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(54) **SIRNA SILENCING OF GENES EXPRESSED IN CANCER**

(75) Inventors: **Ian MacLachlan**, Mission (CA); **Adam Judge**, Vancouver (CA); **Vandana Sood**, Vancouver (CA); **James Heyes**, Vancouver (CA); **Lloyd B. Jeffs**, Delta (CA); **Lorne Palmer**, Vancouver (CA)

(73) Assignee: **Alnylam Pharmaceuticals, Inc.**, Cambridge, MA (US)

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Primary Examiner — Brian Whiteman
(74) *Attorney, Agent, or Firm* — Fenwick & West LLP

(57) **ABSTRACT**

The present invention provides nucleic acid-lipid particles comprising siRNA molecules that silence genes expressed in cancer (e.g., Eg5, EGFR or XIAP) and methods of using such nucleic acid-lipid particles to silence Eg5, EGFR or XIAP gene expression.

8 Claims, 378 Drawing Sheets

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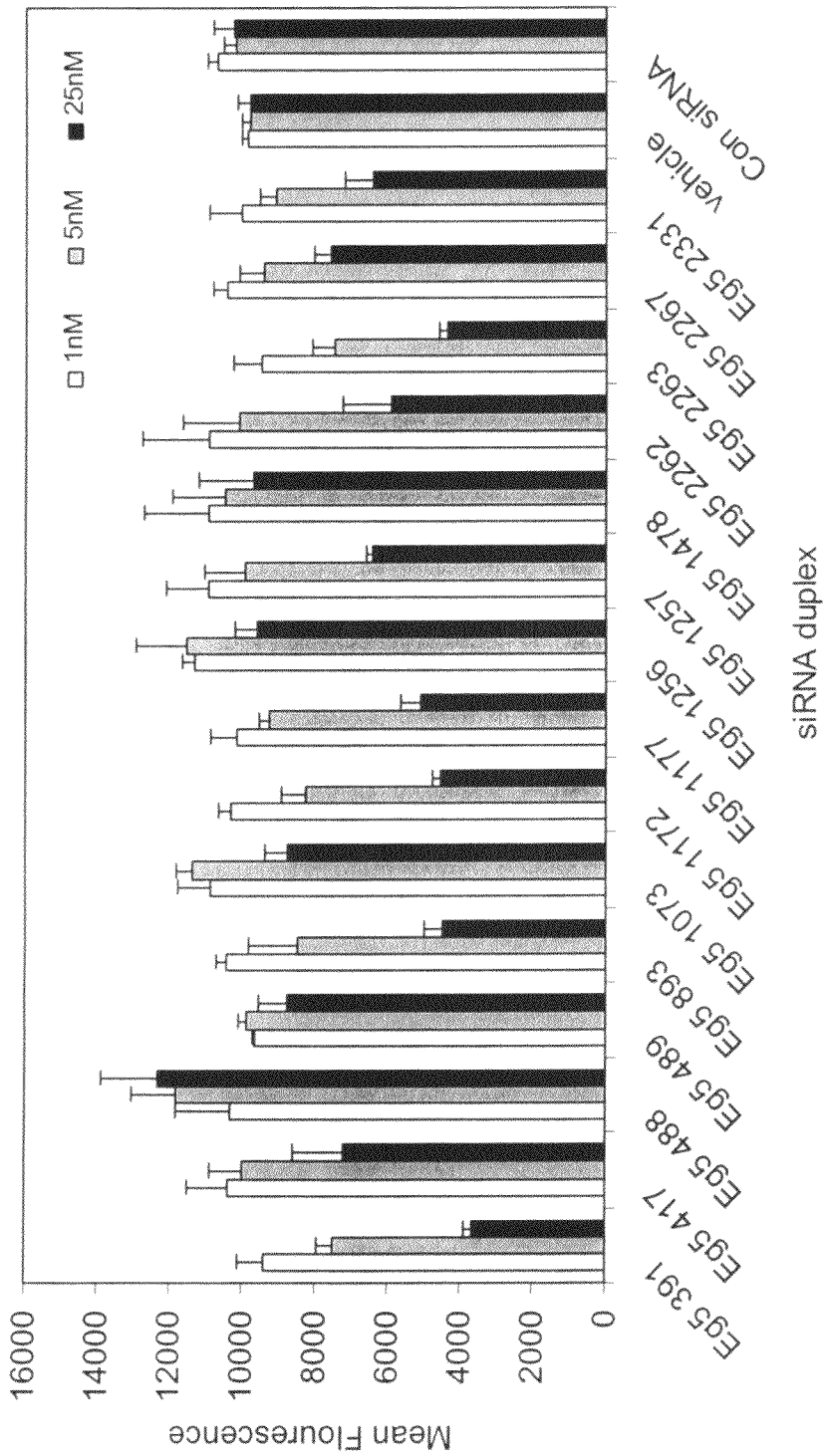

1nM
5nM
25nM
Mean Flourescence
16000
14000
12000
10000
8000
6000
4000
2000
0
EGS 391
EGS 417
EGS 488
EGS 489
EGS 893
EGS 1073
EGS 1172
EGS 1177
EGS 1256
EGS 1257
EGS 1478
EGS 2262
EGS 2263
EGS 2267
EGS 2331
Vehicle
Con siRNA
siRNA duplex

Figure 1

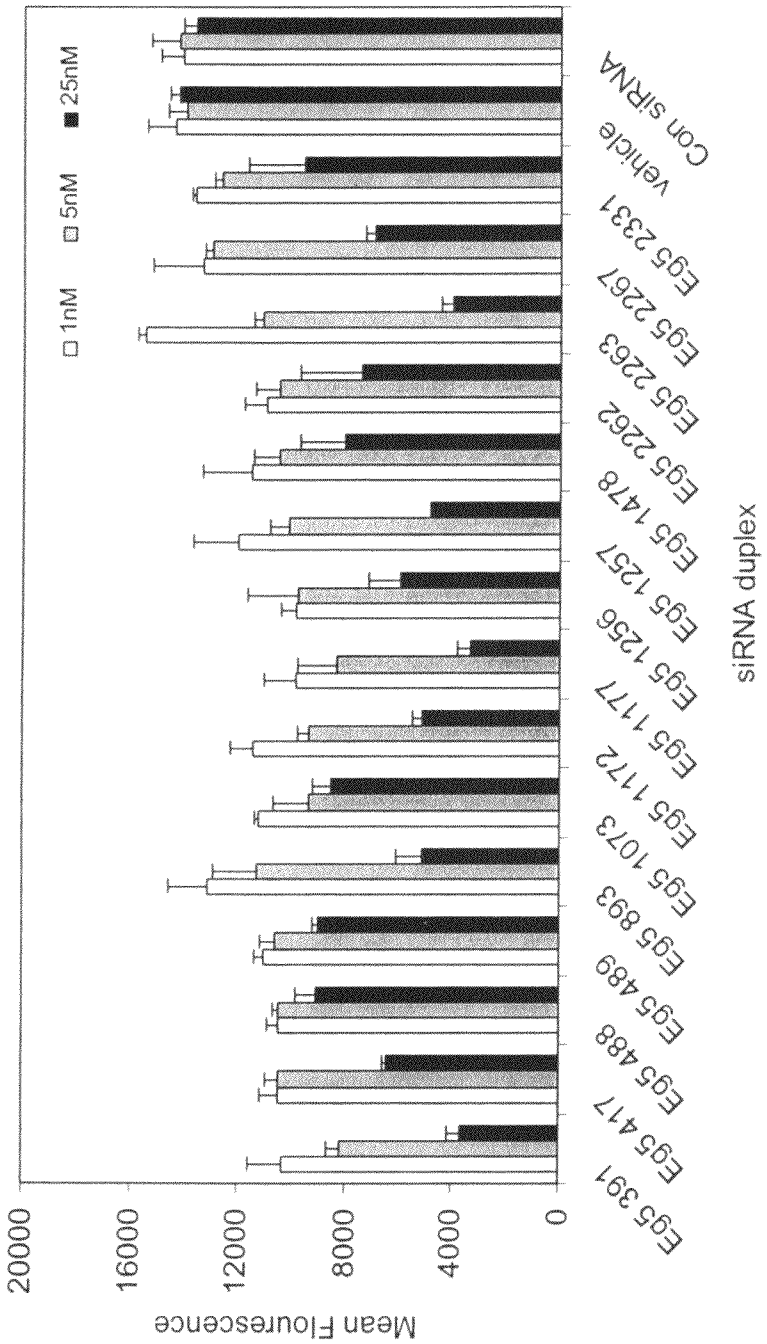

1nM
5nM
25nM
Mean Flourescence
20000
16000
12000
8000
4000
0
siRNA duplex
Con siRNA
vehicle
EGS 2331
EGS 2267
EGS 2263
EGS 2262
EGS 1478
EGS 1257
EGS 1256
EGS 1177
EGS 1172
EGS 1073
EGS 893
EGS 489
EGS 488
EGS 417
EGS 391

Figure 2

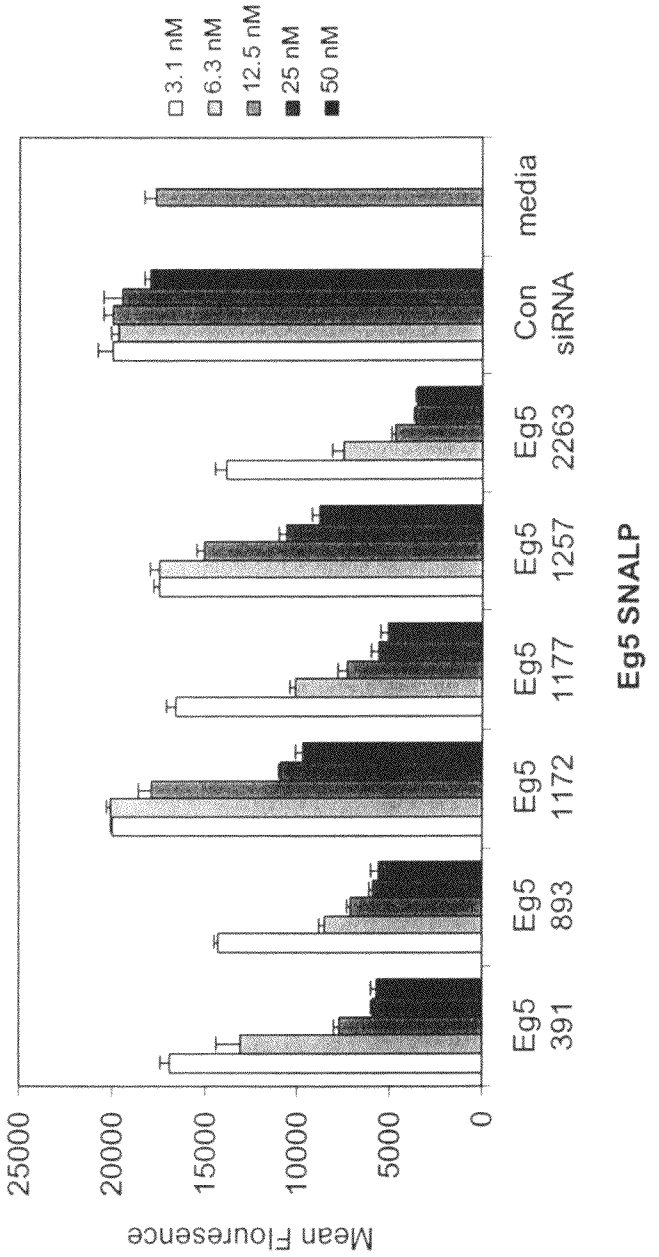

3.1 nM
6.3 nM
12.5 nM
25 nM
50 nM
Mean Flourescence
25000
20000
15000
10000
5000
0
Eg5 391
Eg5 893
Eg5 1172
Eg5 1177
Eg5 1257
Eg5 2263
Con siRNA
media
Eg5 SNALP

Figure 3

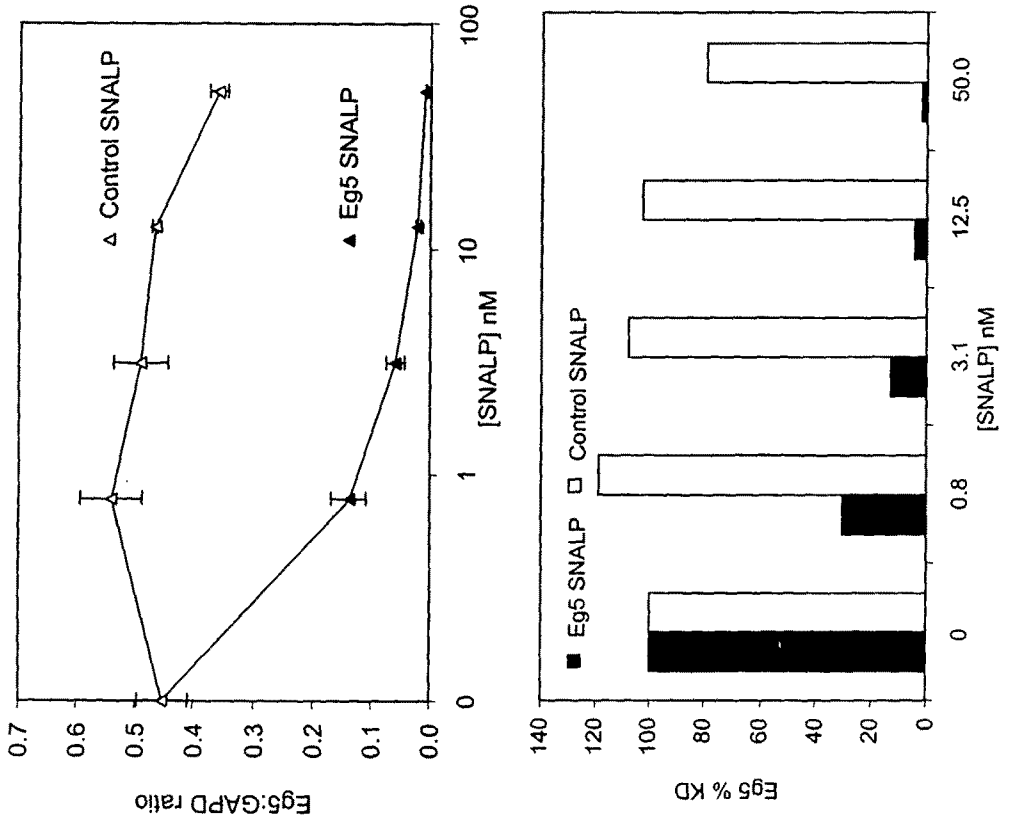

Eg5:GAPD ratio
0.7
0.6
0.5
0.4
0.3
0.2
0.1
0.0
0
1
10
100
[SNALP] nM
Control SNALP
Eg5 SNALP
Eg5 % KD
140
120
100
80
60
40
20
0
0
0.8
3.1
12.5
50.0
[SNALP] nM
Eg5 SNALP
Control SNALP

Figure 4

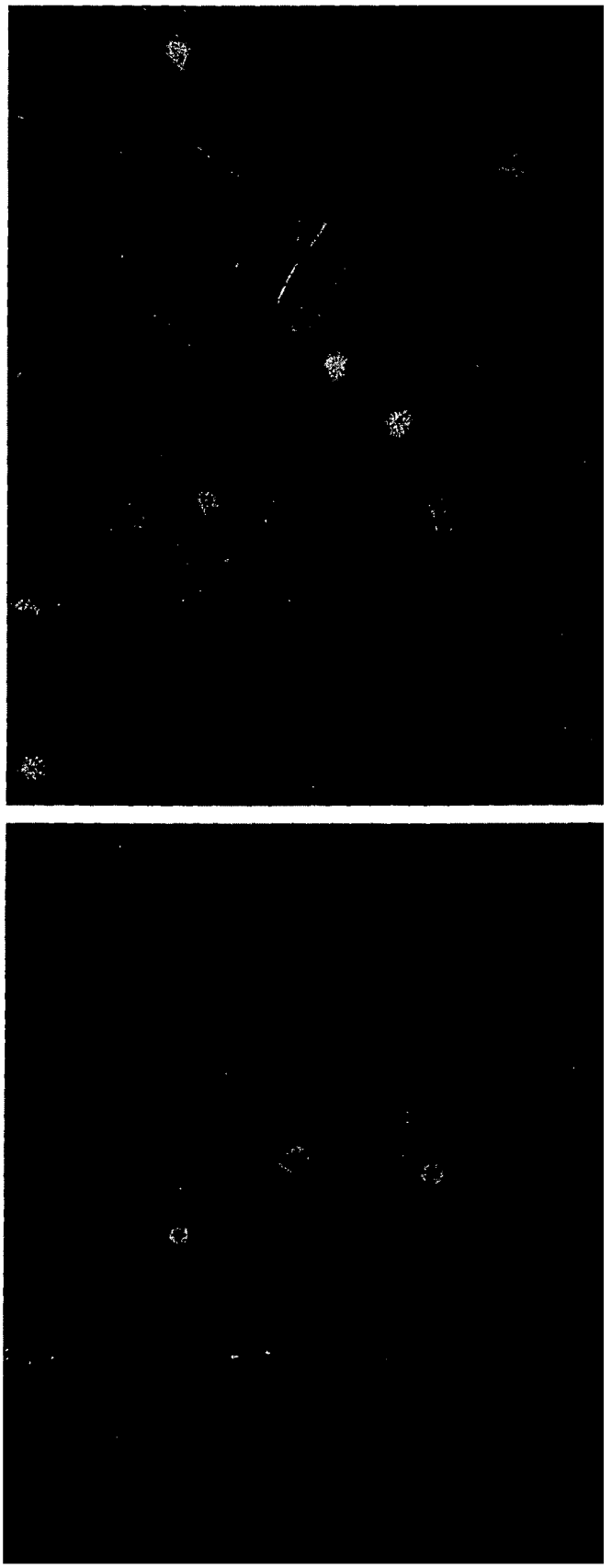


Figure 5

		Sense/AS
5' C U G A A G A C C U G A A G A C A A U dT dT sense 3' dT dT G A C U U C U G G A C U U C U G U U A antisense	1	0/0
5' C [U] G A A G A C C [U] G A A G A C A A [U] dT dT sense 3' dT dT G A C U U C U G G A C U U C U G U U A antisense	2	U/0
5' C U [G] A A [G] A C C U [G] A A [G] A C A A U dT dT sense 3' dT dT G A C U U C U G G A C U U C U G U U A antisense	3	G/0
5' C U G A A G A C C U G A A G A C A A U dT dT sense 3' dT dT G A C [U] U C [U] G G A C [U] U C U G U U A antisense	4	0/U
5' C U G A A G A C C U G A A G A C A A U dT dT sense 3' dT dT [G] A C U U C U [G] G A C U U C U [G] U U A antisense	5	0/G
5' C [U] G A A G A C C [U] G A A G A C A A [U] dT dT sense 3' dT dT G A C [U] U C [U] G G A C [U] U C U G U U A antisense	6	U/U
5' C [U] G A A G A C C [U] G A A G A C A A [U] dT dT sense 3' dT dT [G] A C U U C U [G] G A C U U C U [G] U U A antisense	7	U/G
5' C U [G] A A [G] A C C U [G] A A [G] A C A A U dT dT sense 3' dT dT [G] A C U U C U [G] G A C U U C U [G] U U A antisense	8	G/G
5' C U [G] A A [G] A C C U [G] A A [G] A C A A U dT dT sense 3' dT dT G A C [U] U C [U] G G A C [U] U C U G U U A antisense	9	G/U

Figure 6

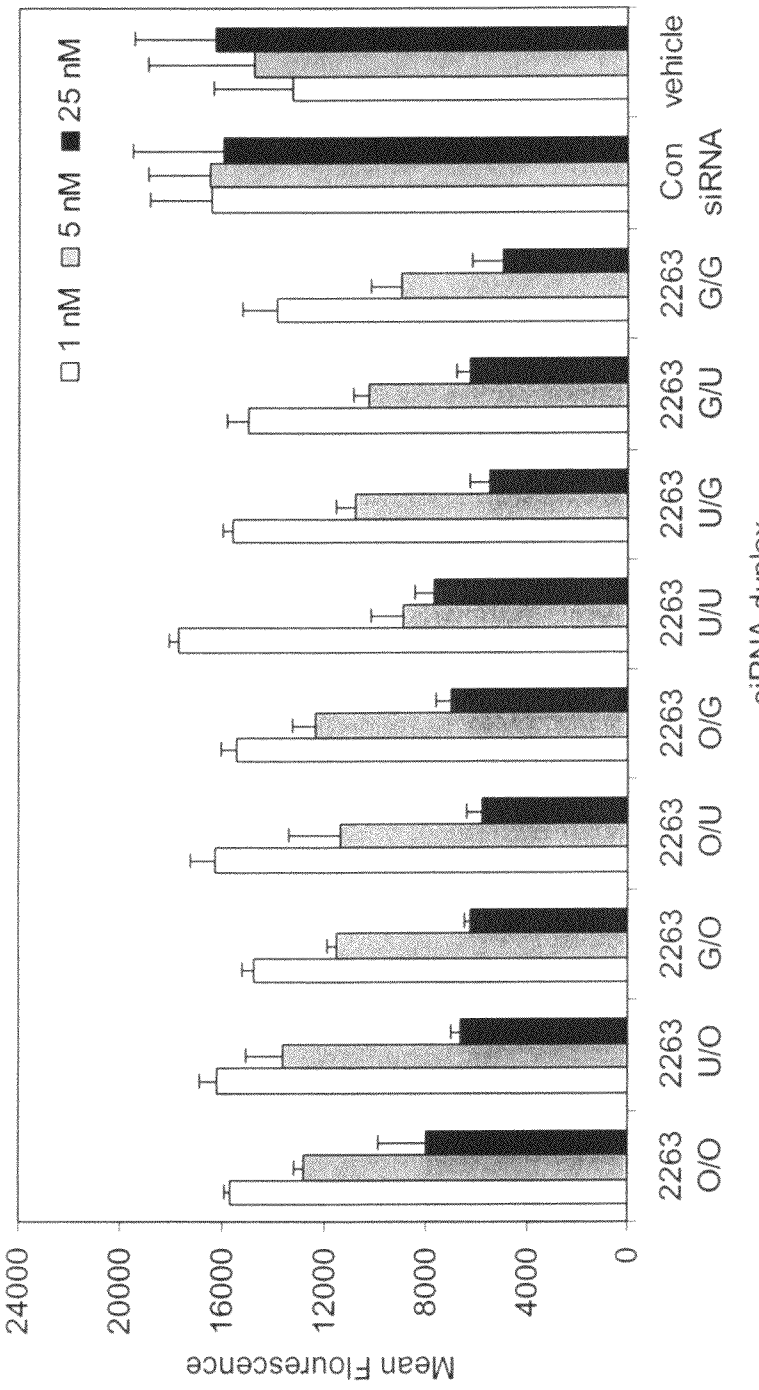

1 nM
5 nM
25 nM
Mean Flourescence
24000
20000
16000
12000
8000
4000
0
2263 O/O
2263 U/O
2263 G/O
2263 O/U
2263 O/G
2263 U/U
2263 U/G
2263 G/U
2263 G/G
Con siRNA
vehicle
siRNA duplex

Figure 7

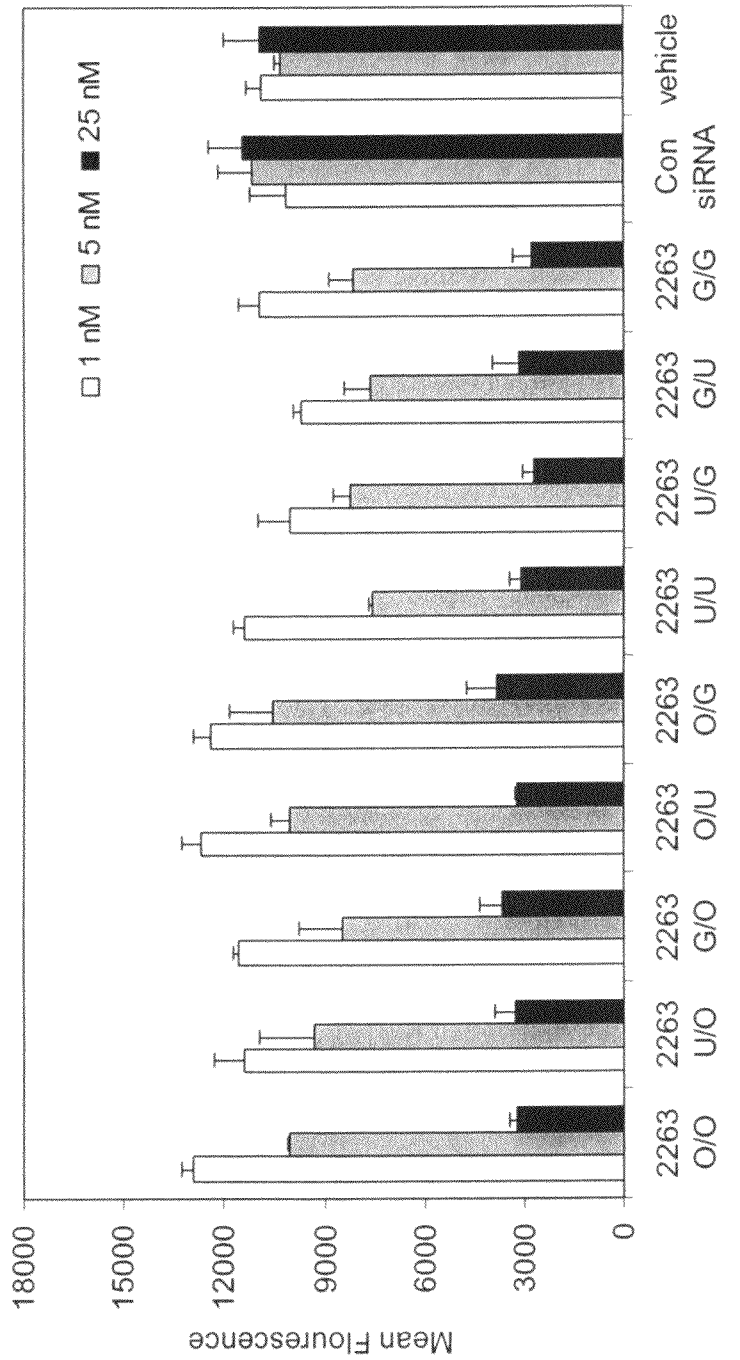

1 nM
5 nM
25 nM
Mean Flourescence
18000
15000
12000
9000
6000
3000
0
2263 O/O
2263 U/O
2263 G/O
2263 O/U
2263 O/G
2263 U/U
2263 U/G
2263 G/U
2263 G/G
Con siRNA
vehicle
siRNA duplex

Figure 8

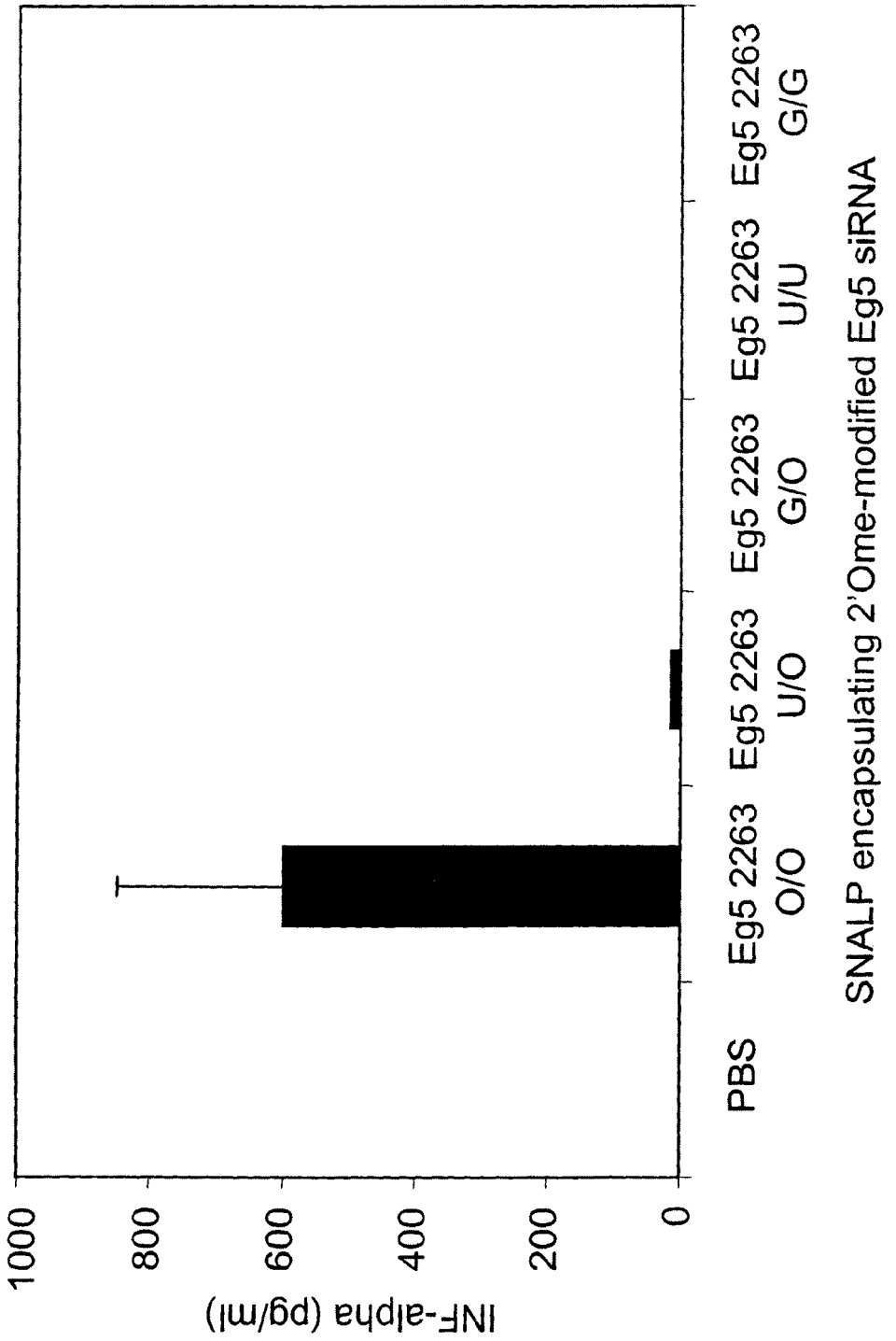

INF-alpha (pg/ml)
1000
800
600
400
200
0
PBS
Eg5 2263 O/O
Eg5 2263 U/O
Eg5 2263 G/O
Eg5 2263 U/U
Eg5 2263 G/G
SNALP encapsulating 2'Ome-modified Eg5 siRNA

Figure 9

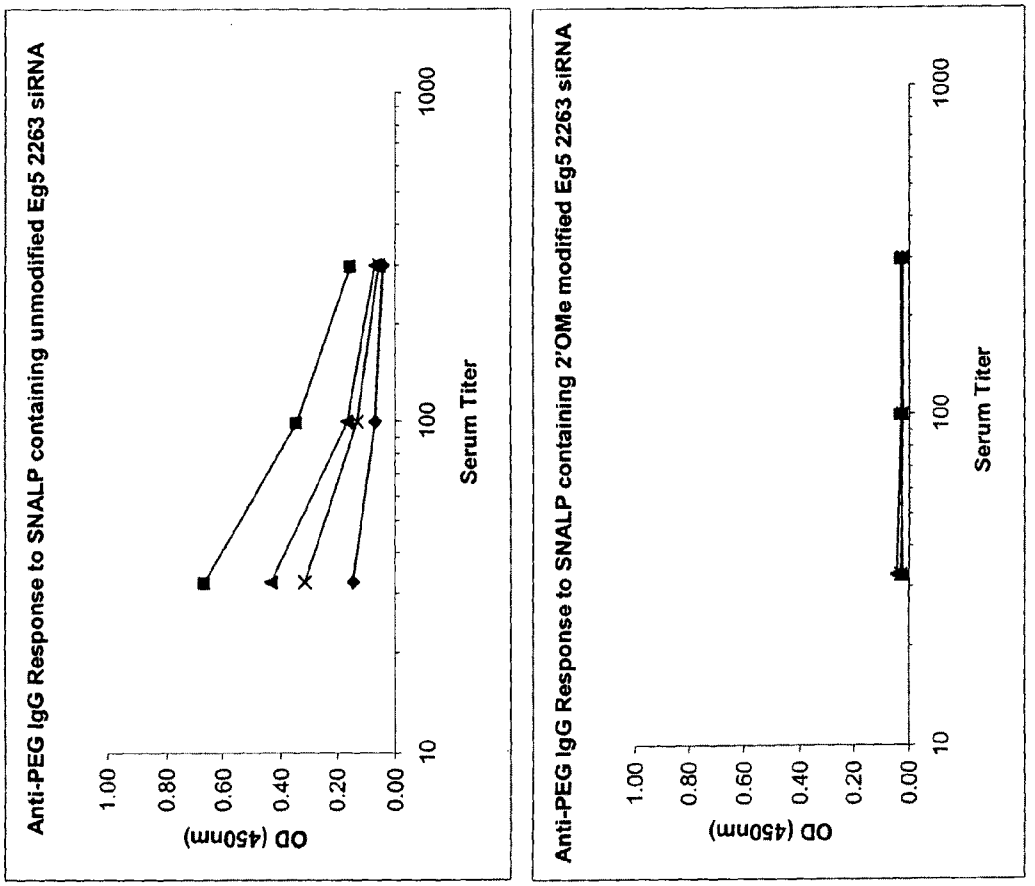

Anti-PEG IgG Response to SNALP containing unmodified Eg5 2263 siRNA
OD (450nm)
1.00
0.80
0.60
0.40
0.20
0.00
10
100
1000
Serum Titer
Anti-PEG IgG Response to SNALP containing 2'OMe modified Eg5 2263 siRNA
OD (450nm)
1.00
0.80
0.60
0.40
0.20
0.00
10
100
1000
Serum Titer

Figure 10

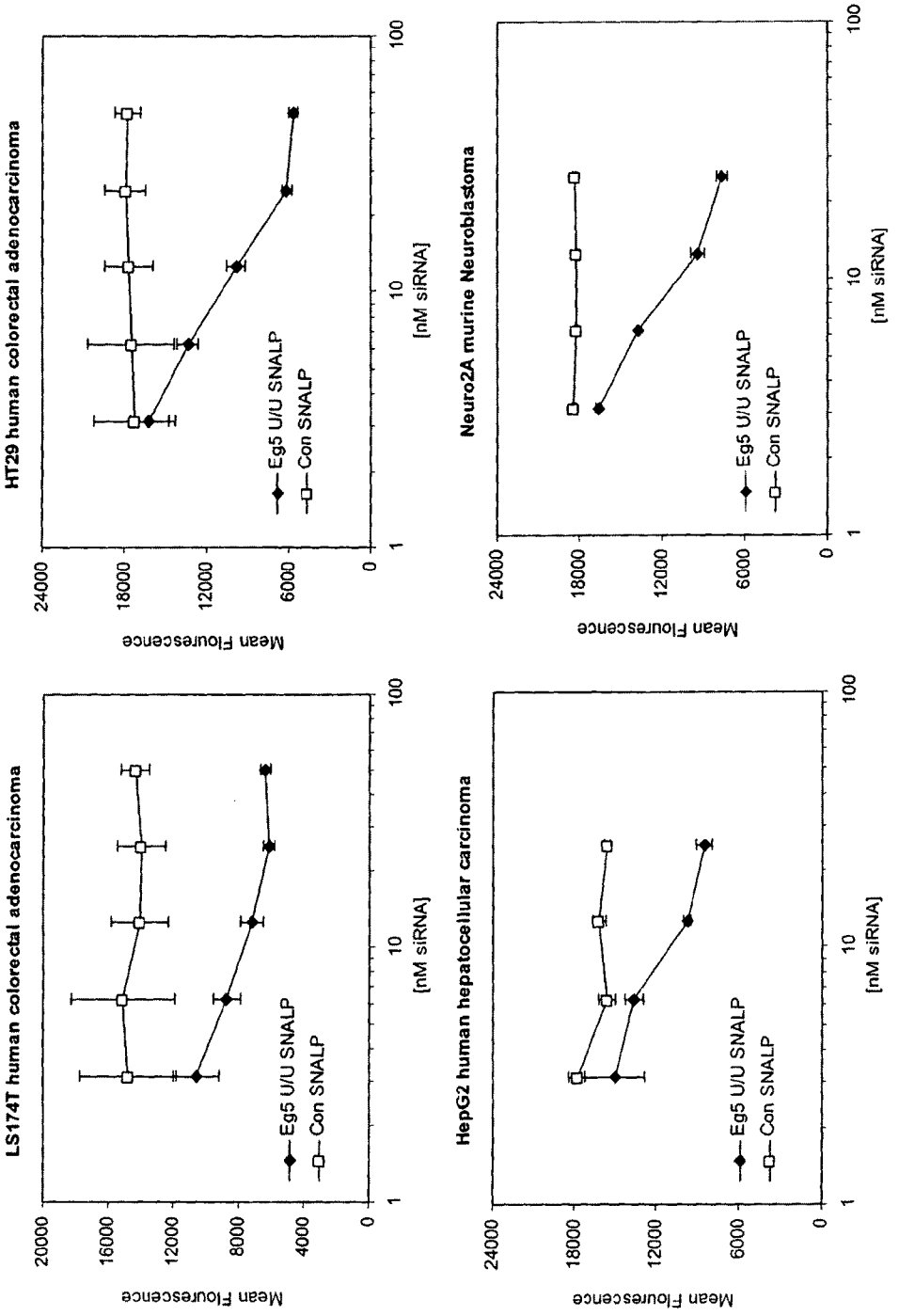

HT29 human colorectal adenocarcinoma
Neuro2A murine Neuroblastoma
LS174T human colorectal adenocarcinoma
HepG2 human hepatocellular carcinoma
Mean Flourescence
[nM siRNA]
Eg5 U/U SNALP
Con SNALP

Figure 11

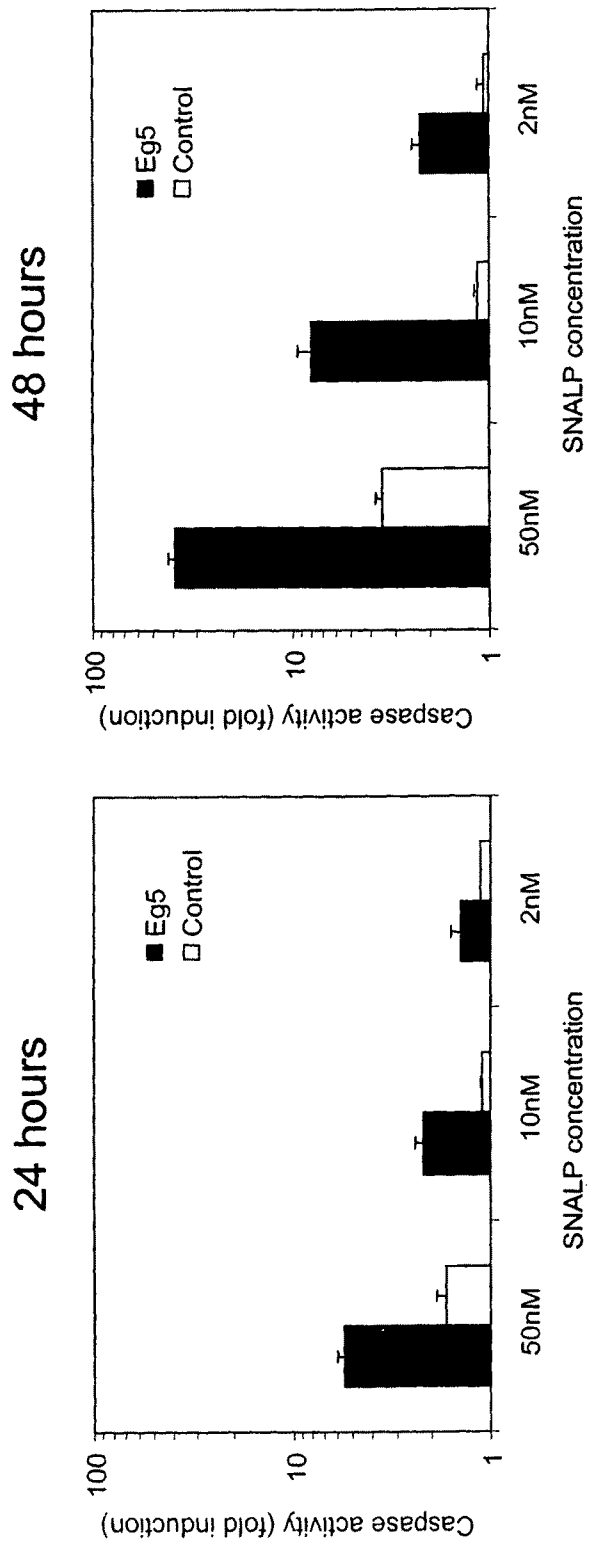
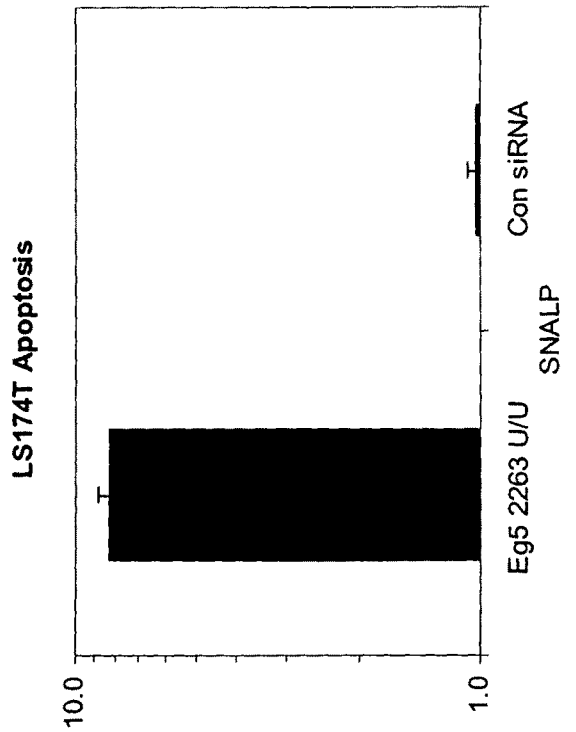

48 hours
Eg5
Control
100
10
1
Caspase activity (fold induction)
50nM
10nM
2nM
SNALP concentration
24 hours
Eg5
Control
100
10
1
Caspase activity (fold induction)
50nM
10nM
2nM
SNALP concentration

Figure 12


LS174T Apoptosis
Caspase activity (fold increase)
10.0
1.0
Eg5 2263 U/U
SNALP
Con siRNA

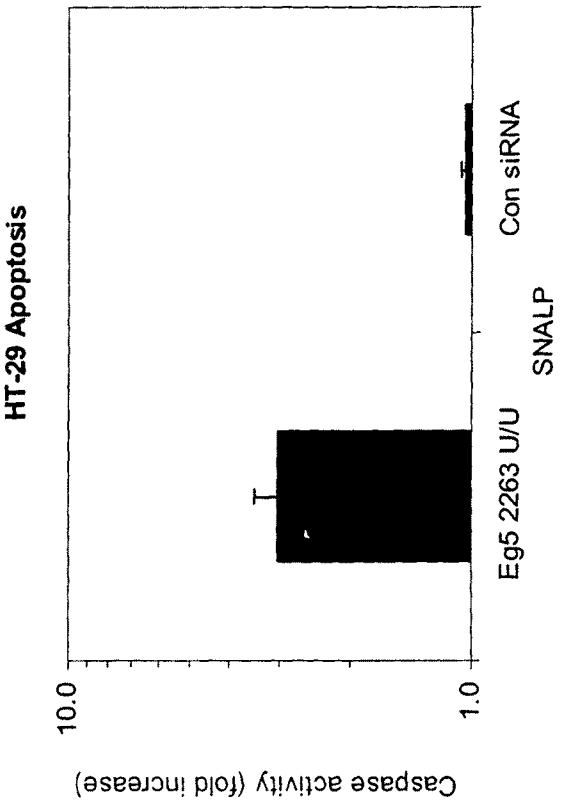

HT-29 Apoptosis
Caspase activity (fold increase)
10.0
1.0
Eg5 2263 U/U
SNALP
Con siRNA

Figure 13

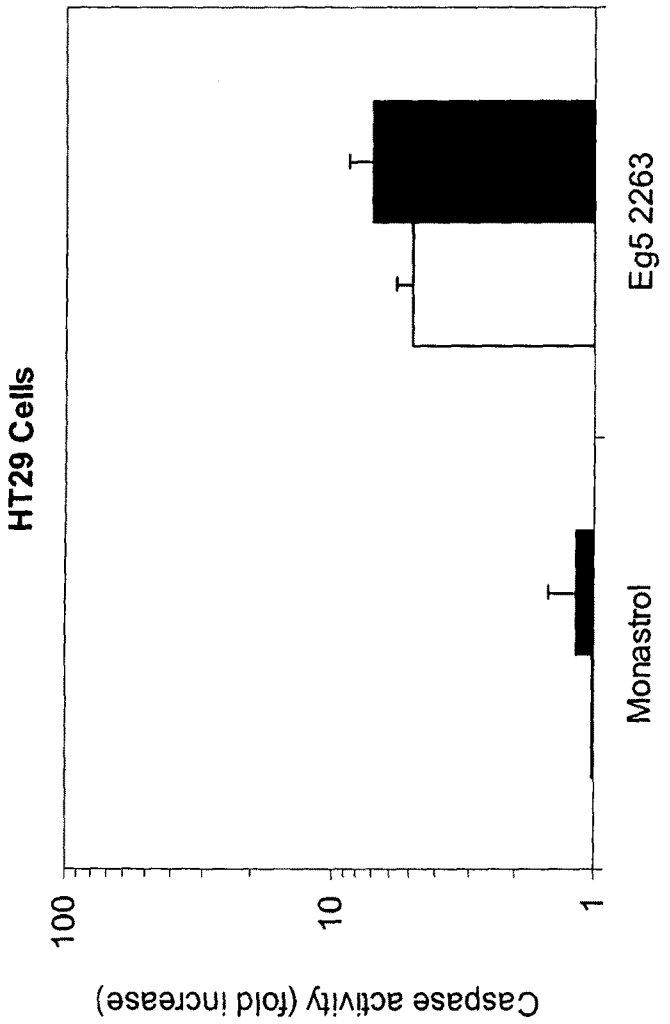

HT29 Cells
Caspase activity (fold increase)
100
10
1
Monastrol
Eg5 2263

Figure 14

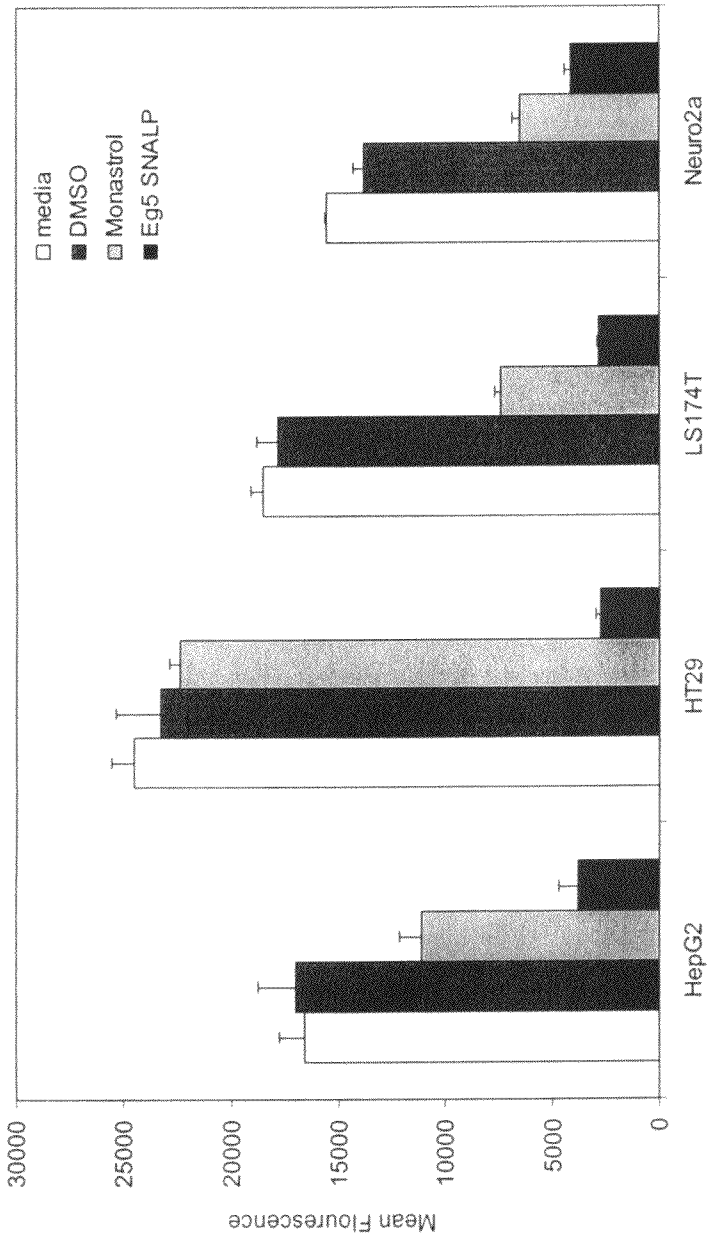

media
DMSO
Monastrol
Eg5 SNALP
Mean Flourescence
30000
25000
20000
15000
10000
5000
0
HepG2
HT29
LS174T
Neuro2a
Cancer Cell Line

Figure 15

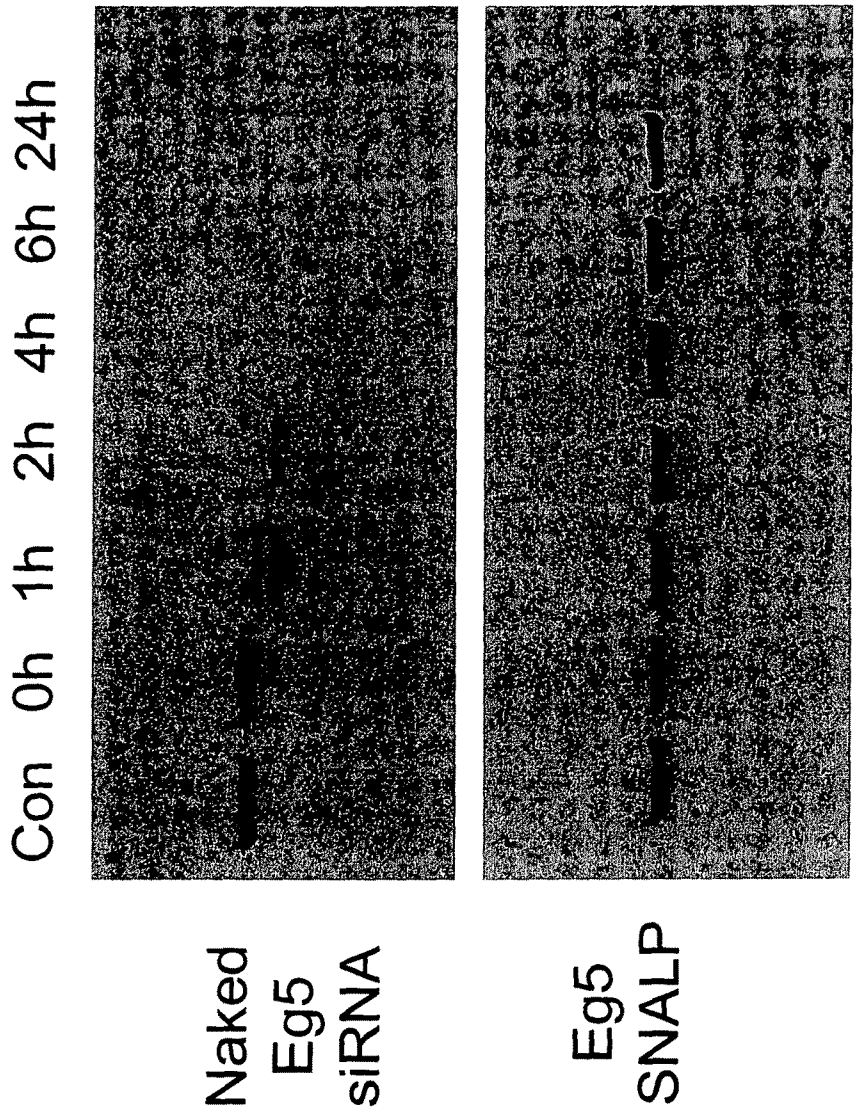


Figure 16

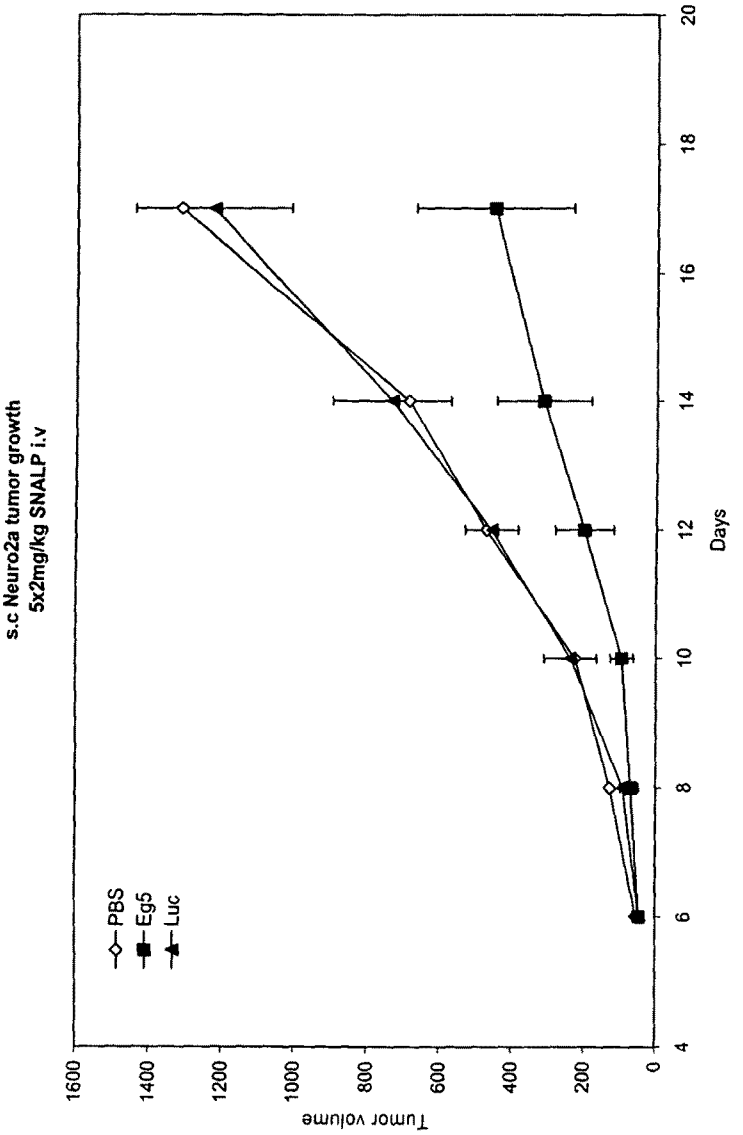

s.c Neuro2a tumor growth
5x2mg/kg SNALP i.v
PBS
Eg5
Luc
Tumor volume
Days
0
200
400
600
800
1000
1200
1400
1600
4
6
8
10
12
14
16
18
20

Figure 17

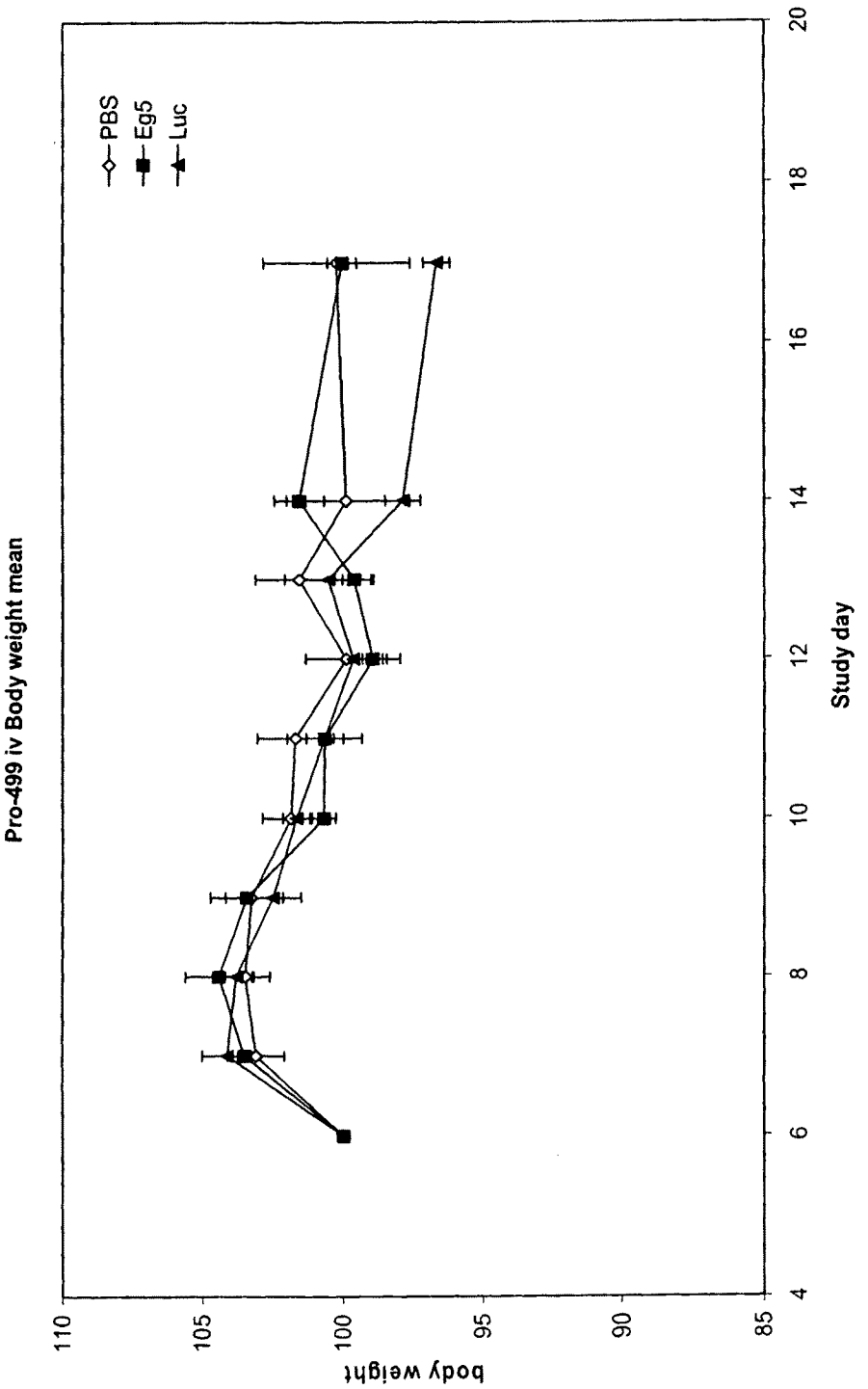

Pro-499 iv Body weight mean
PBS
Eg5
Luc
body weight
110
105
100
95
90
85
4
6
8
10
12
14
16
18
20
Study day

Figure 18

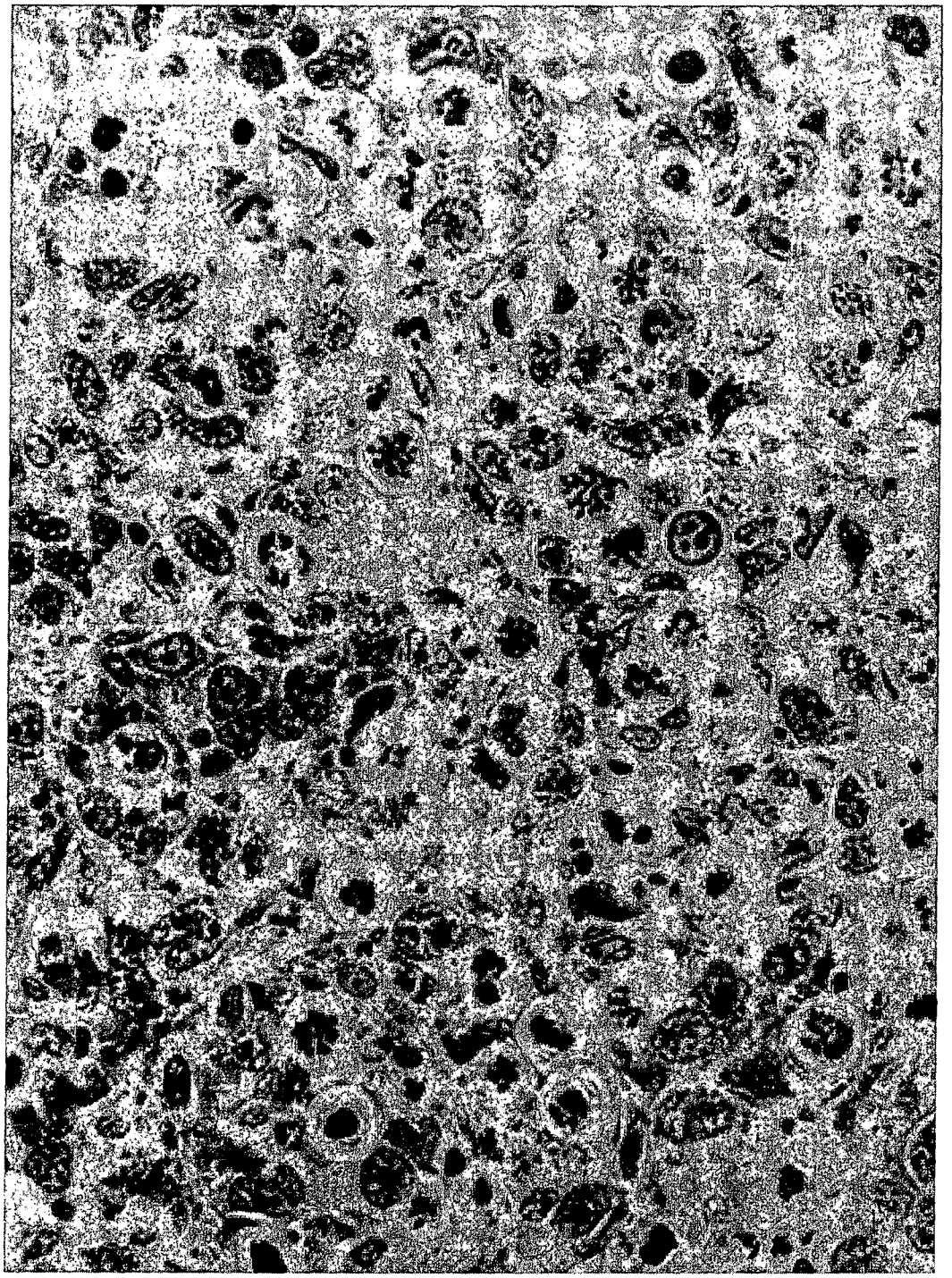


Figure 19

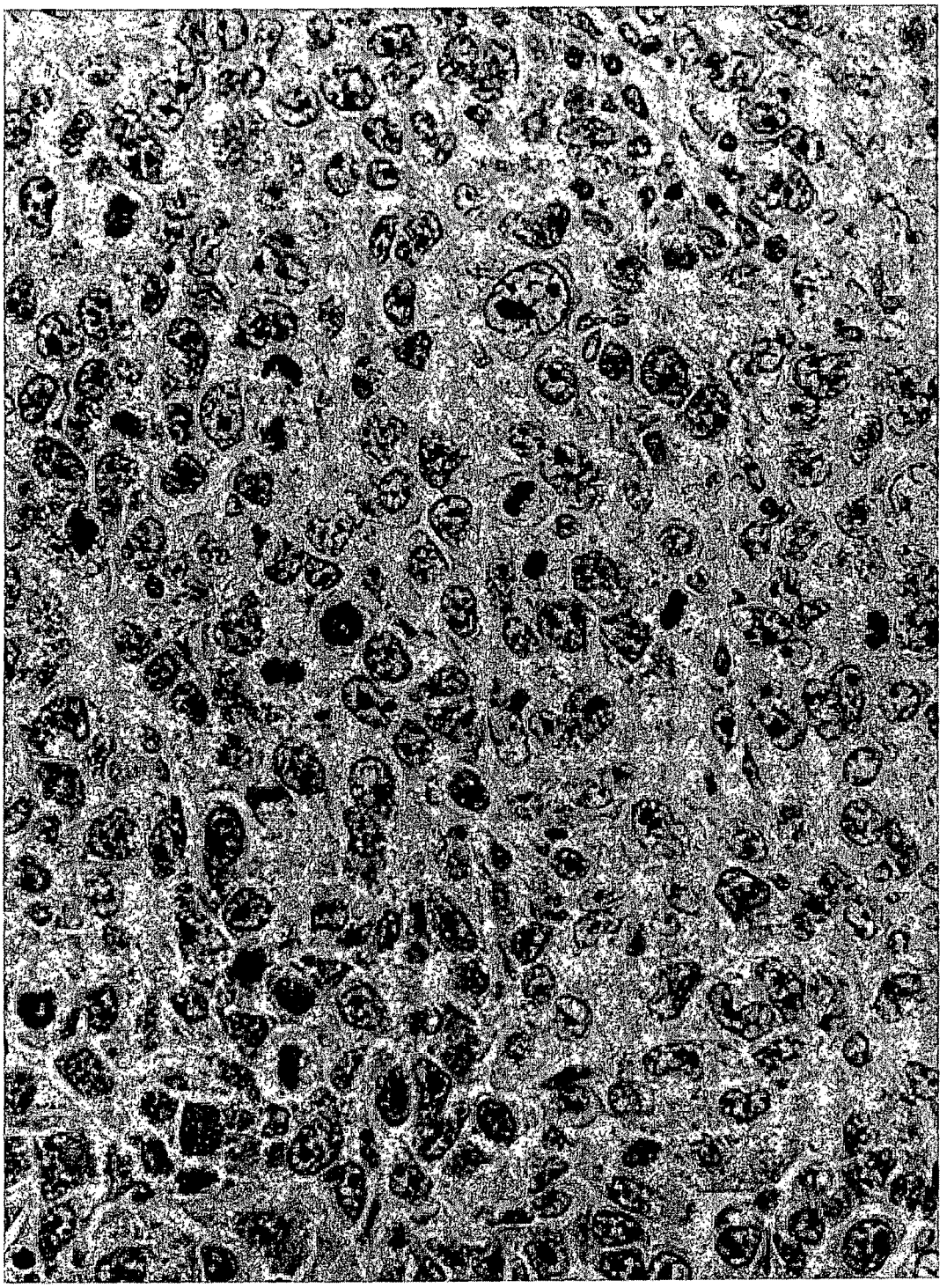


Figure 20

TABLE 1: Eg5 (Kif11) siRNA Sequences

Start site	Sense strand 5p-3p – 19bp core	Sense leader-trailer	Reynolds score	%GC	Thermo (AS-S)	mRNA secondary structure
196	UCCAGGUGGUGGUGAGAUG	CA-CA	5	57.9%	1.7	Y
200	GGUGGUGGUGAGAUGCAGA	CA-CC	3	57.9%	2.0	M
347	UAUGGUGUUUGGAGCAUCU	GA-AC	2	42.1%	0.6	Y
349	UGGUGUUUGGAGCAUCUAC	UA-UA	3	47.4%	0.6	Y
380	UGUUUACCGAAGUGUUGUU	GA-UG	6	36.8%	0.5	M
390	AGUGUUGUUUGUCCAAUUC	GA-UG	5	36.8%	1.7	M
391	**GUGUUGUUUGUCCAAUUCU**	**AA-GG**	**5**	**36.8%**	**2.5**	**M**
413	TGAAGUUAUUAUGGGCUAU	GA-AA	5	31.6%	0.1	M
416	AGUUAUUAUGGGCUAUAAU	GA-UG	3	26.3%	2.1	N
417	**GUUAUUAUGGGCUAUAAUU**	**AA-GC**	**3**	**26.3%**	**2.9**	**N**
488	**AGGUGAAAGGUCACCUAAU**	**GA-GA**	**2**	**42.1%**	**4.3**	**M**
489	**GGUGAAAGGUCACCUAAUG**	**AA-AA**	**3**	**47.4%**	**5.2**	**Y**
893	**UGGAGAAGAGCUUGUUAAA**	**GA-AT**	**5**	**36.8%**	**5.9**	**Y**
1073	**UCGAGAAUCUAAACUAACU**	**UA-AG**	**5**	**31.6%**	**3.3**	**M**
1077	GAAUCUAAACUAACUAGAA	GA-TC	3	26.3%	1.2	Y
1172	**GGAAACUCUGAGUACAUUG**	**GA-GA**	**2**	**42.1%**	**1.9**	**M**
1176	ACUCUGAGUACAUUGGAAU	AA-AU	2	36.8%	1.1	M
1177	**CUCUGAGUACAUUGGAAUA**	**AA-UG**	**3**	**36.8%**	**3.5**	**N**
1256	**AGCUCUUAUUAAGGAGUAU**	**AA-AC**	**0**	**31.6%**	**3.3**	**Y**
1257	**GCUCUUAUUAAGGAGUAUA**	**AA-CG**	**1**	**31.6%**	**5.2**	**M**
1478	**ACUUGACCAGUGUAAAUCU**	**GA-GA**	**6**	**36.8%**	**0.8**	**Y**
1487	GUGUAAAUCUGACCUGCAA	CA-AA	5	42.1%	0.4	Y
2262	**ACUGAAGACCUGAAGACAA**	**UA-UA**	**8**	**42.1%**	**0.7**	**M**
2263	***CUGAAGACCUGAAGACAAU***	***AA-AA***	***8***	***42.1%***	***2.2***	***M***
2267	**AGACCUGAAGACAAUAAAG**	**GA-CA**	**8**	**36.8%**	**3.8**	**M**
2331	**GAGAGAUUCUGUGCUUUGG**	**CA-AG**	**5**	**47.4%**	**2.4**	**M**

Figure 21

TABLE 2: Eg5 (Kif11) siRNA Sequences

HEg5 21bp Start_Pos	19bp core hEg5 start bp	Sense	Antisense
389	391	GUGUUGUUUGUCCAAUUCUdTdT	AGAAUUGGACAAACAACACdTdT
415	417	GUUAUUAUGGGCUAUAAUUdTdT	AAUUAUAGCCCAUAAUAACdTdT
486	488	AGGUGAAAGGUCACCUAAAUdTdT	AUUAGGUGACCUUUCACCUdTdT
487	489	GGUGAAAGGUCACCUAAAUGdTdT	CAUUAGGUGACCUUUCACCdTdT
891	893	UGGAGAAGAGCUUGUUUAAAdTdT	UUUAACAAGCUCUUCUCCAdTdT
1071	1073	UCGAGAAUCUAAACUAACCUdTdT	AGUUAGUUUAGAUUCUCGAdTdT
1170	1172	GGAAACUCUGAGUACAUUGdTdT	CAAUGUACUCAGAGUUUCCdTdT
1175	1177	CUCUGAGUACAUUGGAAUAdTdT	UAUUCCAAUGUACUCAGAGdTdT
1254	1256	AGCUCUUAUUAAGGAGUAUdTdT	AUACUCCUUAAUAAGAGCUdTdT
1255	1257	GCUCUUAUUAAGGAGUAUAdTdT	UAUACUCCUUAAUAAGAGCdTdT
1476	1478	ACUUGACCAGUGUAAAUCUdTdT	AGAUUUACACUGGUCAAGUdTdT
2260	2262	ACUGAAGACCUGAAGACAAdTdT	UUGUCUUCAGGUCUUCAGUdTdT
2261	2263	CUGAAGACCUGAAGACAAUdTdT	AUUGUCUUCAGGUCUUCAGdTdT
2265	2267	AGACCUGAAGACAAUAAAGdTdT	CUUUAUUGUCUUCAGGUCUdTdT
2329	2331	GAGAGAUUCUGUGCUUUGGdTdT	CCAAAGCACAGAAUCUCUCdTdT

Figure 22

TABLE 3: EGFR siRNA Sequences

bp start (human)	Sense strand target 5p-3p – 19bp + TT
510	UGUCCUCAUUGCCCUCAACTT
511	GUCCUCAUUGCCCUCAACATT
512	UCCUCAUUGCCCUCAACACTT
816	UGAUCCAAGCUGUCCCAAUTT
817	GAUCCAAGCUGUCCCAAUGTT
854	GAGAGGAGAACUGCCAGAATT
855	AGAGGAGAACUGCCAGAAATT
928	CCCAGUGACUGCUGCCACATT
929	CCAGUGACUGCUGCCACAATT
1252	GUGUGUAACGGAAUAGGUATT
1986	CCAGUGUGCCCACUACAUUTT
1987	CAGUGUGCCCACUACAUUGTT
1988	AGUGUGCCCACUACAUUGATT
2438	GGAUCCCAGAAGGUGAGAATT
2439	GAUCCCAGAAGGUGAGAAATT
2440	AUCCCAGAAGGUGAGAAAGTT
2441	UCCCAGAAGGUGAGAAAGUTT
2793	GCAUGUCAAGAUCACAGAUTT
2794	CAUGUCAAGAUCACAGAUUTT
2795	AUGUCAAGAUCACAGAUUUTT
2872	GUGCCUAUCAAGUGGAUGGTT
3068	UCGAUGUCUACAUGAUCAUTT
3086	UGGUCAAGUGCUGGAUGAUTT
3087	GGUCAAGUGCUGGAUGAUATT
3088	GUCAAGUGCUGGAUGAUAGTT
3194	GGGAUGAAAGAAUGCAUUUTT
3195	GGAUGAAAGAAUGCAUUUGTT
3755	CUGACUACCAGCAGGACUUTT
3757	GACUACCAGCAGGACUUCUTT
3758	ACUACCAGCAGGACUUCUUTT

Figure 23

TABLE 4: EGFR siRNA Sequences

bp start (human)	Sense 5p-3p – 19bp + TT	AntiSense 5p-3p – 19bp + TT
511	GUCCUCAUUGCCCUCAACATT	UGUUGAGGGCAAUGAGGACTT
512	UCCUCAUUGCCCUCAACACTT	GUGUUGAGGGCAAUGAGGATT
816	UGAUCCAAGCUGUCCCAAUTT	AUUGGGACAGCUUGGAUCATT
817	GAUCCAAGCUGUCCCAAUGTT	CAUUGGGACAGCUUGGAUCTT
1252	GUGUGUAACGGAAUAGGUATT	UACCUAUUCCGUUACACACTT
1986	CCAGUGUGCCCACUACAUUTT	AAUGUAGUGGGCACACUGGTT
2440	AUCCCAGAAGGUGAGAAAGTT	CUUUCUCACCUUCUGGGAUTT
2795	AUGUCAAGAUCACAGAUUUTT	AAAUCUGUGAUCUUGACAUTT
3068	UCGAUGUCUACAUGAUCAUTT	AUGAUCAUGUAGACAUCGATT
3088	GUCAAGUGCUGGAUGAUAGTT	CUAUCAUCCAGCACUUGACTT
3755	CUGACUACCAGCAGGACUUTT	AAGUCCUGCUGGUAGUCAGTT
3757	GACUACCAGCAGGACUUCUTT	AGAAGUCCUGCUGGUAGUCTT
3758	ACUACCAGCAGGACUUCUUTT	AAGAAGUCCUGCUGGUAGUTT

Figure 24

TABLE 5: XIAP siRNA Sequences

bp start (human)	Sense strand target (5p-3p – 19bp + TT)
5'UTR1	AAGGUGGACAAGUCCUAUUTT
5'UTR2	AGGUGGACAAGUCCUAUUUTT
64	GAAUUUGUAGAAGAGUUUATT
67	UUUGUAGAAGAGUUUAAUATT
70	GUAGAAGAGUUUAAUAGAUTT
72	AGAAGAGUUUAAUAGAUUATT
73	GAAGAGUUUAAUAGAUUAATT
74	AAGAGUUUAAUAGAUUAAATT
113	GUGGUAGUCCUGUUUCAGCTT
118	AGUCCUGUUUCAGCAUCAATT
119	GUCCUGUUUCAGCAUCAACTT
120	UCCUGUUUCAGCAUCAACATT
261	CCCAAAUUGCAGAUUUAUCTT
300	UAGUGCCACGCAGUCUACATT
732	GAGUUCUGAUAGGAAUUUCTT
738	UGAUAGGAAUUUCCCAAAUTT
739	GAUAGGAAUUUCCCAAAUUTT
741	UAGGAAUUUCCCAAAUUCATT
742	AGGAAUUUCCCAAAUUCAATT
849	GCUUGCAAGAGCUGGAUUUTT
1307	GUACUGAAGAGCAGCUAAGTT
1353	AAUCUGUAUGGAUAGAAAUTT
1354	AUCUGUAUGGAUAGAAAUATT
1355	UCUGUAUGGAUAGAAAUAUTT
1356	CUGUAUGGAUAGAAAUAUUTT
1361	UGGAUAGAAAUAUUGCUAUTT
1362	GGAUAGAAAUAUUGCUAUCTT

Figure 25

TABLE 6: XIAP siRNA Sequences

bp start (human)	Sense 5p-3p – 19bp + TT	AntiSense 5p-3p – 19bp + TT
64	GAAUUUGUAGAAGAGUUUATT	UAAACUCUUCUACAAAUUCTT
73	GAAGAGUUUAAUAGAUUAATT	UUAAUCUAUUAAACUCUUCTT
74	AAGAGUUUAAUAGAUUAAATT	UUUAAUCUAUUAAACUCUUTT
113	GUGGUAGUCCUGUUUUCAGCTT	GCUGAAACAGGACUACCACTT
120	UCCUGUUUUCAGCAUCAACATT	UGUUGAUGCUGAAACAGGATT
261	CCCAAAUUGCAGAUUUAUCTT	GAUAAAUCUGCAAUUUGGGTT
300	UAGUGCCACGCAGUCUACATT	UGUAGACUGCGUGGCACUATT
732	GAGUUCUGAUAGGAAUUUCTT	GAAAUUCCUAUCAGAACUCTT
741	UAGGAAUUUCCCAAAUUCATT	UGAAUUUGGGAAAUUCCUATT
742	AGGAAUUUCCCAAAUUCAATT	UUGAAUUUGGGAAAUUCCUTT
849	GCUUGCAAGAGCUGGAUUUTT	AAAUCCAGCUCUUGCAAGCTT
1307	GUACUGAAGAGCAGCUAAGTT	CUUAGCUGCUCUUCAGUACTT
1361	UGGAUAGAAAUAUUGCUAUTT	AUAGCAAUAUUUCUAUCCATT
1362	GGAUAGAAAUAUUGCUAUCTT	GAUAGCAAUAUUUCUAUCCTT

Figure 26

TABLE 7

ID	SEQUENCE
1	ACCTGCGTGCAGTCGGTCCTCCA
2	CCTGCGTGCAGTCGGTCCTCCAG
3	CTGCGTGCAGTCGGTCCTCCAGG
4	TGCGTGCAGTCGGTCCTCCAGGC
5	GCGTGCAGTCGGTCCTCCAGGCC
6	CGTGCAGTCGGTCCTCCAGGCCA
7	GTGCAGTCGGTCCTCCAGGCCAC
8	TGCAGTCGGTCCTCCAGGCCACG
9	GCAGTCGGTCCTCCAGGCCACGC
10	CAGTCGGTCCTCCAGGCCACGCA
11	AGTCGGTCCTCCAGGCCACGCAG
12	GTCGGTCCTCCAGGCCACGCAGC
13	TCGGTCCTCCAGGCCACGCAGCG
14	CGGTCCTCCAGGCCACGCAGCGC
15	GGTCCTCCAGGCCACGCAGCGCC
16	GTCCTCCAGGCCACGCAGCGCCC
17	TCCTCCAGGCCACGCAGCGCCCG
18	CCTCCAGGCCACGCAGCGCCCGA
19	CTCCAGGCCACGCAGCGCCCGAG
20	TCCAGGCCACGCAGCGCCCGAGA
21	CCAGGCCACGCAGCGCCCGAGAG
22	CAGGCCACGCAGCGCCCGAGAGT
23	AGGCCACGCAGCGCCCGAGAGTA
24	GGCCACGCAGCGCCCGAGAGTAC
25	GCCACGCAGCGCCCGAGAGTACC
26	CCACGCAGCGCCCGAGAGTACCA
27	CACGCAGCGCCCGAGAGTACCAG
28	ACGCAGCGCCCGAGAGTACCAGG
29	CGCAGCGCCCGAGAGTACCAGGG
30	GCAGCGCCCGAGAGTACCAGGGA
31	CAGCGCCCGAGAGTACCAGGGAG
32	AGCGCCCGAGAGTACCAGGGAGA
33	GCGCCCGAGAGTACCAGGGAGAC
34	CGCCCGAGAGTACCAGGGAGACT
35	GCCCGAGAGTACCAGGGAGACTC
36	CCCGAGAGTACCAGGGAGACTCC
37	CCGAGAGTACCAGGGAGACTCCG
38	CGAGAGTACCAGGGAGACTCCGG
39	GAGAGTACCAGGGAGACTCCGGC
40	AGAGTACCAGGGAGACTCCGGCC
41	GAGTACCAGGGAGACTCCGGCCC
42	AGTACCAGGGAGACTCCGGCCCC
43	GTACCAGGGAGACTCCGGCCCCT
44	TACCAGGGAGACTCCGGCCCCTG
45	ACCAGGGAGACTCCGGCCCCTGT
46	CCAGGGAGACTCCGGCCCCTGTC
47	CAGGGAGACTCCGGCCCCTGTCG
48	AGGGAGACTCCGGCCCCTGTCGG
49	GGGAGACTCCGGCCCCTGTCGGC
50	GGAGACTCCGGCCCCTGTCGGCG
51	GAGACTCCGGCCCCTGTCGGCGC
52	AGACTCCGGCCCCTGTCGGCGCC
53	GACTCCGGCCCCTGTCGGCGCCA
54	ACTCCGGCCCCTGTCGGCGCCAA
55	CTCCGGCCCCTGTCGGCGCCAAG

Fig. 27 cont'd (Sheet 1 of 84)

ID	SEQUENCE
56	TCCGGCCCCTGTCGGCGCCAAGC
57	CCGGCCCCTGTCGGCGCCAAGCC
58	CGGCCCCTGTCGGCGCCAAGCCC
59	GGCCCCTGTCGGCGCCAAGCCCC
60	GCCCCTGTCGGCGCCAAGCCCCT
61	CCCCTGTCGGCGCCAAGCCCCTC
62	CCCTGTCGGCGCCAAGCCCCTCC
63	CCTGTCGGCGCCAAGCCCCTCCG
64	CTGTCGGCGCCAAGCCCCTCCGC
65	TGTCGGCGCCAAGCCCCTCCGCC
66	GTCGGCGCCAAGCCCCTCCGCCC
67	TCGGCGCCAAGCCCCTCCGCCCC
68	CGGCGCCAAGCCCCTCCGCCCCT
69	GGCGCCAAGCCCCTCCGCCCCTC
70	GCGCCAAGCCCCTCCGCCCCTCA
71	CGCCAAGCCCCTCCGCCCCTCAC
72	GCCAAGCCCCTCCGCCCCTCACA
73	CCAAGCCCCTCCGCCCCTCACAG
74	CAAGCCCCTCCGCCCCTCACAGC
75	AAGCCCCTCCGCCCCTCACAGCG
76	AGCCCCTCCGCCCCTCACAGCGC
77	GCCCCTCCGCCCCTCACAGCGCC
78	CCCCTCCGCCCCTCACAGCGCCC
79	CCCTCCGCCCCTCACAGCGCCCA
80	CCTCCGCCCCTCACAGCGCCCAG
81	CTCCGCCCCTCACAGCGCCCAGG
82	TCCGCCCCTCACAGCGCCCAGGT
83	CCGCCCCTCACAGCGCCCAGGTC
84	CGCCCCTCACAGCGCCCAGGTCC
85	GCCCCTCACAGCGCCCAGGTCCG
86	CCCCTCACAGCGCCCAGGTCCGC
87	CCCTCACAGCGCCCAGGTCCGCG
88	CCTCACAGCGCCCAGGTCCGCGG
89	CTCACAGCGCCCAGGTCCGCGGC
90	TCACAGCGCCCAGGTCCGCGGCC
91	GCCGGGCCTTGATTTTTTGGCGG
92	CCGGGCCTTGATTTTTTGGCGGG
93	CGGGCCTTGATTTTTTGGCGGGG
94	GGGCCTTGATTTTTTGGCGGGGA
95	GGCCTTGATTTTTTGGCGGGGAC
96	GCCTTGATTTTTTGGCGGGGACC
97	CCTTGATTTTTTGGCGGGGACCG
98	CTTGATTTTTTGGCGGGGACCGT
99	ATGGCGTCGCAGCCAAATTCGTC
100	TGGCGTCGCAGCCAAATTCGTCT
101	GGCGTCGCAGCCAAATTCGTCTG
102	GCGTCGCAGCCAAATTCGTCTGC
103	CGTCGCAGCCAAATTCGTCTGCG
104	GTCGCAGCCAAATTCGTCTGCGA
105	TCGCAGCCAAATTCGTCTGCGAA
106	CGCAGCCAAATTCGTCTGCGAAG
107	GCAGCCAAATTCGTCTGCGAAGA
108	CAGCCAAATTCGTCTGCGAAGAA
109	AGCCAAATTCGTCTGCGAAGAAG
110	GCCAAATTCGTCTGCGAAGAAGA
111	CCAAATTCGTCTGCGAAGAAGAA
112	CAAATTCGTCTGCGAAGAAGAAA
113	AAATTCGTCTGCGAAGAAGAAAG

Fig. 27 cont'd (Sheet 2 of 84)

ID	SEQUENCE
114	AATTCGTCTGCGAAGAAGAAAGA
115	ATTCGTCTGCGAAGAAGAAAGAG
116	TTCGTCTGCGAAGAAGAAAGAGG
117	TCGTCTGCGAAGAAGAAAGAGGA
118	CGTCTGCGAAGAAGAAAGAGGAG
119	GTCTGCGAAGAAGAAAGAGGAGA
120	TCTGCGAAGAAGAAAGAGGAGAA
121	CTGCGAAGAAGAAAGAGGAGAAG
122	TGCGAAGAAGAAAGAGGAGAAGG
123	GCGAAGAAGAAAGAGGAGAAGGG
124	CGAAGAAGAAAGAGGAGAAGGGG
125	GAAGAAGAAAGAGGAGAAGGGGA
126	AAGAAGAAAGAGGAGAAGGGGAA
127	AGAAGAAAGAGGAGAAGGGGAAG
128	GAAGAAAGAGGAGAAGGGGAAGA
129	AAGAAAGAGGAGAAGGGGAAGAA
130	AGAAAGAGGAGAAGGGGAAGAAC
131	GAAAGAGGAGAAGGGGAAGAACA
132	AAAGAGGAGAAGGGGAAGAACAT
133	AAGAGGAGAAGGGGAAGAACATC
134	AGAGGAGAAGGGGAAGAACATCC
135	GAGGAGAAGGGGAAGAACATCCA
136	AGGAGAAGGGGAAGAACATCCAG
137	GGAGAAGGGGAAGAACATCCAGG
138	GAGAAGGGGAAGAACATCCAGGT
139	AGAAGGGGAAGAACATCCAGGTG
140	GAAGGGGAAGAACATCCAGGTGG
141	AAGGGGAAGAACATCCAGGTGGT
142	AGGGGAAGAACATCCAGGTGGTG
143	GGGGAAGAACATCCAGGTGGTGG
144	GGGAAGAACATCCAGGTGGTGGT
145	GGAAGAACATCCAGGTGGTGGTG
146	GAAGAACATCCAGGTGGTGGTGA
147	AAGAACATCCAGGTGGTGGTGAG
148	AGAACATCCAGGTGGTGGTGAGA
149	GAACATCCAGGTGGTGGTGAGAT
150	AACATCCAGGTGGTGGTGAGATG
151	ACATCCAGGTGGTGGTGAGATGC
152	CATCCAGGTGGTGGTGAGATGCA
153	ATCCAGGTGGTGGTGAGATGCAG
154	TCCAGGTGGTGGTGAGATGCAGA
155	CCAGGTGGTGGTGAGATGCAGAC
156	CAGGTGGTGGTGAGATGCAGACC
157	AGGTGGTGGTGAGATGCAGACCA
158	GGTGGTGGTGAGATGCAGACCAT
159	GTGGTGGTGAGATGCAGACCATT
160	TGGTGGTGAGATGCAGACCATTT
161	GGTGGTGAGATGCAGACCATTTA
162	GTGGTGAGATGCAGACCATTTAA
163	TGGTGAGATGCAGACCATTTAAT
164	GGTGAGATGCAGACCATTTAATT
165	GTGAGATGCAGACCATTTAATTT
166	TGAGATGCAGACCATTTAATTTG
167	GAGATGCAGACCATTTAATTTGG
168	AGATGCAGACCATTTAATTTGGC
169	GATGCAGACCATTTAATTTGGCA
170	ATGCAGACCATTTAATTTGGCAG
171	TGCAGACCATTTAATTTGGCAGA

Fig. 27 cont'd (Sheet 3 of 84)

ID	SEQUENCE
172	GCAGACCATTTAATTTGGCAGAG
173	CAGACCATTTAATTTGGCAGAGC
174	AGACCATTTAATTTGGCAGAGCG
175	GACCATTTAATTTGGCAGAGCGG
176	ACCATTTAATTTGGCAGAGCGGA
177	CCATTTAATTTGGCAGAGCGGAA
178	CATTTAATTTGGCAGAGCGGAAA
179	ATTTAATTTGGCAGAGCGGAAAG
180	TTTAATTTGGCAGAGCGGAAAGC
181	TTAATTTGGCAGAGCGGAAAGCT
182	TAATTTGGCAGAGCGGAAAGCTA
183	AATTTGGCAGAGCGGAAAGCTAG
184	ATTTGGCAGAGCGGAAAGCTAGC
185	TTTGGCAGAGCGGAAAGCTAGCG
186	TTGGCAGAGCGGAAAGCTAGCGC
187	TGGCAGAGCGGAAAGCTAGCGCC
188	GGCAGAGCGGAAAGCTAGCGCCC
189	GCAGAGCGGAAAGCTAGCGCCCA
190	CAGAGCGGAAAGCTAGCGCCCAT
191	AGAGCGGAAAGCTAGCGCCCATT
192	GAGCGGAAAGCTAGCGCCCATTC
193	AGCGGAAAGCTAGCGCCCATTCA
194	GCGGAAAGCTAGCGCCCATTCAA
195	CGGAAAGCTAGCGCCCATTCAAT
196	GGAAAGCTAGCGCCCATTCAATA
197	GAAAGCTAGCGCCCATTCAATAG
198	AAAGCTAGCGCCCATTCAATAGT
199	AAGCTAGCGCCCATTCAATAGTA
200	AGCTAGCGCCCATTCAATAGTAG
201	GCTAGCGCCCATTCAATAGTAGA
202	CTAGCGCCCATTCAATAGTAGAA
203	TAGCGCCCATTCAATAGTAGAAT
204	AGCGCCCATTCAATAGTAGAATG
205	GCGCCCATTCAATAGTAGAATGT
206	CGCCCATTCAATAGTAGAATGTG
207	GCCCATTCAATAGTAGAATGTGA
208	CCCATTCAATAGTAGAATGTGAT
209	CCATTCAATAGTAGAATGTGATC
210	CATTCAATAGTAGAATGTGATCC
211	ATTCAATAGTAGAATGTGATCCT
212	TTCAATAGTAGAATGTGATCCTG
213	TCAATAGTAGAATGTGATCCTGT
214	CAATAGTAGAATGTGATCCTGTA
215	AATAGTAGAATGTGATCCTGTAC
216	ATAGTAGAATGTGATCCTGTACG
217	TAGTAGAATGTGATCCTGTACGA
218	AGTAGAATGTGATCCTGTACGAA
219	GTAGAATGTGATCCTGTACGAAA
220	TAGAATGTGATCCTGTACGAAAA
221	AGAATGTGATCCTGTACGAAAAG
222	GAATGTGATCCTGTACGAAAAGA
223	AATGTGATCCTGTACGAAAAGAA
224	ATGTGATCCTGTACGAAAAGAAG
225	TGTGATCCTGTACGAAAAGAAGT
226	GTGATCCTGTACGAAAAGAAGTT
227	TGATCCTGTACGAAAAGAAGTTA
228	GATCCTGTACGAAAAGAAGTTAG
229	ATCCTGTACGAAAAGAAGTTAGT

Fig. 27 cont'd (Sheet 4 of 84)

ID	SEQUENCE
230	TCCTGTACGAAAAGAAGTTAGTG
231	CCTGTACGAAAAGAAGTTAGTGT
232	CTGTACGAAAAGAAGTTAGTGTA
233	TGTACGAAAAGAAGTTAGTGTAC
234	GTACGAAAAGAAGTTAGTGTACG
235	TACGAAAAGAAGTTAGTGTACGA
236	ACGAAAAGAAGTTAGTGTACGAA
237	CGAAAAGAAGTTAGTGTACGAAC
238	GAAAAGAAGTTAGTGTACGAACT
239	AAAAGAAGTTAGTGTACGAACTG
240	AAAGAAGTTAGTGTACGAACTGG
241	AAGAAGTTAGTGTACGAACTGGA
242	AGAAGTTAGTGTACGAACTGGAG
243	GAAGTTAGTGTACGAACTGGAGG
244	AAGTTAGTGTACGAACTGGAGGA
245	AGTTAGTGTACGAACTGGAGGAT
246	GTTAGTGTACGAACTGGAGGATT
247	TTAGTGTACGAACTGGAGGATTG
248	TAGTGTACGAACTGGAGGATTGG
249	AGTGTACGAACTGGAGGATTGGC
250	GTGTACGAACTGGAGGATTGGCT
251	TGTACGAACTGGAGGATTGGCTG
252	GTACGAACTGGAGGATTGGCTGA
253	TACGAACTGGAGGATTGGCTGAC
254	ACGAACTGGAGGATTGGCTGACA
255	CGAACTGGAGGATTGGCTGACAA
256	GAACTGGAGGATTGGCTGACAAG
257	AACTGGAGGATTGGCTGACAAGA
258	ACTGGAGGATTGGCTGACAAGAG
259	CTGGAGGATTGGCTGACAAGAGC
260	TGGAGGATTGGCTGACAAGAGCT
261	GGAGGATTGGCTGACAAGAGCTC
262	GAGGATTGGCTGACAAGAGCTCA
263	AGGATTGGCTGACAAGAGCTCAA
264	GGATTGGCTGACAAGAGCTCAAG
265	GATTGGCTGACAAGAGCTCAAGG
266	ATTGGCTGACAAGAGCTCAAGGA
267	TTGGCTGACAAGAGCTCAAGGAA
268	TGGCTGACAAGAGCTCAAGGAAA
269	GGCTGACAAGAGCTCAAGGAAAA
270	GCTGACAAGAGCTCAAGGAAAAC
271	CTGACAAGAGCTCAAGGAAAACA
272	TGACAAGAGCTCAAGGAAAACAT
273	GACAAGAGCTCAAGGAAAACATA
274	ACAAGAGCTCAAGGAAAACATAC
275	CAAGAGCTCAAGGAAAACATACA
276	AAGAGCTCAAGGAAAACATACAC
277	AGAGCTCAAGGAAAACATACACT
278	GAGCTCAAGGAAAACATACACTT
279	AGCTCAAGGAAAACATACACTTT
280	GCTCAAGGAAAACATACACTTTT
281	CTCAAGGAAAACATACACTTTTG
282	TCAAGGAAAACATACACTTTTGA
283	CAAGGAAAACATACACTTTTGAT
284	AAGGAAAACATACACTTTTGATA
285	AGGAAAACATACACTTTTGATAT
286	GGAAAACATACACTTTTGATATG
287	GAAAACATACACTTTTGATATGG

Fig. 27 cont'd (Sheet 5 of 84)

ID	SEQUENCE
288	AAAACATACACTTTTGATATGGT
289	AAACATACACTTTTGATATGGTG
290	AACATACACTTTTGATATGGTGT
291	ACATACACTTTTGATATGGTGTT
292	CATACACTTTTGATATGGTGTTT
293	ATACACTTTTGATATGGTGTTTG
294	TACACTTTTGATATGGTGTTTGG
295	ACACTTTTGATATGGTGTTTGGA
296	CACTTTTGATATGGTGTTTGGAG
297	ACTTTTGATATGGTGTTTGGAGC
298	CTTTTGATATGGTGTTTGGAGCA
299	TTTTGATATGGTGTTTGGAGCAT
300	TTTGATATGGTGTTTGGAGCATC
301	TTGATATGGTGTTTGGAGCATCT
302	TGATATGGTGTTTGGAGCATCTA
303	GATATGGTGTTTGGAGCATCTAC
304	ATATGGTGTTTGGAGCATCTACT
305	TATGGTGTTTGGAGCATCTACTA
306	ATGGTGTTTGGAGCATCTACTAA
307	TGGTGTTTGGAGCATCTACTAAA
308	GGTGTTTGGAGCATCTACTAAAC
309	GTGTTTGGAGCATCTACTAAACA
310	TGTTTGGAGCATCTACTAAACAG
311	GTTTGGAGCATCTACTAAACAGA
312	TTTGGAGCATCTACTAAACAGAT
313	TTGGAGCATCTACTAAACAGATT
314	TGGAGCATCTACTAAACAGATTG
315	GGAGCATCTACTAAACAGATTGA
316	GAGCATCTACTAAACAGATTGAT
317	AGCATCTACTAAACAGATTGATG
318	GCATCTACTAAACAGATTGATGT
319	CATCTACTAAACAGATTGATGTT
320	ATCTACTAAACAGATTGATGTTT
321	TCTACTAAACAGATTGATGTTTA
322	CTACTAAACAGATTGATGTTTAC
323	TACTAAACAGATTGATGTTTACC
324	ACTAAACAGATTGATGTTTACCG
325	CTAAACAGATTGATGTTTACCGA
326	TAAACAGATTGATGTTTACCGAA
327	AAACAGATTGATGTTTACCGAAG
328	AACAGATTGATGTTTACCGAAGT
329	ACAGATTGATGTTTACCGAAGTG
330	CAGATTGATGTTTACCGAAGTGT
331	AGATTGATGTTTACCGAAGTGTT
332	GATTGATGTTTACCGAAGTGTTG
333	ATTGATGTTTACCGAAGTGTTGT
334	TTGATGTTTACCGAAGTGTTGTT
335	TGATGTTTACCGAAGTGTTGTTT
336	GATGTTTACCGAAGTGTTGTTTG
337	ATGTTTACCGAAGTGTTGTTTGT
338	TGTTTACCGAAGTGTTGTTTGTC
339	GTTTACCGAAGTGTTGTTTGTCC
340	TTTACCGAAGTGTTGTTTGTCCA
341	TTACCGAAGTGTTGTTTGTCCAA
342	TACCGAAGTGTTGTTTGTCCAAT
343	ACCGAAGTGTTGTTTGTCCAATT
344	CCGAAGTGTTGTTTGTCCAATTC
345	CGAAGTGTTGTTTGTCCAATTCT

Fig. 27 cont'd (Sheet 6 of 84)

ID	SEQUENCE
346	GAAGTGTTGTTTGTCCAATTCTG
347	AAGTGTTGTTTGTCCAATTCTGG
348	AGTGTTGTTTGTCCAATTCTGGA
349	GTGTTGTTTGTCCAATTCTGGAT
350	TGTTGTTTGTCCAATTCTGGATG
351	GTTGTTTGTCCAATTCTGGATGA
352	TTGTTTGTCCAATTCTGGATGAA
353	TGTTTGTCCAATTCTGGATGAAG
354	GTTTGTCCAATTCTGGATGAAGT
355	TTTGTCCAATTCTGGATGAAGTT
356	TTGTCCAATTCTGGATGAAGTTA
357	TGTCCAATTCTGGATGAAGTTAT
358	GTCCAATTCTGGATGAAGTTATT
359	TCCAATTCTGGATGAAGTTATTA
360	CCAATTCTGGATGAAGTTATTAT
361	CAATTCTGGATGAAGTTATTATG
362	AATTCTGGATGAAGTTATTATGG
363	ATTCTGGATGAAGTTATTATGGG
364	TTCTGGATGAAGTTATTATGGGC
365	TCTGGATGAAGTTATTATGGGCT
366	CTGGATGAAGTTATTATGGGCTA
367	TGGATGAAGTTATTATGGGCTAT
368	GGATGAAGTTATTATGGGCTATA
369	GATGAAGTTATTATGGGCTATAA
370	ATGAAGTTATTATGGGCTATAAT
371	TGAAGTTATTATGGGCTATAATT
372	GAAGTTATTATGGGCTATAATTG
373	AAGTTATTATGGGCTATAATTGC
374	AGTTATTATGGGCTATAATTGCA
375	GTTATTATGGGCTATAATTGCAC
376	TTATTATGGGCTATAATTGCACT
377	TATTATGGGCTATAATTGCACTA
378	ATTATGGGCTATAATTGCACTAT
379	TTATGGGCTATAATTGCACTATC
380	TATGGGCTATAATTGCACTATCT
381	ATGGGCTATAATTGCACTATCTT
382	TGGGCTATAATTGCACTATCTTT
383	GGGCTATAATTGCACTATCTTTG
384	GGCTATAATTGCACTATCTTTGC
385	GCTATAATTGCACTATCTTTGCG
386	CTATAATTGCACTATCTTTGCGT
387	TATAATTGCACTATCTTTGCGTA
388	ATAATTGCACTATCTTTGCGTAT
389	TAATTGCACTATCTTTGCGTATG
390	AATTGCACTATCTTTGCGTATGG
391	ATTGCACTATCTTTGCGTATGGC
392	TTGCACTATCTTTGCGTATGGCC
393	TGCACTATCTTTGCGTATGGCCA
394	GCACTATCTTTGCGTATGGCCAA
395	CACTATCTTTGCGTATGGCCAAA
396	ACTATCTTTGCGTATGGCCAAAC
397	CTATCTTTGCGTATGGCCAAACT
398	TATCTTTGCGTATGGCCAAACTG
399	ATCTTTGCGTATGGCCAAACTGG
400	TCTTTGCGTATGGCCAAACTGGC
401	CTTTGCGTATGGCCAAACTGGCA
402	TTTGCGTATGGCCAAACTGGCAC
403	TTGCGTATGGCCAAACTGGCACT

Fig. 27 cont'd (Sheet 7 of 84)

ID	SEQUENCE
404	TGCGTATGGCCAAACTGGCACTG
405	GCGTATGGCCAAACTGGCACTGG
406	CGTATGGCCAAACTGGCACTGGA
407	GTATGGCCAAACTGGCACTGGAA
408	TATGGCCAAACTGGCACTGGAAA
409	ATGGCCAAACTGGCACTGGAAAA
410	TGGCCAAACTGGCACTGGAAAAA
411	GGCCAAACTGGCACTGGAAAAAC
412	GCCAAACTGGCACTGGAAAAACT
413	CCAAACTGGCACTGGAAAAACTT
414	CAAACTGGCACTGGAAAAACTTT
415	AAACTGGCACTGGAAAAACTTTT
416	AACTGGCACTGGAAAAACTTTTA
417	ACTGGCACTGGAAAAACTTTTAC
418	CTGGCACTGGAAAAACTTTTACA
419	TGGCACTGGAAAAACTTTTACAA
420	GGCACTGGAAAAACTTTTACAAT
421	GCACTGGAAAAACTTTTACAATG
422	CACTGGAAAAACTTTTACAATGG
423	ACTGGAAAAACTTTTACAATGGA
424	CTGGAAAAACTTTTACAATGGAA
425	TGGAAAAACTTTTACAATGGAAG
426	GGAAAAACTTTTACAATGGAAGG
427	GAAAAACTTTTACAATGGAAGGT
428	AAAAACTTTTACAATGGAAGGTG
429	AAAACTTTTACAATGGAAGGTGA
430	AAACTTTTACAATGGAAGGTGAA
431	AACTTTTACAATGGAAGGTGAAA
432	ACTTTTACAATGGAAGGTGAAAG
433	CTTTTACAATGGAAGGTGAAAGG
434	TTTTACAATGGAAGGTGAAAGGT
435	TTTACAATGGAAGGTGAAAGGTC
436	TTACAATGGAAGGTGAAAGGTCA
437	TACAATGGAAGGTGAAAGGTCAC
438	ACAATGGAAGGTGAAAGGTCACC
439	CAATGGAAGGTGAAAGGTCACCT
440	AATGGAAGGTGAAAGGTCACCTA
441	ATGGAAGGTGAAAGGTCACCTAA
442	TGGAAGGTGAAAGGTCACCTAAT
443	GGAAGGTGAAAGGTCACCTAATG
444	GAAGGTGAAAGGTCACCTAATGA
445	AAGGTGAAAGGTCACCTAATGAA
446	AGGTGAAAGGTCACCTAATGAAG
447	GGTGAAAGGTCACCTAATGAAGA
448	GTGAAAGGTCACCTAATGAAGAG
449	TGAAAGGTCACCTAATGAAGAGT
450	GAAAGGTCACCTAATGAAGAGTA
451	AAAGGTCACCTAATGAAGAGTAT
452	AAGGTCACCTAATGAAGAGTATA
453	AGGTCACCTAATGAAGAGTATAC
454	GGTCACCTAATGAAGAGTATACC
455	GTCACCTAATGAAGAGTATACCT
456	TCACCTAATGAAGAGTATACCTG
457	CACCTAATGAAGAGTATACCTGG
458	ACCTAATGAAGAGTATACCTGGG
459	CCTAATGAAGAGTATACCTGGGA
460	CTAATGAAGAGTATACCTGGGAA
461	TAATGAAGAGTATACCTGGGAAG

Fig. 27 cont'd (Sheet 8 of 84)

ID	SEQUENCE
462	AATGAAGAGTATACCTGGGAAGA
463	ATGAAGAGTATACCTGGGAAGAG
464	TGAAGAGTATACCTGGGAAGAGG
465	TTCAAATCTTAACCCTTAGGACT
466	TCAAATCTTAACCCTTAGGACTC
467	AGAGTATACCTGGGAAGAGGATC
468	GAGTATACCTGGGAAGAGGATCC
469	AGTATACCTGGGAAGAGGATCCC
470	GTATACCTGGGAAGAGGATCCCT
471	TATACCTGGGAAGAGGATCCCTT
472	ATACCTGGGAAGAGGATCCCTTG
473	TACCTGGGAAGAGGATCCCTTGG
474	ACCTGGGAAGAGGATCCCTTGGC
475	CCTGGGAAGAGGATCCCTTGGCT
476	CTGGGAAGAGGATCCCTTGGCTG
477	TGGGAAGAGGATCCCTTGGCTGG
478	GGGAAGAGGATCCCTTGGCTGGT
479	GGAAGAGGATCCCTTGGCTGGTA
480	GAAGAGGATCCCTTGGCTGGTAT
481	AAGAGGATCCCTTGGCTGGTATA
482	AGAGGATCCCTTGGCTGGTATAA
483	GAGGATCCCTTGGCTGGTATAAT
484	AGGATCCCTTGGCTGGTATAATT
485	GGATCCCTTGGCTGGTATAATTC
486	GATCCCTTGGCTGGTATAATTCC
487	ATCCCTTGGCTGGTATAATTCCA
488	TCCCTTGGCTGGTATAATTCCAC
489	CCCTTGGCTGGTATAATTCCACG
490	CCTTGGCTGGTATAATTCCACGT
491	CTTGGCTGGTATAATTCCACGTA
492	TTGGCTGGTATAATTCCACGTAC
493	TGGCTGGTATAATTCCACGTACC
494	GGCTGGTATAATTCCACGTACCC
495	GCTGGTATAATTCCACGTACCCT
496	CTGGTATAATTCCACGTACCCTT
497	TGGTATAATTCCACGTACCCTTC
498	GGTATAATTCCACGTACCCTTCA
499	GTATAATTCCACGTACCCTTCAT
500	TATAATTCCACGTACCCTTCATC
501	ATAATTCCACGTACCCTTCATCA
502	TAATTCCACGTACCCTTCATCAA
503	AATTCCACGTACCCTTCATCAAA
504	ATTCCACGTACCCTTCATCAAAT
505	TTCCACGTACCCTTCATCAAATT
506	TCCACGTACCCTTCATCAAATTT
507	CCACGTACCCTTCATCAAATTTT
508	CACGTACCCTTCATCAAATTTTT
509	ACGTACCCTTCATCAAATTTTTG
510	CGTACCCTTCATCAAATTTTTGA
511	GTACCCTTCATCAAATTTTTGAG
512	TACCCTTCATCAAATTTTTGAGA
513	ACCCTTCATCAAATTTTTGAGAA
514	CCCTTCATCAAATTTTTGAGAAA
515	CCTTCATCAAATTTTTGAGAAAC
516	CTTCATCAAATTTTTGAGAAACT
517	TTCATCAAATTTTTGAGAAACTT
518	TCATCAAATTTTTGAGAAACTTA
519	CATCAAATTTTTGAGAAACTTAC

Fig. 27 cont'd (Sheet 9 of 84)

ID	SEQUENCE
520	ATCAAATTTTTGAGAAACTTACT
521	TCAAATTTTTGAGAAACTTACTG
522	CAAATTTTTGAGAAACTTACTGA
523	AAATTTTTGAGAAACTTACTGAT
524	AATTTTTGAGAAACTTACTGATA
525	ATTTTTGAGAAACTTACTGATAA
526	TTTTTGAGAAACTTACTGATAAT
527	TTTTGAGAAACTTACTGATAATG
528	TTTGAGAAACTTACTGATAATGG
529	TTGAGAAACTTACTGATAATGGT
530	TGAGAAACTTACTGATAATGGTA
531	GAGAAACTTACTGATAATGGTAC
532	AGAAACTTACTGATAATGGTACT
533	GAAACTTACTGATAATGGTACTG
534	AAACTTACTGATAATGGTACTGA
535	AACTTACTGATAATGGTACTGAA
536	ACTTACTGATAATGGTACTGAAT
537	CTTACTGATAATGGTACTGAATT
538	TTACTGATAATGGTACTGAATTT
539	TACTGATAATGGTACTGAATTTT
540	ACTGATAATGGTACTGAATTTTC
541	CTGATAATGGTACTGAATTTTCA
542	TGATAATGGTACTGAATTTTCAG
543	GATAATGGTACTGAATTTTCAGT
544	ATAATGGTACTGAATTTTCAGTC
545	TAATGGTACTGAATTTTCAGTCA
546	AATGGTACTGAATTTTCAGTCAA
547	ATGGTACTGAATTTTCAGTCAAA
548	TGGTACTGAATTTTCAGTCAAAG
549	GGTACTGAATTTTCAGTCAAAGT
550	GTACTGAATTTTCAGTCAAAGTG
551	TACTGAATTTTCAGTCAAAGTGT
552	ACTGAATTTTCAGTCAAAGTGTC
553	CTGAATTTTCAGTCAAAGTGTCT
554	TGAATTTTCAGTCAAAGTGTCTC
555	GAATTTTCAGTCAAAGTGTCTCT
556	AATTTTCAGTCAAAGTGTCTCTG
557	ATTTTCAGTCAAAGTGTCTCTGT
558	TTTTCAGTCAAAGTGTCTCTGTT
559	TTTCAGTCAAAGTGTCTCTGTTG
560	TTCAGTCAAAGTGTCTCTGTTGG
561	TCAGTCAAAGTGTCTCTGTTGGA
562	CAGTCAAAGTGTCTCTGTTGGAG
563	AGTCAAAGTGTCTCTGTTGGAGA
564	GTCAAAGTGTCTCTGTTGGAGAT
565	TCAAAGTGTCTCTGTTGGAGATC
566	CAAAGTGTCTCTGTTGGAGATCT
567	AAAGTGTCTCTGTTGGAGATCTA
568	AAGTGTCTCTGTTGGAGATCTAT
569	AGTGTCTCTGTTGGAGATCTATA
570	GTGTCTCTGTTGGAGATCTATAA
571	TGTCTCTGTTGGAGATCTATAAT
572	GTCTCTGTTGGAGATCTATAATG
573	TCTCTGTTGGAGATCTATAATGA
574	CTCTGTTGGAGATCTATAATGAA
575	TCTGTTGGAGATCTATAATGAAG
576	CTGTTGGAGATCTATAATGAAGA
577	TGTTGGAGATCTATAATGAAGAG

Fig. 27 cont'd (Sheet 10 of 84)

ID	SEQUENCE
578	GTTGGAGATCTATAATGAAGAGC
579	TTGGAGATCTATAATGAAGAGCT
580	TGGAGATCTATAATGAAGAGCTT
581	GGAGATCTATAATGAAGAGCTTT
582	GAGATCTATAATGAAGAGCTTTT
583	AGATCTATAATGAAGAGCTTTTT
584	GATCTATAATGAAGAGCTTTTTG
585	ATCTATAATGAAGAGCTTTTTGA
586	TCTATAATGAAGAGCTTTTTGAT
587	CTATAATGAAGAGCTTTTTGATC
588	TATAATGAAGAGCTTTTTGATCT
589	ATAATGAAGAGCTTTTTGATCTT
590	TAATGAAGAGCTTTTTGATCTTC
591	AATGAAGAGCTTTTTGATCTTCT
592	ATGAAGAGCTTTTTGATCTTCTT
593	TGAAGAGCTTTTTGATCTTCTTA
594	GAAGAGCTTTTTGATCTTCTTAA
595	AAGAGCTTTTTGATCTTCTTAAT
596	AGAGCTTTTTGATCTTCTTAATC
597	GAGCTTTTTGATCTTCTTAATCC
598	AGCTTTTTGATCTTCTTAATCCA
599	GCTTTTTGATCTTCTTAATCCAT
600	CTTTTTGATCTTCTTAATCCATC
601	TTTTTGATCTTCTTAATCCATCA
602	TTTTGATCTTCTTAATCCATCAT
603	TTTGATCTTCTTAATCCATCATC
604	TTGATCTTCTTAATCCATCATCT
605	TGATCTTCTTAATCCATCATCTG
606	GATCTTCTTAATCCATCATCTGA
607	ATCTTCTTAATCCATCATCTGAT
608	TCTTCTTAATCCATCATCTGATG
609	CTTCTTAATCCATCATCTGATGT
610	TTCTTAATCCATCATCTGATGTT
611	TCTTAATCCATCATCTGATGTTT
612	CTTAATCCATCATCTGATGTTTC
613	TTAATCCATCATCTGATGTTTCT
614	TAATCCATCATCTGATGTTTCTG
615	AATCCATCATCTGATGTTTCTGA
616	ATCCATCATCTGATGTTTCTGAG
617	TCCATCATCTGATGTTTCTGAGA
618	CCATCATCTGATGTTTCTGAGAG
619	CATCATCTGATGTTTCTGAGAGA
620	ATCATCTGATGTTTCTGAGAGAC
621	TCATCTGATGTTTCTGAGAGACT
622	CATCTGATGTTTCTGAGAGACTA
623	ATCTGATGTTTCTGAGAGACTAC
624	TCTGATGTTTCTGAGAGACTACA
625	CTGATGTTTCTGAGAGACTACAG
626	TGATGTTTCTGAGAGACTACAGA
627	GATGTTTCTGAGAGACTACAGAT
628	ATGTTTCTGAGAGACTACAGATG
629	TGTTTCTGAGAGACTACAGATGT
630	GTTTCTGAGAGACTACAGATGTT
631	TTTCTGAGAGACTACAGATGTTT
632	TTCTGAGAGACTACAGATGTTTG
633	TCTGAGAGACTACAGATGTTTGA
634	CTGAGAGACTACAGATGTTTGAT
635	TGAGAGACTACAGATGTTTGATG

Fig. 27 cont'd (Sheet 11 of 84)

ID	SEQUENCE
636	GAGAGACTACAGATGTTTGATGA
637	AGAGACTACAGATGTTTGATGAT
638	GAGACTACAGATGTTTGATGATC
639	AGACTACAGATGTTTGATGATCC
640	GACTACAGATGTTTGATGATCCC
641	ACTACAGATGTTTGATGATCCCC
642	CTACAGATGTTTGATGATCCCCG
643	TACAGATGTTTGATGATCCCCGT
644	ACAGATGTTTGATGATCCCCGTA
645	CAGATGTTTGATGATCCCCGTAA
646	AGATGTTTGATGATCCCCGTAAC
647	GATGTTTGATGATCCCCGTAACA
648	ATGTTTGATGATCCCCGTAACAA
649	TGTTTGATGATCCCCGTAACAAG
650	GTTTGATGATCCCCGTAACAAGA
651	TTTGATGATCCCCGTAACAAGAG
652	TTGATGATCCCCGTAACAAGAGA
653	TGATGATCCCCGTAACAAGAGAG
654	GATGATCCCCGTAACAAGAGAGG
655	ATGATCCCCGTAACAAGAGAGGA
656	TGATCCCCGTAACAAGAGAGGAG
657	GATCCCCGTAACAAGAGAGGAGT
658	ATCCCCGTAACAAGAGAGGAGTG
659	TCCCCGTAACAAGAGAGGAGTGA
660	CCCCGTAACAAGAGAGGAGTGAT
661	CCCGTAACAAGAGAGGAGTGATA
662	CCGTAACAAGAGAGGAGTGATAA
663	CGTAACAAGAGAGGAGTGATAAT
664	GTAACAAGAGAGGAGTGATAATT
665	TAACAAGAGAGGAGTGATAATTA
666	AACAAGAGAGGAGTGATAATTAA
667	ACAAGAGAGGAGTGATAATTAAA
668	CAAGAGAGGAGTGATAATTAAAG
669	AAGAGAGGAGTGATAATTAAAGG
670	AGAGAGGAGTGATAATTAAAGGT
671	GAGAGGAGTGATAATTAAAGGTT
672	AGAGGAGTGATAATTAAAGGTTT
673	GAGGAGTGATAATTAAAGGTTTA
674	AGGAGTGATAATTAAAGGTTTAG
675	GGAGTGATAATTAAAGGTTTAGA
676	GAGTGATAATTAAAGGTTTAGAA
677	AGTGATAATTAAAGGTTTAGAAG
678	GTGATAATTAAAGGTTTAGAAGA
679	TGATAATTAAAGGTTTAGAAGAA
680	GATAATTAAAGGTTTAGAAGAAA
681	ATAATTAAAGGTTTAGAAGAAAT
682	TAATTAAAGGTTTAGAAGAAATT
683	AATTAAAGGTTTAGAAGAAATTA
684	ATTAAAGGTTTAGAAGAAATTAC
685	TTAAAGGTTTAGAAGAAATTACA
686	TAAAGGTTTAGAAGAAATTACAG
687	AAAGGTTTAGAAGAAATTACAGT
688	AAGGTTTAGAAGAAATTACAGTA
689	AGGTTTAGAAGAAATTACAGTAC
690	GGTTTAGAAGAAATTACAGTACA
691	GTTTAGAAGAAATTACAGTACAC
692	TTTAGAAGAAATTACAGTACACA
693	TTAGAAGAAATTACAGTACACAA

Fig. 27 cont'd (Sheet 12 of 84)

ID	SEQUENCE
694	TAGAAGAAATTACAGTACACAAC
695	AGAAGAAATTACAGTACACAACA
696	GAAGAAATTACAGTACACAACAA
697	AAGAAATTACAGTACACAACAAG
698	AGAAATTACAGTACACAACAAGG
699	GAAATTACAGTACACAACAAGGA
700	AAATTACAGTACACAACAAGGAT
701	AATTACAGTACACAACAAGGATG
702	ATTACAGTACACAACAAGGATGA
703	TTACAGTACACAACAAGGATGAA
704	TACAGTACACAACAAGGATGAAG
705	ACAGTACACAACAAGGATGAAGT
706	CAGTACACAACAAGGATGAAGTC
707	AGTACACAACAAGGATGAAGTCT
708	GTACACAACAAGGATGAAGTCTA
709	TACACAACAAGGATGAAGTCTAT
710	ACACAACAAGGATGAAGTCTATC
711	CACAACAAGGATGAAGTCTATCA
712	ACAACAAGGATGAAGTCTATCAA
713	CAACAAGGATGAAGTCTATCAAA
714	AACAAGGATGAAGTCTATCAAAT
715	ACAAGGATGAAGTCTATCAAATT
716	CAAGGATGAAGTCTATCAAATTT
717	AAGGATGAAGTCTATCAAATTTT
718	AGGATGAAGTCTATCAAATTTTA
719	GGATGAAGTCTATCAAATTTTAG
720	GATGAAGTCTATCAAATTTTAGA
721	ATGAAGTCTATCAAATTTTAGAA
722	TGAAGTCTATCAAATTTTAGAAA
723	GAAGTCTATCAAATTTTAGAAAA
724	AAGTCTATCAAATTTTAGAAAAG
725	AGTCTATCAAATTTTAGAAAAGG
726	GTCTATCAAATTTTAGAAAAGGG
727	TCTATCAAATTTTAGAAAAGGGG
728	CTATCAAATTTTAGAAAAGGGGG
729	TATCAAATTTTAGAAAAGGGGGC
730	ATCAAATTTTAGAAAAGGGGGCA
731	TCAAATTTTAGAAAAGGGGGCAG
732	CAAATTTTAGAAAAGGGGGCAGC
733	AAATTTTAGAAAAGGGGGCAGCA
734	AATTTTAGAAAAGGGGGCAGCAA
735	ATTTTAGAAAAGGGGGCAGCAAA
736	TTTTAGAAAAGGGGGCAGCAAAA
737	TTTAGAAAAGGGGGCAGCAAAAA
738	TTAGAAAAGGGGGCAGCAAAAAG
739	TAGAAAAGGGGGCAGCAAAAAGG
740	AGAAAAGGGGGCAGCAAAAAGGA
741	GAAAAGGGGGCAGCAAAAAGGAC
742	AAAAGGGGGCAGCAAAAAGGACA
743	AAAGGGGGCAGCAAAAAGGACAA
744	AAGGGGGCAGCAAAAAGGACAAC
745	AGGGGGCAGCAAAAAGGACAACT
746	GGGGGCAGCAAAAAGGACAACTG
747	GGGGCAGCAAAAAGGACAACTGC
748	GGGCAGCAAAAAGGACAACTGCA
749	GGCAGCAAAAAGGACAACTGCAG
750	GCAGCAAAAAGGACAACTGCAGC
751	CAGCAAAAAGGACAACTGCAGCT

Fig. 27 cont'd (Sheet 13 of 84)

ID	SEQUENCE
752	AGCAAAAAGGACAACTGCAGCTA
753	GCAAAAAGGACAACTGCAGCTAC
754	CAAAAAGGACAACTGCAGCTACT
755	AAAAAGGACAACTGCAGCTACTC
756	AAAAGGACAACTGCAGCTACTCT
757	AAAGGACAACTGCAGCTACTCTG
758	AAGGACAACTGCAGCTACTCTGA
759	AGGACAACTGCAGCTACTCTGAT
760	GGACAACTGCAGCTACTCTGATG
761	GACAACTGCAGCTACTCTGATGA
762	ACAACTGCAGCTACTCTGATGAA
763	CAACTGCAGCTACTCTGATGAAT
764	AACTGCAGCTACTCTGATGAATG
765	ACTGCAGCTACTCTGATGAATGC
766	CTGCAGCTACTCTGATGAATGCA
767	TGCAGCTACTCTGATGAATGCAT
768	GCAGCTACTCTGATGAATGCATA
769	CAGCTACTCTGATGAATGCATAC
770	AGCTACTCTGATGAATGCATACT
771	GCTACTCTGATGAATGCATACTC
772	CTACTCTGATGAATGCATACTCT
773	TACTCTGATGAATGCATACTCTA
774	ACTCTGATGAATGCATACTCTAG
775	CTCTGATGAATGCATACTCTAGT
776	TCTGATGAATGCATACTCTAGTC
777	CTGATGAATGCATACTCTAGTCG
778	TGATGAATGCATACTCTAGTCGT
779	GATGAATGCATACTCTAGTCGTT
780	ATGAATGCATACTCTAGTCGTTC
781	TGAATGCATACTCTAGTCGTTCC
782	GAATGCATACTCTAGTCGTTCCC
783	AATGCATACTCTAGTCGTTCCCA
784	ATGCATACTCTAGTCGTTCCCAC
785	TGCATACTCTAGTCGTTCCCACT
786	GCATACTCTAGTCGTTCCCACTC
787	CATACTCTAGTCGTTCCCACTCA
788	ATACTCTAGTCGTTCCCACTCAG
789	TACTCTAGTCGTTCCCACTCAGT
790	ACTCTAGTCGTTCCCACTCAGTT
791	CTCTAGTCGTTCCCACTCAGTTT
792	TCTAGTCGTTCCCACTCAGTTTT
793	CTAGTCGTTCCCACTCAGTTTTC
794	TAGTCGTTCCCACTCAGTTTTCT
795	AGTCGTTCCCACTCAGTTTTCTC
796	GTCGTTCCCACTCAGTTTTCTCT
797	TCGTTCCCACTCAGTTTTCTCTG
798	CGTTCCCACTCAGTTTTCTCTGT
799	GTTCCCACTCAGTTTTCTCTGTT
800	TTCCCACTCAGTTTTCTCTGTTA
801	TCCCACTCAGTTTTCTCTGTTAC
802	CCCACTCAGTTTTCTCTGTTACA
803	CCACTCAGTTTTCTCTGTTACAA
804	CACTCAGTTTTCTCTGTTACAAT
805	ACTCAGTTTTCTCTGTTACAATA
806	CTCAGTTTTCTCTGTTACAATAC
807	TCAGTTTTCTCTGTTACAATACA
808	CAGTTTTCTCTGTTACAATACAT
809	AGTTTTCTCTGTTACAATACATA

Fig. 27 cont'd (Sheet 14 of 84)

ID	SEQUENCE
810	GTTTTCTCTGTTACAATACATAT
811	TTTTCTCTGTTACAATACATATG
812	TTTCTCTGTTACAATACATATGA
813	TTCTCTGTTACAATACATATGAA
814	TCTCTGTTACAATACATATGAAA
815	CTCTGTTACAATACATATGAAAG
816	TCTGTTACAATACATATGAAAGA
817	CTGTTACAATACATATGAAAGAA
818	TGTTACAATACATATGAAAGAAA
819	GTTACAATACATATGAAAGAAAC
820	TTACAATACATATGAAAGAAACT
821	TACAATACATATGAAAGAAACTA
822	ACAATACATATGAAAGAAACTAC
823	CAATACATATGAAAGAAACTACG
824	AATACATATGAAAGAAACTACGA
825	ATACATATGAAAGAAACTACGAT
826	TACATATGAAAGAAACTACGATT
827	ACATATGAAAGAAACTACGATTG
828	CATATGAAAGAAACTACGATTGA
829	ATATGAAAGAAACTACGATTGAT
830	TATGAAAGAAACTACGATTGATG
831	ATGAAAGAAACTACGATTGATGG
832	TGAAAGAAACTACGATTGATGGA
833	GAAAGAAACTACGATTGATGGAG
834	AAAGAAACTACGATTGATGGAGA
835	AAGAAACTACGATTGATGGAGAA
836	AGAAACTACGATTGATGGAGAAG
837	GAAACTACGATTGATGGAGAAGA
838	AAACTACGATTGATGGAGAAGAG
839	AACTACGATTGATGGAGAAGAGC
840	ACTACGATTGATGGAGAAGAGCT
841	CTACGATTGATGGAGAAGAGCTT
842	TACGATTGATGGAGAAGAGCTTG
843	ACGATTGATGGAGAAGAGCTTGT
844	CGATTGATGGAGAAGAGCTTGTT
845	GATTGATGGAGAAGAGCTTGTTA
846	ATTGATGGAGAAGAGCTTGTTAA
847	TTGATGGAGAAGAGCTTGTTAAA
848	TGATGGAGAAGAGCTTGTTAAAA
849	GATGGAGAAGAGCTTGTTAAAAT
850	ATGGAGAAGAGCTTGTTAAAATC
851	TGGAGAAGAGCTTGTTAAAATCG
852	GGAGAAGAGCTTGTTAAAATCGG
853	GAGAAGAGCTTGTTAAAATCGGA
854	AGAAGAGCTTGTTAAAATCGGAA
855	GAAGAGCTTGTTAAAATCGGAAA
856	AAGAGCTTGTTAAAATCGGAAAG
857	AGAGCTTGTTAAAATCGGAAAGT
858	GAGCTTGTTAAAATCGGAAAGTT
859	AGCTTGTTAAAATCGGAAAGTTG
860	GCTTGTTAAAATCGGAAAGTTGA
861	CTTGTTAAAATCGGAAAGTTGAA
862	TTGTTAAAATCGGAAAGTTGAAC
863	TGTTAAAATCGGAAAGTTGAACT
864	GTTAAAATCGGAAAGTTGAACTT
865	TTAAAATCGGAAAGTTGAACTTG
866	TAAAATCGGAAAGTTGAACTTGG
867	AAAATCGGAAAGTTGAACTTGGT

Fig. 27 cont'd (Sheet 15 of 84)

ID	SEQUENCE
868	AAATCGGAAAGTTGAACTTGGTT
869	AATCGGAAAGTTGAACTTGGTTG
870	ATCGGAAAGTTGAACTTGGTTGA
871	TCGGAAAGTTGAACTTGGTTGAT
872	CGGAAAGTTGAACTTGGTTGATC
873	GGAAAGTTGAACTTGGTTGATCT
874	GAAAGTTGAACTTGGTTGATCTT
875	AAAGTTGAACTTGGTTGATCTTG
876	AAGTTGAACTTGGTTGATCTTGC
877	AGTTGAACTTGGTTGATCTTGCA
878	GTTGAACTTGGTTGATCTTGCAG
879	TTGAACTTGGTTGATCTTGCAGG
880	TGAACTTGGTTGATCTTGCAGGA
881	GAACTTGGTTGATCTTGCAGGAA
882	AACTTGGTTGATCTTGCAGGAAG
883	ACTTGGTTGATCTTGCAGGAAGT
884	CTTGGTTGATCTTGCAGGAAGTG
885	TTGGTTGATCTTGCAGGAAGTGA
886	TGGTTGATCTTGCAGGAAGTGAA
887	GGTTGATCTTGCAGGAAGTGAAA
888	GTTGATCTTGCAGGAAGTGAAAA
889	TTGATCTTGCAGGAAGTGAAAAC
890	TGATCTTGCAGGAAGTGAAAACA
891	GATCTTGCAGGAAGTGAAAACAT
892	ATCTTGCAGGAAGTGAAAACATT
893	TCTTGCAGGAAGTGAAAACATTG
894	CTTGCAGGAAGTGAAAACATTGG
895	TTGCAGGAAGTGAAAACATTGGC
896	TGCAGGAAGTGAAAACATTGGCC
897	GCAGGAAGTGAAAACATTGGCCG
898	CAGGAAGTGAAAACATTGGCCGT
899	AGGAAGTGAAAACATTGGCCGTT
900	GGAAGTGAAAACATTGGCCGTTC
901	GAAGTGAAAACATTGGCCGTTCT
902	AAGTGAAAACATTGGCCGTTCTG
903	AGTGAAAACATTGGCCGTTCTGG
904	GTGAAAACATTGGCCGTTCTGGA
905	TGAAAACATTGGCCGTTCTGGAG
906	GAAAACATTGGCCGTTCTGGAGC
907	AAAACATTGGCCGTTCTGGAGCT
908	AAACATTGGCCGTTCTGGAGCTG
909	AACATTGGCCGTTCTGGAGCTGT
910	ACATTGGCCGTTCTGGAGCTGTT
911	CATTGGCCGTTCTGGAGCTGTTG
912	ATTGGCCGTTCTGGAGCTGTTGA
913	TTGGCCGTTCTGGAGCTGTTGAT
914	TGGCCGTTCTGGAGCTGTTGATA
915	GGCCGTTCTGGAGCTGTTGATAA
916	GCCGTTCTGGAGCTGTTGATAAG
917	CCGTTCTGGAGCTGTTGATAAGA
918	CGTTCTGGAGCTGTTGATAAGAG
919	GTTCTGGAGCTGTTGATAAGAGA
920	TTCTGGAGCTGTTGATAAGAGAG
921	TCTGGAGCTGTTGATAAGAGAGC
922	CTGGAGCTGTTGATAAGAGAGCT
923	TGGAGCTGTTGATAAGAGAGCTC
924	GGAGCTGTTGATAAGAGAGCTCG
925	GAGCTGTTGATAAGAGAGCTCGG

Fig. 27 cont'd (Sheet 16 of 84)

ID	SEQUENCE
926	AGCTGTTGATAAGAGAGCTCGGG
927	GCTGTTGATAAGAGAGCTCGGGA
928	CTGTTGATAAGAGAGCTCGGGAA
929	TGTTGATAAGAGAGCTCGGGAAG
930	GTTGATAAGAGAGCTCGGGAAGC
931	TTGATAAGAGAGCTCGGGAAGCT
932	TGATAAGAGAGCTCGGGAAGCTG
933	GATAAGAGAGCTCGGGAAGCTGG
934	ATAAGAGAGCTCGGGAAGCTGGA
935	TAAGAGAGCTCGGGAAGCTGGAA
936	AAGAGAGCTCGGGAAGCTGGAAA
937	AGAGAGCTCGGGAAGCTGGAAAT
938	GAGAGCTCGGGAAGCTGGAAATA
939	AGAGCTCGGGAAGCTGGAAATAT
940	GAGCTCGGGAAGCTGGAAATATA
941	AGCTCGGGAAGCTGGAAATATAA
942	GCTCGGGAAGCTGGAAATATAAA
943	CTCGGGAAGCTGGAAATATAAAT
944	TCGGGAAGCTGGAAATATAAATC
945	CGGGAAGCTGGAAATATAAATCA
946	GGGAAGCTGGAAATATAAATCAA
947	GGAAGCTGGAAATATAAATCAAT
948	GAAGCTGGAAATATAAATCAATC
949	AAGCTGGAAATATAAATCAATCC
950	AGCTGGAAATATAAATCAATCCC
951	GCTGGAAATATAAATCAATCCCT
952	CTGGAAATATAAATCAATCCCTG
953	TGGAAATATAAATCAATCCCTGT
954	GGAAATATAAATCAATCCCTGTT
955	GAAATATAAATCAATCCCTGTTG
956	AAATATAAATCAATCCCTGTTGA
957	AATATAAATCAATCCCTGTTGAC
958	ATATAAATCAATCCCTGTTGACT
959	TATAAATCAATCCCTGTTGACTT
960	ATAAATCAATCCCTGTTGACTTT
961	TAAATCAATCCCTGTTGACTTTG
962	AAATCAATCCCTGTTGACTTTGG
963	AATCAATCCCTGTTGACTTTGGG
964	ATCAATCCCTGTTGACTTTGGGA
965	TCAATCCCTGTTGACTTTGGGAA
966	CAATCCCTGTTGACTTTGGGAAG
967	AATCCCTGTTGACTTTGGGAAGG
968	ATCCCTGTTGACTTTGGGAAGGG
969	TCCCTGTTGACTTTGGGAAGGGT
970	CCCTGTTGACTTTGGGAAGGGTC
971	CCTGTTGACTTTGGGAAGGGTCA
972	CTGTTGACTTTGGGAAGGGTCAT
973	TGTTGACTTTGGGAAGGGTCATT
974	GTTGACTTTGGGAAGGGTCATTA
975	TTGACTTTGGGAAGGGTCATTAC
976	TGACTTTGGGAAGGGTCATTACT
977	GACTTTGGGAAGGGTCATTACTG
978	ACTTTGGGAAGGGTCATTACTGC
979	CTTTGGGAAGGGTCATTACTGCC
980	TTTGGGAAGGGTCATTACTGCCC
981	TTGGGAAGGGTCATTACTGCCCT
982	TGGGAAGGGTCATTACTGCCCTT
983	GGGAAGGGTCATTACTGCCCTTG

Fig. 27 cont'd (Sheet 17 of 84)

ID	SEQUENCE
984	GGAAGGGTCATTACTGCCCTTGT
985	GAAGGGTCATTACTGCCCTTGTA
986	AAGGGTCATTACTGCCCTTGTAG
987	AGGGTCATTACTGCCCTTGTAGA
988	GGGTCATTACTGCCCTTGTAGAA
989	GGTCATTACTGCCCTTGTAGAAA
990	GTCATTACTGCCCTTGTAGAAAG
991	TCATTACTGCCCTTGTAGAAAGA
992	CATTACTGCCCTTGTAGAAAGAA
993	ATTACTGCCCTTGTAGAAAGAAC
994	TTACTGCCCTTGTAGAAAGAACA
995	TACTGCCCTTGTAGAAAGAACAC
996	ACTGCCCTTGTAGAAAGAACACC
997	CTGCCCTTGTAGAAAGAACACCT
998	TGCCCTTGTAGAAAGAACACCTC
999	GCCCTTGTAGAAAGAACACCTCA
1000	CCCTTGTAGAAAGAACACCTCAT
1001	CCTTGTAGAAAGAACACCTCATG
1002	CTTGTAGAAAGAACACCTCATGT
1003	TTGTAGAAAGAACACCTCATGTT
1004	TGTAGAAAGAACACCTCATGTTC
1005	GTAGAAAGAACACCTCATGTTCC
1006	TAGAAAGAACACCTCATGTTCCT
1007	AGAAAGAACACCTCATGTTCCTT
1008	GAAAGAACACCTCATGTTCCTTA
1009	AAAGAACACCTCATGTTCCTTAT
1010	AAGAACACCTCATGTTCCTTATC
1011	AGAACACCTCATGTTCCTTATCG
1012	GAACACCTCATGTTCCTTATCGA
1013	AACACCTCATGTTCCTTATCGAG
1014	ACACCTCATGTTCCTTATCGAGA
1015	CACCTCATGTTCCTTATCGAGAA
1016	ACCTCATGTTCCTTATCGAGAAT
1017	CCTCATGTTCCTTATCGAGAATC
1018	CTCATGTTCCTTATCGAGAATCT
1019	TCATGTTCCTTATCGAGAATCTA
1020	CATGTTCCTTATCGAGAATCTAA
1021	ATGTTCCTTATCGAGAATCTAAA
1022	TGTTCCTTATCGAGAATCTAAAC
1023	GTTCCTTATCGAGAATCTAAACT
1024	TTCCTTATCGAGAATCTAAACTA
1025	TCCTTATCGAGAATCTAAACTAA
1026	CCTTATCGAGAATCTAAACTAAC
1027	CTTATCGAGAATCTAAACTAACT
1028	TTATCGAGAATCTAAACTAACTA
1029	TATCGAGAATCTAAACTAACTAG
1030	ATCGAGAATCTAAACTAACTAGA
1031	TCGAGAATCTAAACTAACTAGAA
1032	CGAGAATCTAAACTAACTAGAAT
1033	GAGAATCTAAACTAACTAGAATC
1034	AGAATCTAAACTAACTAGAATCC
1035	GAATCTAAACTAACTAGAATCCT
1036	AATCTAAACTAACTAGAATCCTC
1037	ATCTAAACTAACTAGAATCCTCC
1038	TCTAAACTAACTAGAATCCTCCA
1039	CTAAACTAACTAGAATCCTCCAG
1040	TAAACTAACTAGAATCCTCCAGG
1041	AAACTAACTAGAATCCTCCAGGA

Fig. 27 cont'd (Sheet 18 of 84)

ID	SEQUENCE
1042	AACTAACTAGAATCCTCCAGGAT
1043	ACTAACTAGAATCCTCCAGGATT
1044	CTAACTAGAATCCTCCAGGATTC
1045	TAACTAGAATCCTCCAGGATTCT
1046	AACTAGAATCCTCCAGGATTCTC
1047	ACTAGAATCCTCCAGGATTCTCT
1048	CTAGAATCCTCCAGGATTCTCTT
1049	TAGAATCCTCCAGGATTCTCTTG
1050	AGAATCCTCCAGGATTCTCTTGG
1051	GAATCCTCCAGGATTCTCTTGGA
1052	AATCCTCCAGGATTCTCTTGGAG
1053	ATCCTCCAGGATTCTCTTGGAGG
1054	TCCTCCAGGATTCTCTTGGAGGG
1055	CCTCCAGGATTCTCTTGGAGGGC
1056	CTCCAGGATTCTCTTGGAGGGCG
1057	TCCAGGATTCTCTTGGAGGGCGT
1058	CCAGGATTCTCTTGGAGGGCGTA
1059	CAGGATTCTCTTGGAGGGCGTAC
1060	AGGATTCTCTTGGAGGGCGTACA
1061	GGATTCTCTTGGAGGGCGTACAA
1062	GATTCTCTTGGAGGGCGTACAAG
1063	ATTCTCTTGGAGGGCGTACAAGA
1064	TTCTCTTGGAGGGCGTACAAGAA
1065	TCTCTTGGAGGGCGTACAAGAAC
1066	CTCTTGGAGGGCGTACAAGAACA
1067	TCTTGGAGGGCGTACAAGAACAT
1068	CTTGGAGGGCGTACAAGAACATC
1069	TTGGAGGGCGTACAAGAACATCT
1070	TGGAGGGCGTACAAGAACATCTA
1071	GGAGGGCGTACAAGAACATCTAT
1072	GAGGGCGTACAAGAACATCTATA
1073	AGGGCGTACAAGAACATCTATAA
1074	GGGCGTACAAGAACATCTATAAT
1075	GGCGTACAAGAACATCTATAATT
1076	GCGTACAAGAACATCTATAATTG
1077	CGTACAAGAACATCTATAATTGC
1078	GTACAAGAACATCTATAATTGCA
1079	TACAAGAACATCTATAATTGCAA
1080	ACAAGAACATCTATAATTGCAAC
1081	CAAGAACATCTATAATTGCAACA
1082	AAGAACATCTATAATTGCAACAA
1083	AGAACATCTATAATTGCAACAAT
1084	GAACATCTATAATTGCAACAATT
1085	AACATCTATAATTGCAACAATTT
1086	ACATCTATAATTGCAACAATTTC
1087	CATCTATAATTGCAACAATTTCT
1088	ATCTATAATTGCAACAATTTCTC
1089	TCTATAATTGCAACAATTTCTCC
1090	CTATAATTGCAACAATTTCTCCT
1091	TATAATTGCAACAATTTCTCCTG
1092	ATAATTGCAACAATTTCTCCTGC
1093	TAATTGCAACAATTTCTCCTGCA
1094	AATTGCAACAATTTCTCCTGCAT
1095	ATTGCAACAATTTCTCCTGCATC
1096	TTGCAACAATTTCTCCTGCATCT
1097	TGCAACAATTTCTCCTGCATCTC
1098	GCAACAATTTCTCCTGCATCTCT
1099	CAACAATTTCTCCTGCATCTCTC

Fig. 27 cont'd (Sheet 19 of 84)

ID	SEQUENCE
1100	AACAATTTCTCCTGCATCTCTCA
1101	ACAATTTCTCCTGCATCTCTCAA
1102	CAATTTCTCCTGCATCTCTCAAT
1103	AATTTCTCCTGCATCTCTCAATC
1104	ATTTCTCCTGCATCTCTCAATCT
1105	TTTCTCCTGCATCTCTCAATCTT
1106	TTCTCCTGCATCTCTCAATCTTG
1107	TCTCCTGCATCTCTCAATCTTGA
1108	CTCCTGCATCTCTCAATCTTGAG
1109	TCCTGCATCTCTCAATCTTGAGG
1110	CCTGCATCTCTCAATCTTGAGGA
1111	CTGCATCTCTCAATCTTGAGGAA
1112	TGCATCTCTCAATCTTGAGGAAA
1113	GCATCTCTCAATCTTGAGGAAAC
1114	CATCTCTCAATCTTGAGGAAACT
1115	ATCTCTCAATCTTGAGGAAACTC
1116	TCTCTCAATCTTGAGGAAACTCT
1117	CTCTCAATCTTGAGGAAACTCTG
1118	TCTCAATCTTGAGGAAACTCTGA
1119	CTCAATCTTGAGGAAACTCTGAG
1120	TCAATCTTGAGGAAACTCTGAGT
1121	CAATCTTGAGGAAACTCTGAGTA
1122	AATCTTGAGGAAACTCTGAGTAC
1123	ATCTTGAGGAAACTCTGAGTACA
1124	TCTTGAGGAAACTCTGAGTACAT
1125	CTTGAGGAAACTCTGAGTACATT
1126	TTGAGGAAACTCTGAGTACATTG
1127	TGAGGAAACTCTGAGTACATTGG
1128	GAGGAAACTCTGAGTACATTGGA
1129	AGGAAACTCTGAGTACATTGGAA
1130	GGAAACTCTGAGTACATTGGAAT
1131	GAAACTCTGAGTACATTGGAATA
1132	AAACTCTGAGTACATTGGAATAT
1133	AACTCTGAGTACATTGGAATATG
1134	ACTCTGAGTACATTGGAATATGC
1135	CTCTGAGTACATTGGAATATGCT
1136	TCTGAGTACATTGGAATATGCTC
1137	CTGAGTACATTGGAATATGCTCA
1138	TGAGTACATTGGAATATGCTCAT
1139	GAGTACATTGGAATATGCTCATA
1140	AGTACATTGGAATATGCTCATAG
1141	GTACATTGGAATATGCTCATAGA
1142	TACATTGGAATATGCTCATAGAG
1143	ACATTGGAATATGCTCATAGAGC
1144	CATTGGAATATGCTCATAGAGCA
1145	ATTGGAATATGCTCATAGAGCAA
1146	TTGGAATATGCTCATAGAGCAAA
1147	TGGAATATGCTCATAGAGCAAAG
1148	GGAATATGCTCATAGAGCAAAGA
1149	GAATATGCTCATAGAGCAAAGAA
1150	AATATGCTCATAGAGCAAAGAAC
1151	ATATGCTCATAGAGCAAAGAACA
1152	TATGCTCATAGAGCAAAGAACAT
1153	ATGCTCATAGAGCAAAGAACATA
1154	TGCTCATAGAGCAAAGAACATAT
1155	GCTCATAGAGCAAAGAACATATT
1156	CTCATAGAGCAAAGAACATATTG
1157	TCATAGAGCAAAGAACATATTGA

Fig. 27 cont'd (Sheet 20 of 84)

ID	SEQUENCE
1158	CATAGAGCAAAGAACATATTGAA
1159	ATAGAGCAAAGAACATATTGAAT
1160	TAGAGCAAAGAACATATTGAATA
1161	AGAGCAAAGAACATATTGAATAA
1162	GAGCAAAGAACATATTGAATAAG
1163	AGCAAAGAACATATTGAATAAGC
1164	GCAAAGAACATATTGAATAAGCC
1165	CAAAGAACATATTGAATAAGCCT
1166	AAAGAACATATTGAATAAGCCTG
1167	AAGAACATATTGAATAAGCCTGA
1168	AGAACATATTGAATAAGCCTGAA
1169	GAACATATTGAATAAGCCTGAAG
1170	AACATATTGAATAAGCCTGAAGT
1171	ACATATTGAATAAGCCTGAAGTG
1172	CATATTGAATAAGCCTGAAGTGA
1173	ATATTGAATAAGCCTGAAGTGAA
1174	TATTGAATAAGCCTGAAGTGAAT
1175	ATTGAATAAGCCTGAAGTGAATC
1176	TTGAATAAGCCTGAAGTGAATCA
1177	TGAATAAGCCTGAAGTGAATCAG
1178	GAATAAGCCTGAAGTGAATCAGA
1179	AATAAGCCTGAAGTGAATCAGAA
1180	ATAAGCCTGAAGTGAATCAGAAA
1181	TAAGCCTGAAGTGAATCAGAAAC
1182	AAGCCTGAAGTGAATCAGAAACT
1183	AGCCTGAAGTGAATCAGAAACTC
1184	GCCTGAAGTGAATCAGAAACTCA
1185	CCTGAAGTGAATCAGAAACTCAC
1186	CTGAAGTGAATCAGAAACTCACC
1187	TGAAGTGAATCAGAAACTCACCA
1188	GAAGTGAATCAGAAACTCACCAA
1189	AAGTGAATCAGAAACTCACCAAA
1190	AGTGAATCAGAAACTCACCAAAA
1191	GTGAATCAGAAACTCACCAAAAA
1192	TGAATCAGAAACTCACCAAAAAA
1193	GAATCAGAAACTCACCAAAAAAG
1194	AATCAGAAACTCACCAAAAAAGC
1195	ATCAGAAACTCACCAAAAAAGCT
1196	TCAGAAACTCACCAAAAAAGCTC
1197	CAGAAACTCACCAAAAAAGCTCT
1198	AGAAACTCACCAAAAAAGCTCTT
1199	GAAACTCACCAAAAAAGCTCTTA
1200	AAACTCACCAAAAAAGCTCTTAT
1201	AACTCACCAAAAAAGCTCTTATT
1202	ACTCACCAAAAAAGCTCTTATTA
1203	CTCACCAAAAAAGCTCTTATTAA
1204	TCACCAAAAAAGCTCTTATTAAG
1205	CACCAAAAAAGCTCTTATTAAGG
1206	ACCAAAAAAGCTCTTATTAAGGA
1207	CCAAAAAAGCTCTTATTAAGGAG
1208	CAAAAAAGCTCTTATTAAGGAGT
1209	AAAAAAGCTCTTATTAAGGAGTA
1210	AAAAAGCTCTTATTAAGGAGTAT
1211	AAAAGCTCTTATTAAGGAGTATA
1212	AAAGCTCTTATTAAGGAGTATAC
1213	AAGCTCTTATTAAGGAGTATACG
1214	AGCTCTTATTAAGGAGTATACGG
1215	GCTCTTATTAAGGAGTATACGGA

Fig. 27 cont'd (Sheet 21 of 84)

ID	SEQUENCE
1216	CTCTTATTAAGGAGTATACGGAG
1217	TCTTATTAAGGAGTATACGGAGG
1218	CTTATTAAGGAGTATACGGAGGA
1219	TTATTAAGGAGTATACGGAGGAG
1220	TATTAAGGAGTATACGGAGGAGA
1221	ATTAAGGAGTATACGGAGGAGAT
1222	TTAAGGAGTATACGGAGGAGATA
1223	TAAGGAGTATACGGAGGAGATAG
1224	AAGGAGTATACGGAGGAGATAGA
1225	AGGAGTATACGGAGGAGATAGAA
1226	GGAGTATACGGAGGAGATAGAAC
1227	GAGTATACGGAGGAGATAGAACG
1228	AGTATACGGAGGAGATAGAACGT
1229	GTATACGGAGGAGATAGAACGTT
1230	TATACGGAGGAGATAGAACGTTT
1231	ATACGGAGGAGATAGAACGTTTA
1232	TACGGAGGAGATAGAACGTTTAA
1233	ACGGAGGAGATAGAACGTTTAAA
1234	CGGAGGAGATAGAACGTTTAAAA
1235	GGAGGAGATAGAACGTTTAAAAC
1236	GAGGAGATAGAACGTTTAAAACG
1237	AGGAGATAGAACGTTTAAAACGA
1238	GGAGATAGAACGTTTAAAACGAG
1239	GAGATAGAACGTTTAAAACGAGA
1240	AGATAGAACGTTTAAAACGAGAT
1241	GATAGAACGTTTAAAACGAGATC
1242	ATAGAACGTTTAAAACGAGATCT
1243	TAGAACGTTTAAAACGAGATCTT
1244	AGAACGTTTAAAACGAGATCTTG
1245	GAACGTTTAAAACGAGATCTTGC
1246	AACGTTTAAAACGAGATCTTGCT
1247	ACGTTTAAAACGAGATCTTGCTG
1248	CGTTTAAAACGAGATCTTGCTGC
1249	GTTTAAAACGAGATCTTGCTGCA
1250	TTTAAAACGAGATCTTGCTGCAG
1251	TTAAAACGAGATCTTGCTGCAGC
1252	TAAAACGAGATCTTGCTGCAGCC
1253	AAAACGAGATCTTGCTGCAGCCC
1254	AAACGAGATCTTGCTGCAGCCCG
1255	AACGAGATCTTGCTGCAGCCCGT
1256	ACGAGATCTTGCTGCAGCCCGTG
1257	CGAGATCTTGCTGCAGCCCGTGA
1258	GAGATCTTGCTGCAGCCCGTGAG
1259	AGATCTTGCTGCAGCCCGTGAGA
1260	GATCTTGCTGCAGCCCGTGAGAA
1261	ATCTTGCTGCAGCCCGTGAGAAA
1262	TCTTGCTGCAGCCCGTGAGAAAA
1263	CTTGCTGCAGCCCGTGAGAAAAA
1264	TTGCTGCAGCCCGTGAGAAAAAT
1265	TGCTGCAGCCCGTGAGAAAAATG
1266	GCTGCAGCCCGTGAGAAAAATGG
1267	CTGCAGCCCGTGAGAAAAATGGA
1268	TGCAGCCCGTGAGAAAAATGGAG
1269	GCAGCCCGTGAGAAAAATGGAGT
1270	CAGCCCGTGAGAAAAATGGAGTG
1271	AGCCCGTGAGAAAAATGGAGTGT
1272	GCCCGTGAGAAAAATGGAGTGTA
1273	CCCGTGAGAAAAATGGAGTGTAT

Fig. 27 cont'd (Sheet 22 of 84)

ID	SEQUENCE
1274	CCGTGAGAAAAATGGAGTGTATA
1275	CGTGAGAAAAATGGAGTGTATAT
1276	GTGAGAAAAATGGAGTGTATATT
1277	TGAGAAAAATGGAGTGTATATTT
1278	GAGAAAAATGGAGTGTATATTTC
1279	AGAAAAATGGAGTGTATATTTCT
1280	GAAAAATGGAGTGTATATTTCTG
1281	AAAAATGGAGTGTATATTTCTGA
1282	AAAATGGAGTGTATATTTCTGAA
1283	AAATGGAGTGTATATTTCTGAAG
1284	AATGGAGTGTATATTTCTGAAGA
1285	ATGGAGTGTATATTTCTGAAGAA
1286	TGGAGTGTATATTTCTGAAGAAA
1287	GGAGTGTATATTTCTGAAGAAAA
1288	GAGTGTATATTTCTGAAGAAAAT
1289	AGTGTATATTTCTGAAGAAAATT
1290	GTGTATATTTCTGAAGAAAATTT
1291	TGTATATTTCTGAAGAAAATTTT
1292	GTATATTTCTGAAGAAAATTTTA
1293	TATATTTCTGAAGAAAATTTTAG
1294	ATATTTCTGAAGAAAATTTTAGA
1295	TATTTCTGAAGAAAATTTTAGAG
1296	ATTTCTGAAGAAAATTTTAGAGT
1297	TTTCTGAAGAAAATTTTAGAGTC
1298	TTCTGAAGAAAATTTTAGAGTCA
1299	TCTGAAGAAAATTTTAGAGTCAT
1300	CTGAAGAAAATTTTAGAGTCATG
1301	TGAAGAAAATTTTAGAGTCATGA
1302	GAAGAAAATTTTAGAGTCATGAG
1303	AAGAAAATTTTAGAGTCATGAGT
1304	AGAAAATTTTAGAGTCATGAGTG
1305	GAAAATTTTAGAGTCATGAGTGG
1306	AAAATTTTAGAGTCATGAGTGGA
1307	AAATTTTAGAGTCATGAGTGGAA
1308	AATTTTAGAGTCATGAGTGGAAA
1309	ATTTTAGAGTCATGAGTGGAAAA
1310	TTTTAGAGTCATGAGTGGAAAAT
1311	TTTAGAGTCATGAGTGGAAAATT
1312	TTAGAGTCATGAGTGGAAAATTA
1313	TAGAGTCATGAGTGGAAAATTAA
1314	AGAGTCATGAGTGGAAAATTAAC
1315	GAGTCATGAGTGGAAAATTAACT
1316	AGTCATGAGTGGAAAATTAACTG
1317	GTCATGAGTGGAAAATTAACTGT
1318	TCATGAGTGGAAAATTAACTGTT
1319	CATGAGTGGAAAATTAACTGTTC
1320	ATGAGTGGAAAATTAACTGTTCA
1321	TGAGTGGAAAATTAACTGTTCAA
1322	GAGTGGAAAATTAACTGTTCAAG
1323	AGTGGAAAATTAACTGTTCAAGA
1324	GTGGAAAATTAACTGTTCAAGAA
1325	TGGAAAATTAACTGTTCAAGAAG
1326	GGAAAATTAACTGTTCAAGAAGA
1327	GAAAATTAACTGTTCAAGAAGAG
1328	AAAATTAACTGTTCAAGAAGAGC
1329	AAATTAACTGTTCAAGAAGAGCA
1330	AATTAACTGTTCAAGAAGAGCAG
1331	ATTAACTGTTCAAGAAGAGCAGA

Fig. 27 cont'd (Sheet 23 of 84)

ID	SEQUENCE
1332	TTAACTGTTCAAGAAGAGCAGAT
1333	TAACTGTTCAAGAAGAGCAGATT
1334	AACTGTTCAAGAAGAGCAGATTG
1335	ACTGTTCAAGAAGAGCAGATTGT
1336	CTGTTCAAGAAGAGCAGATTGTA
1337	TGTTCAAGAAGAGCAGATTGTAG
1338	GTTCAAGAAGAGCAGATTGTAGA
1339	TTCAAGAAGAGCAGATTGTAGAA
1340	TCAAGAAGAGCAGATTGTAGAAT
1341	CAAGAAGAGCAGATTGTAGAATT
1342	AAGAAGAGCAGATTGTAGAATTG
1343	AGAAGAGCAGATTGTAGAATTGA
1344	GAAGAGCAGATTGTAGAATTGAT
1345	AAGAGCAGATTGTAGAATTGATT
1346	AGAGCAGATTGTAGAATTGATTG
1347	GAGCAGATTGTAGAATTGATTGA
1348	AGCAGATTGTAGAATTGATTGAA
1349	GCAGATTGTAGAATTGATTGAAA
1350	CAGATTGTAGAATTGATTGAAAA
1351	AGATTGTAGAATTGATTGAAAAA
1352	GATTGTAGAATTGATTGAAAAAA
1353	ATTGTAGAATTGATTGAAAAAAT
1354	TTGTAGAATTGATTGAAAAAATT
1355	TGTAGAATTGATTGAAAAAATTG
1356	GTAGAATTGATTGAAAAAATTGG
1357	TAGAATTGATTGAAAAAATTGGT
1358	AGAATTGATTGAAAAAATTGGTG
1359	GAATTGATTGAAAAAATTGGTGC
1360	AATTGATTGAAAAAATTGGTGCT
1361	ATTGATTGAAAAAATTGGTGCTG
1362	TTGATTGAAAAAATTGGTGCTGT
1363	TGATTGAAAAAATTGGTGCTGTT
1364	GATTGAAAAAATTGGTGCTGTTG
1365	ATTGAAAAAATTGGTGCTGTTGA
1366	TTGAAAAAATTGGTGCTGTTGAG
1367	TGAAAAAATTGGTGCTGTTGAGG
1368	GAAAAAATTGGTGCTGTTGAGGA
1369	AAAAAATTGGTGCTGTTGAGGAG
1370	AAAAATTGGTGCTGTTGAGGAGG
1371	AAAATTGGTGCTGTTGAGGAGGA
1372	AAATTGGTGCTGTTGAGGAGGAG
1373	AATTGGTGCTGTTGAGGAGGAGC
1374	ATTGGTGCTGTTGAGGAGGAGCT
1375	TTGGTGCTGTTGAGGAGGAGCTG
1376	TGGTGCTGTTGAGGAGGAGCTGA
1377	GGTGCTGTTGAGGAGGAGCTGAA
1378	GTGCTGTTGAGGAGGAGCTGAAT
1379	TGCTGTTGAGGAGGAGCTGAATA
1380	GCTGTTGAGGAGGAGCTGAATAG
1381	CTGTTGAGGAGGAGCTGAATAGG
1382	TGTTGAGGAGGAGCTGAATAGGG
1383	GTTGAGGAGGAGCTGAATAGGGT
1384	TTGAGGAGGAGCTGAATAGGGTT
1385	TGAGGAGGAGCTGAATAGGGTTA
1386	GAGGAGGAGCTGAATAGGGTTAC
1387	AGGAGGAGCTGAATAGGGTTACA
1388	GGAGGAGCTGAATAGGGTTACAG
1389	GAGGAGCTGAATAGGGTTACAGA

Fig. 27 cont'd (Sheet 24 of 84)

ID	SEQUENCE
1390	AGGAGCTGAATAGGGTTACAGAG
1391	GGAGCTGAATAGGGTTACAGAGT
1392	GAGCTGAATAGGGTTACAGAGTT
1393	AGCTGAATAGGGTTACAGAGTTG
1394	GCTGAATAGGGTTACAGAGTTGT
1395	CTGAATAGGGTTACAGAGTTGTT
1396	TGAATAGGGTTACAGAGTTGTTT
1397	GAATAGGGTTACAGAGTTGTTTA
1398	AATAGGGTTACAGAGTTGTTTAT
1399	ATAGGGTTACAGAGTTGTTTATG
1400	TAGGGTTACAGAGTTGTTTATGG
1401	AGGGTTACAGAGTTGTTTATGGA
1402	GGGTTACAGAGTTGTTTATGGAT
1403	GGTTACAGAGTTGTTTATGGATA
1404	GTTACAGAGTTGTTTATGGATAA
1405	TTACAGAGTTGTTTATGGATAAT
1406	TACAGAGTTGTTTATGGATAATA
1407	ACAGAGTTGTTTATGGATAATAA
1408	CAGAGTTGTTTATGGATAATAAA
1409	AGAGTTGTTTATGGATAATAAAA
1410	GAGTTGTTTATGGATAATAAAAA
1411	AGTTGTTTATGGATAATAAAAAT
1412	GTTGTTTATGGATAATAAAAATG
1413	TTGTTTATGGATAATAAAAATGA
1414	TGTTTATGGATAATAAAAATGAA
1415	GTTTATGGATAATAAAAATGAAC
1416	TTTATGGATAATAAAAATGAACT
1417	TTATGGATAATAAAAATGAACTT
1418	TATGGATAATAAAAATGAACTTG
1419	ATGGATAATAAAAATGAACTTGA
1420	TGGATAATAAAAATGAACTTGAC
1421	GGATAATAAAAATGAACTTGACC
1422	GATAATAAAAATGAACTTGACCA
1423	ATAATAAAAATGAACTTGACCAG
1424	TAATAAAAATGAACTTGACCAGT
1425	AATAAAAATGAACTTGACCAGTG
1426	ATAAAAATGAACTTGACCAGTGT
1427	TAAAAATGAACTTGACCAGTGTA
1428	AAAAATGAACTTGACCAGTGTAA
1429	AAAATGAACTTGACCAGTGTAAA
1430	AAATGAACTTGACCAGTGTAAAT
1431	AATGAACTTGACCAGTGTAAATC
1432	ATGAACTTGACCAGTGTAAATCT
1433	TGAACTTGACCAGTGTAAATCTG
1434	GAACTTGACCAGTGTAAATCTGA
1435	AACTTGACCAGTGTAAATCTGAC
1436	ACTTGACCAGTGTAAATCTGACC
1437	CTTGACCAGTGTAAATCTGACCT
1438	TTGACCAGTGTAAATCTGACCTG
1439	TGACCAGTGTAAATCTGACCTGC
1440	GACCAGTGTAAATCTGACCTGCA
1441	ACCAGTGTAAATCTGACCTGCAA
1442	CCAGTGTAAATCTGACCTGCAAA
1443	CAGTGTAAATCTGACCTGCAAAA
1444	AGTGTAAATCTGACCTGCAAAAT
1445	GTGTAAATCTGACCTGCAAAATA
1446	TGTAAATCTGACCTGCAAAATAA
1447	GTAAATCTGACCTGCAAAATAAA

Fig. 27 cont'd (Sheet 25 of 84)

ID	SEQUENCE
1448	TAAATCTGACCTGCAAAATAAAA
1449	AAATCTGACCTGCAAAATAAAAC
1450	AATCTGACCTGCAAAATAAAACA
1451	ATCTGACCTGCAAAATAAAACAC
1452	TCTGACCTGCAAAATAAAACACA
1453	CTGACCTGCAAAATAAAACACAA
1454	TGACCTGCAAAATAAAACACAAG
1455	GACCTGCAAAATAAAACACAAGA
1456	ACCTGCAAAATAAAACACAAGAA
1457	CCTGCAAAATAAAACACAAGAAC
1458	CTGCAAAATAAAACACAAGAACT
1459	TGCAAAATAAAACACAAGAACTT
1460	GCAAAATAAAACACAAGAACTTG
1461	CAAAATAAAACACAAGAACTTGA
1462	AAAATAAAACACAAGAACTTGAA
1463	AAATAAAACACAAGAACTTGAAA
1464	AATAAAACACAAGAACTTGAAAC
1465	ATAAAACACAAGAACTTGAAACC
1466	TAAAACACAAGAACTTGAAACCA
1467	AAAACACAAGAACTTGAAACCAC
1468	AAACACAAGAACTTGAAACCACT
1469	AACACAAGAACTTGAAACCACTC
1470	ACACAAGAACTTGAAACCACTCA
1471	CACAAGAACTTGAAACCACTCAA
1472	ACAAGAACTTGAAACCACTCAAA
1473	CAAGAACTTGAAACCACTCAAAA
1474	AAGAACTTGAAACCACTCAAAAA
1475	AGAACTTGAAACCACTCAAAAAC
1476	GAACTTGAAACCACTCAAAAACA
1477	AACTTGAAACCACTCAAAAACAT
1478	ACTTGAAACCACTCAAAAACATT
1479	CTTGAAACCACTCAAAAACATTT
1480	TTGAAACCACTCAAAAACATTTG
1481	TGAAACCACTCAAAAACATTTGC
1482	GAAACCACTCAAAAACATTTGCA
1483	AAACCACTCAAAAACATTTGCAA
1484	AACCACTCAAAAACATTTGCAAG
1485	ACCACTCAAAAACATTTGCAAGA
1486	CCACTCAAAAACATTTGCAAGAA
1487	CACTCAAAAACATTTGCAAGAAA
1488	ACTCAAAAACATTTGCAAGAAAC
1489	CTCAAAAACATTTGCAAGAAACT
1490	TCAAAAACATTTGCAAGAAACTA
1491	CAAAAACATTTGCAAGAAACTAA
1492	AAAAACATTTGCAAGAAACTAAA
1493	AAAACATTTGCAAGAAACTAAAT
1494	AAACATTTGCAAGAAACTAAATT
1495	AACATTTGCAAGAAACTAAATTA
1496	ACATTTGCAAGAAACTAAATTAC
1497	CATTTGCAAGAAACTAAATTACA
1498	ATTTGCAAGAAACTAAATTACAA
1499	TTTGCAAGAAACTAAATTACAAC
1500	TTGCAAGAAACTAAATTACAACT
1501	TGCAAGAAACTAAATTACAACTT
1502	GCAAGAAACTAAATTACAACTTG
1503	CAAGAAACTAAATTACAACTTGT
1504	AAGAAACTAAATTACAACTTGTT
1505	AGAAACTAAATTACAACTTGTTA

Fig. 27 cont'd (Sheet 26 of 84)

ID	SEQUENCE
1506	GAAACTAAATTACAACTTGTTAA
1507	AAACTAAATTACAACTTGTTAAA
1508	AACTAAATTACAACTTGTTAAAG
1509	ACTAAATTACAACTTGTTAAAGA
1510	CTAAATTACAACTTGTTAAAGAA
1511	TAAATTACAACTTGTTAAAGAAG
1512	AAATTACAACTTGTTAAAGAAGA
1513	AATTACAACTTGTTAAAGAAGAA
1514	ATTACAACTTGTTAAAGAAGAAT
1515	TTACAACTTGTTAAAGAAGAATA
1516	TACAACTTGTTAAAGAAGAATAT
1517	ACAACTTGTTAAAGAAGAATATA
1518	CAACTTGTTAAAGAAGAATATAT
1519	AACTTGTTAAAGAAGAATATATC
1520	ACTTGTTAAAGAAGAATATATCA
1521	CTTGTTAAAGAAGAATATATCAC
1522	TTGTTAAAGAAGAATATATCACA
1523	TGTTAAAGAAGAATATATCACAT
1524	GTTAAAGAAGAATATATCACATC
1525	TTAAAGAAGAATATATCACATCA
1526	TAAAGAAGAATATATCACATCAG
1527	AAAGAAGAATATATCACATCAGC
1528	AAGAAGAATATATCACATCAGCT
1529	AGAAGAATATATCACATCAGCTT
1530	GAAGAATATATCACATCAGCTTT
1531	AAGAATATATCACATCAGCTTTG
1532	AGAATATATCACATCAGCTTTGG
1533	GAATATATCACATCAGCTTTGGA
1534	AATATATCACATCAGCTTTGGAA
1535	ATATATCACATCAGCTTTGGAAA
1536	TATATCACATCAGCTTTGGAAAG
1537	ATATCACATCAGCTTTGGAAAGT
1538	TATCACATCAGCTTTGGAAAGTA
1539	ATCACATCAGCTTTGGAAAGTAC
1540	TCACATCAGCTTTGGAAAGTACT
1541	CACATCAGCTTTGGAAAGTACTG
1542	ACATCAGCTTTGGAAAGTACTGA
1543	CATCAGCTTTGGAAAGTACTGAG
1544	ATCAGCTTTGGAAAGTACTGAGG
1545	TCAGCTTTGGAAAGTACTGAGGA
1546	CAGCTTTGGAAAGTACTGAGGAG
1547	AGCTTTGGAAAGTACTGAGGAGA
1548	GCTTTGGAAAGTACTGAGGAGAA
1549	CTTTGGAAAGTACTGAGGAGAAA
1550	TTTGGAAAGTACTGAGGAGAAAC
1551	TTGGAAAGTACTGAGGAGAAACT
1552	TGGAAAGTACTGAGGAGAAACTT
1553	GGAAAGTACTGAGGAGAAACTTC
1554	GAAAGTACTGAGGAGAAACTTCA
1555	AAAGTACTGAGGAGAAACTTCAT
1556	AAGTACTGAGGAGAAACTTCATG
1557	AGTACTGAGGAGAAACTTCATGA
1558	GTACTGAGGAGAAACTTCATGAT
1559	TACTGAGGAGAAACTTCATGATG
1560	ACTGAGGAGAAACTTCATGATGC
1561	CTGAGGAGAAACTTCATGATGCT
1562	TGAGGAGAAACTTCATGATGCTG
1563	GAGGAGAAACTTCATGATGCTGC

Fig. 27 cont'd (Sheet 27 of 84)

ID	SEQUENCE
1564	AGGAGAAACTTCATGATGCTGCC
1565	GGAGAAACTTCATGATGCTGCCA
1566	GAGAAACTTCATGATGCTGCCAG
1567	AGAAACTTCATGATGCTGCCAGC
1568	GAAACTTCATGATGCTGCCAGCA
1569	AAACTTCATGATGCTGCCAGCAA
1570	AACTTCATGATGCTGCCAGCAAG
1571	ACTTCATGATGCTGCCAGCAAGC
1572	CTTCATGATGCTGCCAGCAAGCT
1573	TTCATGATGCTGCCAGCAAGCTG
1574	TCATGATGCTGCCAGCAAGCTGC
1575	CATGATGCTGCCAGCAAGCTGCT
1576	ATGATGCTGCCAGCAAGCTGCTT
1577	TGATGCTGCCAGCAAGCTGCTTA
1578	GATGCTGCCAGCAAGCTGCTTAA
1579	ATGCTGCCAGCAAGCTGCTTAAC
1580	TGCTGCCAGCAAGCTGCTTAACA
1581	GCTGCCAGCAAGCTGCTTAACAC
1582	CTGCCAGCAAGCTGCTTAACACA
1583	TGCCAGCAAGCTGCTTAACACAG
1584	GCCAGCAAGCTGCTTAACACAGT
1585	CCAGCAAGCTGCTTAACACAGTT
1586	CAGCAAGCTGCTTAACACAGTTG
1587	AGCAAGCTGCTTAACACAGTTGA
1588	GCAAGCTGCTTAACACAGTTGAA
1589	CAAGCTGCTTAACACAGTTGAAG
1590	AAGCTGCTTAACACAGTTGAAGA
1591	AGCTGCTTAACACAGTTGAAGAA
1592	GCTGCTTAACACAGTTGAAGAAA
1593	CTGCTTAACACAGTTGAAGAAAC
1594	TGCTTAACACAGTTGAAGAAACT
1595	GCTTAACACAGTTGAAGAAACTA
1596	CTTAACACAGTTGAAGAAACTAC
1597	TTAACACAGTTGAAGAAACTACA
1598	TAACACAGTTGAAGAAACTACAA
1599	AACACAGTTGAAGAAACTACAAA
1600	ACACAGTTGAAGAAACTACAAAA
1601	CACAGTTGAAGAAACTACAAAAG
1602	ACAGTTGAAGAAACTACAAAAGA
1603	CAGTTGAAGAAACTACAAAAGAT
1604	AGTTGAAGAAACTACAAAAGATG
1605	GTTGAAGAAACTACAAAAGATGT
1606	TTGAAGAAACTACAAAAGATGTA
1607	TGAAGAAACTACAAAAGATGTAT
1608	GAAGAAACTACAAAAGATGTATC
1609	AAGAAACTACAAAAGATGTATCT
1610	AGAAACTACAAAAGATGTATCTG
1611	GAAACTACAAAAGATGTATCTGG
1612	AAACTACAAAAGATGTATCTGGT
1613	AACTACAAAAGATGTATCTGGTC
1614	ACTACAAAAGATGTATCTGGTCT
1615	CTACAAAAGATGTATCTGGTCTC
1616	TACAAAAGATGTATCTGGTCTCC
1617	ACAAAAGATGTATCTGGTCTCCA
1618	CAAAAGATGTATCTGGTCTCCAT
1619	AAAAGATGTATCTGGTCTCCATT
1620	AAAGATGTATCTGGTCTCCATTC
1621	AAGATGTATCTGGTCTCCATTCC

Fig. 27 cont'd (Sheet 28 of 84)

ID	SEQUENCE
1622	AGATGTATCTGGTCTCCATTCCA
1623	GATGTATCTGGTCTCCATTCCAA
1624	ATGTATCTGGTCTCCATTCCAAA
1625	TGTATCTGGTCTCCATTCCAAAC
1626	GTATCTGGTCTCCATTCCAAACT
1627	TATCTGGTCTCCATTCCAAACTG
1628	ATCTGGTCTCCATTCCAAACTGG
1629	TCTGGTCTCCATTCCAAACTGGA
1630	CTGGTCTCCATTCCAAACTGGAT
1631	TGGTCTCCATTCCAAACTGGATC
1632	GGTCTCCATTCCAAACTGGATCG
1633	GTCTCCATTCCAAACTGGATCGT
1634	TCTCCATTCCAAACTGGATCGTA
1635	CTCCATTCCAAACTGGATCGTAA
1636	TCCATTCCAAACTGGATCGTAAG
1637	CCATTCCAAACTGGATCGTAAGA
1638	CATTCCAAACTGGATCGTAAGAA
1639	ATTCCAAACTGGATCGTAAGAAG
1640	TTCCAAACTGGATCGTAAGAAGG
1641	TCCAAACTGGATCGTAAGAAGGC
1642	CCAAACTGGATCGTAAGAAGGCA
1643	CAAACTGGATCGTAAGAAGGCAG
1644	AAACTGGATCGTAAGAAGGCAGT
1645	AACTGGATCGTAAGAAGGCAGTT
1646	ACTGGATCGTAAGAAGGCAGTTG
1647	CTGGATCGTAAGAAGGCAGTTGA
1648	TGGATCGTAAGAAGGCAGTTGAC
1649	GGATCGTAAGAAGGCAGTTGACC
1650	GATCGTAAGAAGGCAGTTGACCA
1651	ATCGTAAGAAGGCAGTTGACCAA
1652	TCGTAAGAAGGCAGTTGACCAAC
1653	CGTAAGAAGGCAGTTGACCAACA
1654	GTAAGAAGGCAGTTGACCAACAC
1655	TAAGAAGGCAGTTGACCAACACA
1656	AAGAAGGCAGTTGACCAACACAA
1657	AGAAGGCAGTTGACCAACACAAT
1658	GAAGGCAGTTGACCAACACAATG
1659	AAGGCAGTTGACCAACACAATGC
1660	AGGCAGTTGACCAACACAATGCA
1661	GGCAGTTGACCAACACAATGCAG
1662	GCAGTTGACCAACACAATGCAGA
1663	CAGTTGACCAACACAATGCAGAA
1664	AGTTGACCAACACAATGCAGAAG
1665	GTTGACCAACACAATGCAGAAGC
1666	TTGACCAACACAATGCAGAAGCT
1667	TGACCAACACAATGCAGAAGCTC
1668	GACCAACACAATGCAGAAGCTCA
1669	ACCAACACAATGCAGAAGCTCAG
1670	CCAACACAATGCAGAAGCTCAGG
1671	CAACACAATGCAGAAGCTCAGGA
1672	AACACAATGCAGAAGCTCAGGAT
1673	ACACAATGCAGAAGCTCAGGATA
1674	CACAATGCAGAAGCTCAGGATAT
1675	ACAATGCAGAAGCTCAGGATATT
1676	CAATGCAGAAGCTCAGGATATTT
1677	AATGCAGAAGCTCAGGATATTTT
1678	ATGCAGAAGCTCAGGATATTTTT
1679	TGCAGAAGCTCAGGATATTTTTG

Fig. 27 cont'd (Sheet 29 of 84)

ID	SEQUENCE
1680	GCAGAAGCTCAGGATATTTTTGG
1681	CAGAAGCTCAGGATATTTTTGGC
1682	AGAAGCTCAGGATATTTTTGGCA
1683	GAAGCTCAGGATATTTTTGGCAA
1684	AAGCTCAGGATATTTTTGGCAAA
1685	AGCTCAGGATATTTTTGGCAAAA
1686	GCTCAGGATATTTTTGGCAAAAA
1687	CTCAGGATATTTTTGGCAAAAAC
1688	TCAGGATATTTTTGGCAAAAACC
1689	CAGGATATTTTTGGCAAAAACCT
1690	AGGATATTTTTGGCAAAAACCTG
1691	GGATATTTTTGGCAAAAACCTGA
1692	GATATTTTTGGCAAAAACCTGAA
1693	ATATTTTTGGCAAAAACCTGAAT
1694	TATTTTTGGCAAAAACCTGAATA
1695	ATTTTTGGCAAAAACCTGAATAG
1696	TTTTTGGCAAAAACCTGAATAGT
1697	TTTTGGCAAAAACCTGAATAGTC
1698	TTTGGCAAAAACCTGAATAGTCT
1699	TTGGCAAAAACCTGAATAGTCTG
1700	TGGCAAAAACCTGAATAGTCTGT
1701	GGCAAAAACCTGAATAGTCTGTT
1702	GCAAAAACCTGAATAGTCTGTTT
1703	CAAAAACCTGAATAGTCTGTTTA
1704	AAAAACCTGAATAGTCTGTTTAA
1705	AAAACCTGAATAGTCTGTTTAAT
1706	AAACCTGAATAGTCTGTTTAATA
1707	AACCTGAATAGTCTGTTTAATAA
1708	ACCTGAATAGTCTGTTTAATAAT
1709	CCTGAATAGTCTGTTTAATAATA
1710	CTGAATAGTCTGTTTAATAATAT
1711	TGAATAGTCTGTTTAATAATATG
1712	GAATAGTCTGTTTAATAATATGG
1713	AATAGTCTGTTTAATAATATGGA
1714	ATAGTCTGTTTAATAATATGGAA
1715	TAGTCTGTTTAATAATATGGAAG
1716	AGTCTGTTTAATAATATGGAAGA
1717	GTCTGTTTAATAATATGGAAGAA
1718	TCTGTTTAATAATATGGAAGAAT
1719	CTGTTTAATAATATGGAAGAATT
1720	TGTTTAATAATATGGAAGAATTA
1721	GTTTAATAATATGGAAGAATTAA
1722	TTTAATAATATGGAAGAATTAAT
1723	TTAATAATATGGAAGAATTAATT
1724	TAATAATATGGAAGAATTAATTA
1725	AATAATATGGAAGAATTAATTAA
1726	ATAATATGGAAGAATTAATTAAG
1727	TAATATGGAAGAATTAATTAAGG
1728	AATATGGAAGAATTAATTAAGGA
1729	ATATGGAAGAATTAATTAAGGAT
1730	TATGGAAGAATTAATTAAGGATG
1731	ATGGAAGAATTAATTAAGGATGG
1732	TGGAAGAATTAATTAAGGATGGC
1733	GGAAGAATTAATTAAGGATGGCA
1734	GAAGAATTAATTAAGGATGGCAG
1735	AAGAATTAATTAAGGATGGCAGC
1736	AGAATTAATTAAGGATGGCAGCT
1737	GAATTAATTAAGGATGGCAGCTC

Fig. 27 cont'd (Sheet 30 of 84)

ID	SEQUENCE
1738	AATTAATTAAGGATGGCAGCTCA
1739	ATTAATTAAGGATGGCAGCTCAA
1740	TTAATTAAGGATGGCAGCTCAAA
1741	TAATTAAGGATGGCAGCTCAAAG
1742	AATTAAGGATGGCAGCTCAAAGC
1743	ATTAAGGATGGCAGCTCAAAGCA
1744	TTAAGGATGGCAGCTCAAAGCAA
1745	TAAGGATGGCAGCTCAAAGCAAA
1746	AAGGATGGCAGCTCAAAGCAAAA
1747	AGGATGGCAGCTCAAAGCAAAAG
1748	GGATGGCAGCTCAAAGCAAAAGG
1749	GATGGCAGCTCAAAGCAAAAGGC
1750	ATGGCAGCTCAAAGCAAAAGGCC
1751	TGGCAGCTCAAAGCAAAAGGCCA
1752	GGCAGCTCAAAGCAAAAGGCCAT
1753	GCAGCTCAAAGCAAAAGGCCATG
1754	CAGCTCAAAGCAAAAGGCCATGC
1755	AGCTCAAAGCAAAAGGCCATGCT
1756	GCTCAAAGCAAAAGGCCATGCTA
1757	CTCAAAGCAAAAGGCCATGCTAG
1758	TCAAAGCAAAAGGCCATGCTAGA
1759	CAAAGCAAAAGGCCATGCTAGAA
1760	AAAGCAAAAGGCCATGCTAGAAG
1761	AAGCAAAAGGCCATGCTAGAAGT
1762	AGCAAAAGGCCATGCTAGAAGTA
1763	GCAAAAGGCCATGCTAGAAGTAC
1764	CAAAAGGCCATGCTAGAAGTACA
1765	AAAAGGCCATGCTAGAAGTACAT
1766	AAAGGCCATGCTAGAAGTACATA
1767	AAGGCCATGCTAGAAGTACATAA
1768	AGGCCATGCTAGAAGTACATAAG
1769	GGCCATGCTAGAAGTACATAAGA
1770	GCCATGCTAGAAGTACATAAGAC
1771	CCATGCTAGAAGTACATAAGACC
1772	CATGCTAGAAGTACATAAGACCT
1773	ATGCTAGAAGTACATAAGACCTT
1774	TGCTAGAAGTACATAAGACCTTA
1775	GCTAGAAGTACATAAGACCTTAT
1776	CTAGAAGTACATAAGACCTTATT
1777	TAGAAGTACATAAGACCTTATTT
1778	AGAAGTACATAAGACCTTATTTG
1779	GAAGTACATAAGACCTTATTTGG
1780	AAGTACATAAGACCTTATTTGGT
1781	AGTACATAAGACCTTATTTGGTA
1782	GTACATAAGACCTTATTTGGTAA
1783	TACATAAGACCTTATTTGGTAAT
1784	ACATAAGACCTTATTTGGTAATC
1785	CATAAGACCTTATTTGGTAATCT
1786	ATAAGACCTTATTTGGTAATCTG
1787	TAAGACCTTATTTGGTAATCTGC
1788	AAGACCTTATTTGGTAATCTGCT
1789	AGACCTTATTTGGTAATCTGCTG
1790	GACCTTATTTGGTAATCTGCTGT
1791	ACCTTATTTGGTAATCTGCTGTC
1792	CCTTATTTGGTAATCTGCTGTCT
1793	CTTATTTGGTAATCTGCTGTCTT
1794	TTATTTGGTAATCTGCTGTCTTC
1795	TATTTGGTAATCTGCTGTCTTCC

Fig. 27 cont'd (Sheet 31 of 84)

ID	SEQUENCE
1796	ATTTGGTAATCTGCTGTCTTCCA
1797	TTTGGTAATCTGCTGTCTTCCAG
1798	TTGGTAATCTGCTGTCTTCCAGT
1799	TGGTAATCTGCTGTCTTCCAGTG
1800	GGTAATCTGCTGTCTTCCAGTGT
1801	GTAATCTGCTGTCTTCCAGTGTC
1802	TAATCTGCTGTCTTCCAGTGTCT
1803	AATCTGCTGTCTTCCAGTGTCTC
1804	ATCTGCTGTCTTCCAGTGTCTCT
1805	TCTGCTGTCTTCCAGTGTCTCTG
1806	CTGCTGTCTTCCAGTGTCTCTGC
1807	TGCTGTCTTCCAGTGTCTCTGCA
1808	GCTGTCTTCCAGTGTCTCTGCAT
1809	CTGTCTTCCAGTGTCTCTGCATT
1810	TGTCTTCCAGTGTCTCTGCATTA
1811	GTCTTCCAGTGTCTCTGCATTAG
1812	TCTTCCAGTGTCTCTGCATTAGA
1813	CTTCCAGTGTCTCTGCATTAGAT
1814	TTCCAGTGTCTCTGCATTAGATA
1815	TCCAGTGTCTCTGCATTAGATAC
1816	CCAGTGTCTCTGCATTAGATACC
1817	CAGTGTCTCTGCATTAGATACCA
1818	AGTGTCTCTGCATTAGATACCAT
1819	GTGTCTCTGCATTAGATACCATT
1820	TGTCTCTGCATTAGATACCATTA
1821	GTCTCTGCATTAGATACCATTAC
1822	TCTCTGCATTAGATACCATTACT
1823	CTCTGCATTAGATACCATTACTA
1824	TCTGCATTAGATACCATTACTAC
1825	CTGCATTAGATACCATTACTACA
1826	TGCATTAGATACCATTACTACAG
1827	GCATTAGATACCATTACTACAGT
1828	CATTAGATACCATTACTACAGTA
1829	ATTAGATACCATTACTACAGTAG
1830	TTAGATACCATTACTACAGTAGC
1831	TAGATACCATTACTACAGTAGCA
1832	AGATACCATTACTACAGTAGCAC
1833	GATACCATTACTACAGTAGCACT
1834	ATACCATTACTACAGTAGCACTT
1835	TACCATTACTACAGTAGCACTTG
1836	ACCATTACTACAGTAGCACTTGG
1837	CCATTACTACAGTAGCACTTGGA
1838	CATTACTACAGTAGCACTTGGAT
1839	ATTACTACAGTAGCACTTGGATC
1840	TTACTACAGTAGCACTTGGATCT
1841	TACTACAGTAGCACTTGGATCTC
1842	ACTACAGTAGCACTTGGATCTCT
1843	CTACAGTAGCACTTGGATCTCTC
1844	TACAGTAGCACTTGGATCTCTCA
1845	ACAGTAGCACTTGGATCTCTCAC
1846	CAGTAGCACTTGGATCTCTCACA
1847	AGTAGCACTTGGATCTCTCACAT
1848	GTAGCACTTGGATCTCTCACATC
1849	TAGCACTTGGATCTCTCACATCT
1850	AGCACTTGGATCTCTCACATCTA
1851	GCACTTGGATCTCTCACATCTAT
1852	CACTTGGATCTCTCACATCTATT
1853	ACTTGGATCTCTCACATCTATTC

Fig. 27 cont'd (Sheet 32 of 84)

ID	SEQUENCE
1854	CTTGGATCTCTCACATCTATTCC
1855	TTGGATCTCTCACATCTATTCCA
1856	TGGATCTCTCACATCTATTCCAG
1857	GGATCTCTCACATCTATTCCAGA
1858	GATCTCTCACATCTATTCCAGAA
1859	ATCTCTCACATCTATTCCAGAAA
1860	TCTCTCACATCTATTCCAGAAAA
1861	CTCTCACATCTATTCCAGAAAAT
1862	TCTCACATCTATTCCAGAAAATG
1863	CTCACATCTATTCCAGAAAATGT
1864	TCACATCTATTCCAGAAAATGTG
1865	CACATCTATTCCAGAAAATGTGT
1866	ACATCTATTCCAGAAAATGTGTC
1867	CATCTATTCCAGAAAATGTGTCT
1868	ATCTATTCCAGAAAATGTGTCTA
1869	TCTATTCCAGAAAATGTGTCTAC
1870	CTATTCCAGAAAATGTGTCTACT
1871	TATTCCAGAAAATGTGTCTACTC
1872	ATTCCAGAAAATGTGTCTACTCA
1873	TTCCAGAAAATGTGTCTACTCAT
1874	TCCAGAAAATGTGTCTACTCATG
1875	CCAGAAAATGTGTCTACTCATGT
1876	CAGAAAATGTGTCTACTCATGTT
1877	AGAAAATGTGTCTACTCATGTTT
1878	GAAAATGTGTCTACTCATGTTTC
1879	AAAATGTGTCTACTCATGTTTCT
1880	AAATGTGTCTACTCATGTTTCTC
1881	AATGTGTCTACTCATGTTTCTCA
1882	ATGTGTCTACTCATGTTTCTCAG
1883	TGTGTCTACTCATGTTTCTCAGA
1884	GTGTCTACTCATGTTTCTCAGAT
1885	TGTCTACTCATGTTTCTCAGATT
1886	GTCTACTCATGTTTCTCAGATTT
1887	TCTACTCATGTTTCTCAGATTTT
1888	CTACTCATGTTTCTCAGATTTTT
1889	TACTCATGTTTCTCAGATTTTTA
1890	ACTCATGTTTCTCAGATTTTTAA
1891	CTCATGTTTCTCAGATTTTTAAT
1892	TCATGTTTCTCAGATTTTTAATA
1893	CATGTTTCTCAGATTTTTAATAT
1894	ATGTTTCTCAGATTTTTAATATG
1895	TGTTTCTCAGATTTTTAATATGA
1896	GTTTCTCAGATTTTTAATATGAT
1897	TTTCTCAGATTTTTAATATGATA
1898	TTCTCAGATTTTTAATATGATAC
1899	TCTCAGATTTTTAATATGATACT
1900	CTCAGATTTTTAATATGATACTA
1901	TCAGATTTTTAATATGATACTAA
1902	CAGATTTTTAATATGATACTAAA
1903	AGATTTTTAATATGATACTAAAA
1904	GATTTTTAATATGATACTAAAAG
1905	ATTTTTAATATGATACTAAAAGA
1906	TTTTTAATATGATACTAAAAGAA
1907	TTTTAATATGATACTAAAAGAAC
1908	TTTAATATGATACTAAAAGAACA
1909	TTAATATGATACTAAAAGAACAA
1910	TAATATGATACTAAAAGAACAAT
1911	AATATGATACTAAAAGAACAATC

Fig. 27 cont'd (Sheet 33 of 84)

ID	SEQUENCE
1912	ATATGATACTAAAAGAACAATCA
1913	TATGATACTAAAAGAACAATCAT
1914	ATGATACTAAAAGAACAATCATT
1915	TGATACTAAAAGAACAATCATTA
1916	GATACTAAAAGAACAATCATTAG
1917	ATACTAAAAGAACAATCATTAGC
1918	TACTAAAAGAACAATCATTAGCA
1919	ACTAAAAGAACAATCATTAGCAG
1920	CTAAAAGAACAATCATTAGCAGC
1921	TAAAAGAACAATCATTAGCAGCA
1922	AAAAGAACAATCATTAGCAGCAG
1923	AAAGAACAATCATTAGCAGCAGA
1924	AAGAACAATCATTAGCAGCAGAA
1925	AGAACAATCATTAGCAGCAGAAA
1926	GAACAATCATTAGCAGCAGAAAG
1927	AACAATCATTAGCAGCAGAAAGT
1928	ACAATCATTAGCAGCAGAAAGTA
1929	CAATCATTAGCAGCAGAAAGTAA
1930	AATCATTAGCAGCAGAAAGTAAA
1931	ATCATTAGCAGCAGAAAGTAAAA
1932	TCATTAGCAGCAGAAAGTAAAAC
1933	CATTAGCAGCAGAAAGTAAAACT
1934	ATTAGCAGCAGAAAGTAAAACTG
1935	TTAGCAGCAGAAAGTAAAACTGT
1936	TAGCAGCAGAAAGTAAAACTGTA
1937	AGCAGCAGAAAGTAAAACTGTAC
1938	GCAGCAGAAAGTAAAACTGTACT
1939	CAGCAGAAAGTAAAACTGTACTA
1940	AGCAGAAAGTAAAACTGTACTAC
1941	GCAGAAAGTAAAACTGTACTACA
1942	CAGAAAGTAAAACTGTACTACAG
1943	AGAAAGTAAAACTGTACTACAGG
1944	GAAAGTAAAACTGTACTACAGGA
1945	AAAGTAAAACTGTACTACAGGAA
1946	AAGTAAAACTGTACTACAGGAAT
1947	AGTAAAACTGTACTACAGGAATT
1948	GTAAAACTGTACTACAGGAATTG
1949	TAAAACTGTACTACAGGAATTGA
1950	AAAACTGTACTACAGGAATTGAT
1951	AAACTGTACTACAGGAATTGATT
1952	AACTGTACTACAGGAATTGATTA
1953	ACTGTACTACAGGAATTGATTAA
1954	CTGTACTACAGGAATTGATTAAT
1955	TGTACTACAGGAATTGATTAATG
1956	GTACTACAGGAATTGATTAATGT
1957	TACTACAGGAATTGATTAATGTA
1958	ACTACAGGAATTGATTAATGTAC
1959	CTACAGGAATTGATTAATGTACT
1960	TACAGGAATTGATTAATGTACTC
1961	ACAGGAATTGATTAATGTACTCA
1962	CAGGAATTGATTAATGTACTCAA
1963	AGGAATTGATTAATGTACTCAAG
1964	GGAATTGATTAATGTACTCAAGA
1965	GAATTGATTAATGTACTCAAGAC
1966	AATTGATTAATGTACTCAAGACT
1967	ATTGATTAATGTACTCAAGACTG
1968	TTGATTAATGTACTCAAGACTGA
1969	TGATTAATGTACTCAAGACTGAT

Fig. 27 cont'd (Sheet 34 of 84)

ID	SEQUENCE
1970	GATTAATGTACTCAAGACTGATC
1971	ATTAATGTACTCAAGACTGATCT
1972	TTAATGTACTCAAGACTGATCTT
1973	TAATGTACTCAAGACTGATCTTC
1974	AATGTACTCAAGACTGATCTTCT
1975	ATGTACTCAAGACTGATCTTCTA
1976	TGTACTCAAGACTGATCTTCTAA
1977	GTACTCAAGACTGATCTTCTAAG
1978	TACTCAAGACTGATCTTCTAAGT
1979	ACTCAAGACTGATCTTCTAAGTT
1980	CTCAAGACTGATCTTCTAAGTTC
1981	TCAAGACTGATCTTCTAAGTTCA
1982	CAAGACTGATCTTCTAAGTTCAC
1983	AAGACTGATCTTCTAAGTTCACT
1984	AGACTGATCTTCTAAGTTCACTG
1985	GACTGATCTTCTAAGTTCACTGG
1986	ACTGATCTTCTAAGTTCACTGGA
1987	CTGATCTTCTAAGTTCACTGGAA
1988	TGATCTTCTAAGTTCACTGGAAA
1989	GATCTTCTAAGTTCACTGGAAAT
1990	ATCTTCTAAGTTCACTGGAAATG
1991	TCTTCTAAGTTCACTGGAAATGA
1992	CTTCTAAGTTCACTGGAAATGAT
1993	TTCTAAGTTCACTGGAAATGATT
1994	TCTAAGTTCACTGGAAATGATTT
1995	CTAAGTTCACTGGAAATGATTTT
1996	TAAGTTCACTGGAAATGATTTTA
1997	AAGTTCACTGGAAATGATTTTAT
1998	AGTTCACTGGAAATGATTTTATC
1999	GTTCACTGGAAATGATTTTATCC
2000	TTCACTGGAAATGATTTTATCCC
2001	TCACTGGAAATGATTTTATCCCC
2002	CACTGGAAATGATTTTATCCCCA
2003	ACTGGAAATGATTTTATCCCCAA
2004	CTGGAAATGATTTTATCCCCAAC
2005	TGGAAATGATTTTATCCCCAACT
2006	GGAAATGATTTTATCCCCAACTG
2007	GAAATGATTTTATCCCCAACTGT
2008	AAATGATTTTATCCCCAACTGTG
2009	AATGATTTTATCCCCAACTGTGG
2010	ATGATTTTATCCCCAACTGTGGT
2011	TGATTTTATCCCCAACTGTGGTG
2012	GATTTTATCCCCAACTGTGGTGT
2013	ATTTTATCCCCAACTGTGGTGTC
2014	TTTTATCCCCAACTGTGGTGTCT
2015	TTTATCCCCAACTGTGGTGTCTA
2016	TTATCCCCAACTGTGGTGTCTAT
2017	TATCCCCAACTGTGGTGTCTATA
2018	ATCCCCAACTGTGGTGTCTATAC
2019	TCCCCAACTGTGGTGTCTATACT
2020	CCCCAACTGTGGTGTCTATACTG
2021	CCCAACTGTGGTGTCTATACTGA
2022	CCAACTGTGGTGTCTATACTGAA
2023	CAACTGTGGTGTCTATACTGAAA
2024	AACTGTGGTGTCTATACTGAAAA
2025	ACTGTGGTGTCTATACTGAAAAT
2026	CTGTGGTGTCTATACTGAAAATC
2027	TGTGGTGTCTATACTGAAAATCA

Fig. 27 cont'd (Sheet 35 of 84)

ID	SEQUENCE
2028	GTGGTGTCTATACTGAAAATCAA
2029	TGGTGTCTATACTGAAAATCAAT
2030	GGTGTCTATACTGAAAATCAATA
2031	GTGTCTATACTGAAAATCAATAG
2032	TGTCTATACTGAAAATCAATAGT
2033	GTCTATACTGAAAATCAATAGTC
2034	TCTATACTGAAAATCAATAGTCA
2035	CTATACTGAAAATCAATAGTCAA
2036	TATACTGAAAATCAATAGTCAAC
2037	ATACTGAAAATCAATAGTCAACT
2038	TACTGAAAATCAATAGTCAACTA
2039	ACTGAAAATCAATAGTCAACTAA
2040	CTGAAAATCAATAGTCAACTAAA
2041	TGAAAATCAATAGTCAACTAAAG
2042	GAAAATCAATAGTCAACTAAAGC
2043	AAAATCAATAGTCAACTAAAGCA
2044	AAATCAATAGTCAACTAAAGCAT
2045	AATCAATAGTCAACTAAAGCATA
2046	ATCAATAGTCAACTAAAGCATAT
2047	TCAATAGTCAACTAAAGCATATT
2048	CAATAGTCAACTAAAGCATATTT
2049	AATAGTCAACTAAAGCATATTTT
2050	ATAGTCAACTAAAGCATATTTTC
2051	TAGTCAACTAAAGCATATTTTCA
2052	AGTCAACTAAAGCATATTTTCAA
2053	GTCAACTAAAGCATATTTTCAAG
2054	TCAACTAAAGCATATTTTCAAGA
2055	CAACTAAAGCATATTTTCAAGAC
2056	AACTAAAGCATATTTTCAAGACT
2057	ACTAAAGCATATTTTCAAGACTT
2058	CTAAAGCATATTTTCAAGACTTC
2059	TAAAGCATATTTTCAAGACTTCA
2060	AAAGCATATTTTCAAGACTTCAT
2061	AAGCATATTTTCAAGACTTCATT
2062	AGCATATTTTCAAGACTTCATTG
2063	GCATATTTTCAAGACTTCATTGA
2064	CATATTTTCAAGACTTCATTGAC
2065	ATATTTTCAAGACTTCATTGACA
2066	TATTTTCAAGACTTCATTGACAG
2067	ATTTTCAAGACTTCATTGACAGT
2068	TTTTCAAGACTTCATTGACAGTG
2069	TTTCAAGACTTCATTGACAGTGG
2070	TTCAAGACTTCATTGACAGTGGC
2071	TCAAGACTTCATTGACAGTGGCC
2072	CAAGACTTCATTGACAGTGGCCG
2073	AAGACTTCATTGACAGTGGCCGA
2074	AGACTTCATTGACAGTGGCCGAT
2075	GACTTCATTGACAGTGGCCGATA
2076	ACTTCATTGACAGTGGCCGATAA
2077	CTTCATTGACAGTGGCCGATAAG
2078	TTCATTGACAGTGGCCGATAAGA
2079	TCATTGACAGTGGCCGATAAGAT
2080	CATTGACAGTGGCCGATAAGATA
2081	ATTGACAGTGGCCGATAAGATAG
2082	TTGACAGTGGCCGATAAGATAGA
2083	TGACAGTGGCCGATAAGATAGAA
2084	GACAGTGGCCGATAAGATAGAAG
2085	ACAGTGGCCGATAAGATAGAAGA

Fig. 27 cont'd (Sheet 36 of 84)

ID	SEQUENCE
2086	CAGTGGCCGATAAGATAGAAGAT
2087	AGTGGCCGATAAGATAGAAGATC
2088	GTGGCCGATAAGATAGAAGATCA
2089	TGGCCGATAAGATAGAAGATCAA
2090	GGCCGATAAGATAGAAGATCAAA
2091	GCCGATAAGATAGAAGATCAAAA
2092	CCGATAAGATAGAAGATCAAAAA
2093	CGATAAGATAGAAGATCAAAAAA
2094	GATAAGATAGAAGATCAAAAAAA
2095	ATAAGATAGAAGATCAAAAAAAG
2096	TAAGATAGAAGATCAAAAAAAGG
2097	AAGATAGAAGATCAAAAAAAGGA
2098	AGATAGAAGATCAAAAAAAGGAA
2099	GATAGAAGATCAAAAAAAGGAAC
2100	ATAGAAGATCAAAAAAAGGAACT
2101	TAGAAGATCAAAAAAAGGAACTA
2102	AGAAGATCAAAAAAAGGAACTAG
2103	GAAGATCAAAAAAAGGAACTAGA
2104	AAGATCAAAAAAAGGAACTAGAT
2105	AGATCAAAAAAAGGAACTAGATG
2106	GATCAAAAAAAGGAACTAGATGG
2107	ATCAAAAAAAGGAACTAGATGGC
2108	TCAAAAAAAGGAACTAGATGGCT
2109	CAAAAAAAGGAACTAGATGGCTT
2110	AAAAAAAGGAACTAGATGGCTTT
2111	AAAAAAGGAACTAGATGGCTTTC
2112	AAAAAGGAACTAGATGGCTTTCT
2113	AAAAGGAACTAGATGGCTTTCTC
2114	AAAGGAACTAGATGGCTTTCTCA
2115	AAGGAACTAGATGGCTTTCTCAG
2116	AGGAACTAGATGGCTTTCTCAGT
2117	GGAACTAGATGGCTTTCTCAGTA
2118	GAACTAGATGGCTTTCTCAGTAT
2119	AACTAGATGGCTTTCTCAGTATA
2120	ACTAGATGGCTTTCTCAGTATAC
2121	CTAGATGGCTTTCTCAGTATACT
2122	TAGATGGCTTTCTCAGTATACTG
2123	AGATGGCTTTCTCAGTATACTGT
2124	GATGGCTTTCTCAGTATACTGTG
2125	ATGGCTTTCTCAGTATACTGTGT
2126	TGGCTTTCTCAGTATACTGTGTA
2127	GGCTTTCTCAGTATACTGTGTAA
2128	GCTTTCTCAGTATACTGTGTAAC
2129	CTTTCTCAGTATACTGTGTAACA
2130	TTTCTCAGTATACTGTGTAACAA
2131	TTCTCAGTATACTGTGTAACAAT
2132	TCTCAGTATACTGTGTAACAATC
2133	CTCAGTATACTGTGTAACAATCT
2134	TCAGTATACTGTGTAACAATCTA
2135	CAGTATACTGTGTAACAATCTAC
2136	AGTATACTGTGTAACAATCTACA
2137	GTATACTGTGTAACAATCTACAT
2138	TATACTGTGTAACAATCTACATG
2139	ATACTGTGTAACAATCTACATGA
2140	TACTGTGTAACAATCTACATGAA
2141	ACTGTGTAACAATCTACATGAAC
2142	CTGTGTAACAATCTACATGAACT
2143	TGTGTAACAATCTACATGAACTA

Fig. 27 cont'd (Sheet 37 of 84)

ID	SEQUENCE
2144	GTGTAACAATCTACATGAACTAC
2145	TGTAACAATCTACATGAACTACA
2146	GTAACAATCTACATGAACTACAA
2147	TAACAATCTACATGAACTACAAG
2148	AACAATCTACATGAACTACAAGA
2149	ACAATCTACATGAACTACAAGAA
2150	CAATCTACATGAACTACAAGAAA
2151	AATCTACATGAACTACAAGAAAA
2152	ATCTACATGAACTACAAGAAAAT
2153	TCTACATGAACTACAAGAAAATA
2154	CTACATGAACTACAAGAAAATAC
2155	TACATGAACTACAAGAAAATACC
2156	ACATGAACTACAAGAAAATACCA
2157	CATGAACTACAAGAAAATACCAT
2158	ATGAACTACAAGAAAATACCATT
2159	TGAACTACAAGAAAATACCATTT
2160	GAACTACAAGAAAATACCATTTG
2161	AACTACAAGAAAATACCATTTGT
2162	ACTACAAGAAAATACCATTTGTT
2163	CTACAAGAAAATACCATTTGTTC
2164	TACAAGAAAATACCATTTGTTCC
2165	ACAAGAAAATACCATTTGTTCCT
2166	CAAGAAAATACCATTTGTTCCTT
2167	AAGAAAATACCATTTGTTCCTTG
2168	AGAAAATACCATTTGTTCCTTGG
2169	GAAAATACCATTTGTTCCTTGGT
2170	AAAATACCATTTGTTCCTTGGTT
2171	AAATACCATTTGTTCCTTGGTTG
2172	AATACCATTTGTTCCTTGGTTGA
2173	ATACCATTTGTTCCTTGGTTGAG
2174	TACCATTTGTTCCTTGGTTGAGT
2175	ACCATTTGTTCCTTGGTTGAGTC
2176	CCATTTGTTCCTTGGTTGAGTCA
2177	CATTTGTTCCTTGGTTGAGTCAC
2178	ATTTGTTCCTTGGTTGAGTCACA
2179	TTTGTTCCTTGGTTGAGTCACAA
2180	TTGTTCCTTGGTTGAGTCACAAA
2181	TGTTCCTTGGTTGAGTCACAAAA
2182	GTTCCTTGGTTGAGTCACAAAAG
2183	TTCCTTGGTTGAGTCACAAAAGC
2184	TCCTTGGTTGAGTCACAAAAGCA
2185	CCTTGGTTGAGTCACAAAAGCAA
2186	CTTGGTTGAGTCACAAAAGCAAT
2187	TTGGTTGAGTCACAAAAGCAATG
2188	TGGTTGAGTCACAAAAGCAATGT
2189	GGTTGAGTCACAAAAGCAATGTG
2190	GTTGAGTCACAAAAGCAATGTGG
2191	TTGAGTCACAAAAGCAATGTGGA
2192	TGAGTCACAAAAGCAATGTGGAA
2193	GAGTCACAAAAGCAATGTGGAAA
2194	AGTCACAAAAGCAATGTGGAAAC
2195	GTCACAAAAGCAATGTGGAAACC
2196	TCACAAAAGCAATGTGGAAACCT
2197	CACAAAAGCAATGTGGAAACCTA
2198	ACAAAAGCAATGTGGAAACCTAA
2199	CAAAAGCAATGTGGAAACCTAAC
2200	AAAAGCAATGTGGAAACCTAACT
2201	AAAGCAATGTGGAAACCTAACTG

Fig. 27 cont'd (Sheet 38 of 84)

ID	SEQUENCE
2202	AAGCAATGTGGAAACCTAACTGA
2203	AGCAATGTGGAAACCTAACTGAA
2204	GCAATGTGGAAACCTAACTGAAG
2205	CAATGTGGAAACCTAACTGAAGA
2206	AATGTGGAAACCTAACTGAAGAC
2207	ATGTGGAAACCTAACTGAAGACC
2208	TGTGGAAACCTAACTGAAGACCT
2209	GTGGAAACCTAACTGAAGACCTG
2210	TGGAAACCTAACTGAAGACCTGA
2211	GGAAACCTAACTGAAGACCTGAA
2212	GAAACCTAACTGAAGACCTGAAG
2213	AAACCTAACTGAAGACCTGAAGA
2214	AACCTAACTGAAGACCTGAAGAC
2215	ACCTAACTGAAGACCTGAAGACA
2216	CCTAACTGAAGACCTGAAGACAA
2217	CTAACTGAAGACCTGAAGACAAT
2218	TAACTGAAGACCTGAAGACAATA
2219	AACTGAAGACCTGAAGACAATAA
2220	ACTGAAGACCTGAAGACAATAAA
2221	CTGAAGACCTGAAGACAATAAAG
2222	TGAAGACCTGAAGACAATAAAGC
2223	GAAGACCTGAAGACAATAAAGCA
2224	AAGACCTGAAGACAATAAAGCAG
2225	AGACCTGAAGACAATAAAGCAGA
2226	GACCTGAAGACAATAAAGCAGAC
2227	ACCTGAAGACAATAAAGCAGACC
2228	CCTGAAGACAATAAAGCAGACCC
2229	CTGAAGACAATAAAGCAGACCCA
2230	TGAAGACAATAAAGCAGACCCAT
2231	GAAGACAATAAAGCAGACCCATT
2232	AAGACAATAAAGCAGACCCATTC
2233	AGACAATAAAGCAGACCCATTCC
2234	GACAATAAAGCAGACCCATTCCC
2235	ACAATAAAGCAGACCCATTCCCA
2236	CAATAAAGCAGACCCATTCCCAG
2237	AATAAAGCAGACCCATTCCCAGG
2238	ATAAAGCAGACCCATTCCCAGGA
2239	TAAAGCAGACCCATTCCCAGGAA
2240	AAAGCAGACCCATTCCCAGGAAC
2241	AAGCAGACCCATTCCCAGGAACT
2242	AGCAGACCCATTCCCAGGAACTT
2243	GCAGACCCATTCCCAGGAACTTT
2244	CAGACCCATTCCCAGGAACTTTG
2245	AGACCCATTCCCAGGAACTTTGC
2246	GACCCATTCCCAGGAACTTTGCA
2247	ACCCATTCCCAGGAACTTTGCAA
2248	CCCATTCCCAGGAACTTTGCAAG
2249	CCATTCCCAGGAACTTTGCAAGT
2250	CATTCCCAGGAACTTTGCAAGTT
2251	ATTCCCAGGAACTTTGCAAGTTA
2252	TTCCCAGGAACTTTGCAAGTTAA
2253	TCCCAGGAACTTTGCAAGTTAAT
2254	CCCAGGAACTTTGCAAGTTAATG
2255	CCAGGAACTTTGCAAGTTAATGA
2256	CAGGAACTTTGCAAGTTAATGAA
2257	AGGAACTTTGCAAGTTAATGAAT
2258	GGAACTTTGCAAGTTAATGAATC
2259	GAACTTTGCAAGTTAATGAATCT

Fig. 27 cont'd (Sheet 39 of 84)

ID	SEQUENCE
2260	AACTTTGCAAGTTAATGAATCTT
2261	ACTTTGCAAGTTAATGAATCTTT
2262	CTTTGCAAGTTAATGAATCTTTG
2263	TTTGCAAGTTAATGAATCTTTGG
2264	TTGCAAGTTAATGAATCTTTGGA
2265	TGCAAGTTAATGAATCTTTGGAC
2266	GCAAGTTAATGAATCTTTGGACA
2267	CAAGTTAATGAATCTTTGGACAG
2268	AAGTTAATGAATCTTTGGACAGA
2269	AGTTAATGAATCTTTGGACAGAG
2270	GTTAATGAATCTTTGGACAGAGA
2271	TTAATGAATCTTTGGACAGAGAG
2272	TAATGAATCTTTGGACAGAGAGA
2273	AATGAATCTTTGGACAGAGAGAT
2274	ATGAATCTTTGGACAGAGAGATT
2275	TGAATCTTTGGACAGAGAGATTC
2276	GAATCTTTGGACAGAGAGATTCT
2277	AATCTTTGGACAGAGAGATTCTG
2278	ATCTTTGGACAGAGAGATTCTGT
2279	TCTTTGGACAGAGAGATTCTGTG
2280	CTTTGGACAGAGAGATTCTGTGC
2281	TTTGGACAGAGAGATTCTGTGCT
2282	TTGGACAGAGAGATTCTGTGCTT
2283	TGGACAGAGAGATTCTGTGCTTT
2284	GGACAGAGAGATTCTGTGCTTTG
2285	GACAGAGAGATTCTGTGCTTTGG
2286	ACAGAGAGATTCTGTGCTTTGGA
2287	CAGAGAGATTCTGTGCTTTGGAG
2288	AGAGAGATTCTGTGCTTTGGAGG
2289	GAGAGATTCTGTGCTTTGGAGGA
2290	AGAGATTCTGTGCTTTGGAGGAA
2291	GAGATTCTGTGCTTTGGAGGAAA
2292	AGATTCTGTGCTTTGGAGGAAAA
2293	GATTCTGTGCTTTGGAGGAAAAG
2294	ATTCTGTGCTTTGGAGGAAAAGT
2295	TTCTGTGCTTTGGAGGAAAAGTG
2296	TCTGTGCTTTGGAGGAAAAGTGT
2297	CTGTGCTTTGGAGGAAAAGTGTG
2298	TGTGCTTTGGAGGAAAAGTGTGA
2299	GTGCTTTGGAGGAAAAGTGTGAA
2300	TGCTTTGGAGGAAAAGTGTGAAA
2301	GCTTTGGAGGAAAAGTGTGAAAA
2302	CTTTGGAGGAAAAGTGTGAAAAT
2303	TTTGGAGGAAAAGTGTGAAAATA
2304	TTGGAGGAAAAGTGTGAAAATAT
2305	TGGAGGAAAAGTGTGAAAATATA
2306	GGAGGAAAAGTGTGAAAATATAC
2307	GAGGAAAAGTGTGAAAATATACA
2308	AGGAAAAGTGTGAAAATATACAG
2309	GGAAAAGTGTGAAAATATACAGA
2310	GAAAAGTGTGAAAATATACAGAA
2311	AAAAGTGTGAAAATATACAGAAA
2312	AAAGTGTGAAAATATACAGAAAC
2313	AAGTGTGAAAATATACAGAAACC
2314	AGTGTGAAAATATACAGAAACCA
2315	GTGTGAAAATATACAGAAACCAC
2316	TGTGAAAATATACAGAAACCACT
2317	GTGAAAATATACAGAAACCACTT

Fig. 27 cont'd (Sheet 40 of 84)

ID	SEQUENCE
2318	TGAAAATATACAGAAACCACTTA
2319	GAAAATATACAGAAACCACTTAG
2320	AAAATATACAGAAACCACTTAGT
2321	AAATATACAGAAACCACTTAGTA
2322	AATATACAGAAACCACTTAGTAG
2323	ATATACAGAAACCACTTAGTAGT
2324	TATACAGAAACCACTTAGTAGTG
2325	ATACAGAAACCACTTAGTAGTGT
2326	TACAGAAACCACTTAGTAGTGTC
2327	ACAGAAACCACTTAGTAGTGTCC
2328	CAGAAACCACTTAGTAGTGTCCA
2329	AGAAACCACTTAGTAGTGTCCAG
2330	GAAACCACTTAGTAGTGTCCAGG
2331	AAACCACTTAGTAGTGTCCAGGA
2332	AACCACTTAGTAGTGTCCAGGAA
2333	ACCACTTAGTAGTGTCCAGGAAA
2334	CCACTTAGTAGTGTCCAGGAAAA
2335	CACTTAGTAGTGTCCAGGAAAAT
2336	ACTTAGTAGTGTCCAGGAAAATA
2337	CTTAGTAGTGTCCAGGAAAATAT
2338	TTAGTAGTGTCCAGGAAAATATA
2339	TAGTAGTGTCCAGGAAAATATAC
2340	AGTAGTGTCCAGGAAAATATACA
2341	GTAGTGTCCAGGAAAATATACAG
2342	TAGTGTCCAGGAAAATATACAGC
2343	AGTGTCCAGGAAAATATACAGCA
2344	GTGTCCAGGAAAATATACAGCAG
2345	TGTCCAGGAAAATATACAGCAGA
2346	GTCCAGGAAAATATACAGCAGAA
2347	TCCAGGAAAATATACAGCAGAAA
2348	CCAGGAAAATATACAGCAGAAAT
2349	CAGGAAAATATACAGCAGAAATC
2350	AGGAAAATATACAGCAGAAATCT
2351	GGAAAATATACAGCAGAAATCTA
2352	GAAAATATACAGCAGAAATCTAA
2353	AAAATATACAGCAGAAATCTAAG
2354	AAATATACAGCAGAAATCTAAGG
2355	AATATACAGCAGAAATCTAAGGA
2356	ATATACAGCAGAAATCTAAGGAT
2357	TATACAGCAGAAATCTAAGGATA
2358	ATACAGCAGAAATCTAAGGATAT
2359	TACAGCAGAAATCTAAGGATATA
2360	ACAGCAGAAATCTAAGGATATAG
2361	CAGCAGAAATCTAAGGATATAGT
2362	AGCAGAAATCTAAGGATATAGTC
2363	GCAGAAATCTAAGGATATAGTCA
2364	CAGAAATCTAAGGATATAGTCAA
2365	AGAAATCTAAGGATATAGTCAAC
2366	GAAATCTAAGGATATAGTCAACA
2367	AAATCTAAGGATATAGTCAACAA
2368	AATCTAAGGATATAGTCAACAAA
2369	ATCTAAGGATATAGTCAACAAAA
2370	TCTAAGGATATAGTCAACAAAAT
2371	CTAAGGATATAGTCAACAAAATG
2372	TAAGGATATAGTCAACAAAATGA
2373	AAGGATATAGTCAACAAAATGAC
2374	AGGATATAGTCAACAAAATGACT
2375	GGATATAGTCAACAAAATGACTT

Fig. 27 cont'd (Sheet 41 of 84)

ID	SEQUENCE
2376	GATATAGTCAACAAAATGACTTT
2377	ATATAGTCAACAAAATGACTTTT
2378	TATAGTCAACAAAATGACTTTTC
2379	ATAGTCAACAAAATGACTTTTCA
2380	TAGTCAACAAAATGACTTTTCAC
2381	AGTCAACAAAATGACTTTTCACA
2382	GTCAACAAAATGACTTTTCACAG
2383	TCAACAAAATGACTTTTCACAGT
2384	CAACAAAATGACTTTTCACAGTC
2385	AACAAAATGACTTTTCACAGTCA
2386	ACAAAATGACTTTTCACAGTCAA
2387	CAAAATGACTTTTCACAGTCAAA
2388	AAAATGACTTTTCACAGTCAAAA
2389	AAATGACTTTTCACAGTCAAAAA
2390	AATGACTTTTCACAGTCAAAAAT
2391	ATGACTTTTCACAGTCAAAAATT
2392	TGACTTTTCACAGTCAAAAATTT
2393	GACTTTTCACAGTCAAAAATTTT
2394	ACTTTTCACAGTCAAAAATTTTG
2395	CTTTTCACAGTCAAAAATTTTGT
2396	TTTTCACAGTCAAAAATTTTGTG
2397	TTTCACAGTCAAAAATTTTGTGC
2398	TTCACAGTCAAAAATTTTGTGCT
2399	TCACAGTCAAAAATTTTGTGCTG
2400	CACAGTCAAAAATTTTGTGCTGA
2401	ACAGTCAAAAATTTTGTGCTGAT
2402	CAGTCAAAAATTTTGTGCTGATT
2403	AGTCAAAAATTTTGTGCTGATTC
2404	GTCAAAAATTTTGTGCTGATTCT
2405	TCAAAAATTTTGTGCTGATTCTG
2406	CAAAAATTTTGTGCTGATTCTGA
2407	AAAAATTTTGTGCTGATTCTGAT
2408	AAAATTTTGTGCTGATTCTGATG
2409	AAATTTTGTGCTGATTCTGATGG
2410	AATTTTGTGCTGATTCTGATGGC
2411	ATTTTGTGCTGATTCTGATGGCT
2412	TTTTGTGCTGATTCTGATGGCTT
2413	TTTGTGCTGATTCTGATGGCTTC
2414	TTGTGCTGATTCTGATGGCTTCT
2415	TGTGCTGATTCTGATGGCTTCTC
2416	GTGCTGATTCTGATGGCTTCTCA
2417	TGCTGATTCTGATGGCTTCTCAC
2418	GCTGATTCTGATGGCTTCTCACA
2419	CTGATTCTGATGGCTTCTCACAG
2420	TGATTCTGATGGCTTCTCACAGG
2421	GATTCTGATGGCTTCTCACAGGA
2422	ATTCTGATGGCTTCTCACAGGAA
2423	TTCTGATGGCTTCTCACAGGAAC
2424	TCTGATGGCTTCTCACAGGAACT
2425	CTGATGGCTTCTCACAGGAACTC
2426	TGATGGCTTCTCACAGGAACTCA
2427	GATGGCTTCTCACAGGAACTCAG
2428	ATGGCTTCTCACAGGAACTCAGA
2429	TGGCTTCTCACAGGAACTCAGAA
2430	GGCTTCTCACAGGAACTCAGAAA
2431	GCTTCTCACAGGAACTCAGAAAT
2432	CTTCTCACAGGAACTCAGAAATT
2433	TTCTCACAGGAACTCAGAAATTT

Fig. 27 cont'd (Sheet 42 of 84)

ID	SEQUENCE
2434	TCTCACAGGAACTCAGAAATTTT
2435	CTCACAGGAACTCAGAAATTTTA
2436	TCACAGGAACTCAGAAATTTTAA
2437	CACAGGAACTCAGAAATTTTAAC
2438	ACAGGAACTCAGAAATTTTAACC
2439	CAGGAACTCAGAAATTTTAACCA
2440	AGGAACTCAGAAATTTTAACCAA
2441	GGAACTCAGAAATTTTAACCAAG
2442	GAACTCAGAAATTTTAACCAAGA
2443	AACTCAGAAATTTTAACCAAGAA
2444	ACTCAGAAATTTTAACCAAGAAG
2445	CTCAGAAATTTTAACCAAGAAGG
2446	TCAGAAATTTTAACCAAGAAGGT
2447	CAGAAATTTTAACCAAGAAGGTA
2448	AGAAATTTTAACCAAGAAGGTAC
2449	GAAATTTTAACCAAGAAGGTACA
2450	AAATTTTAACCAAGAAGGTACAA
2451	AATTTTAACCAAGAAGGTACAAA
2452	ATTTTAACCAAGAAGGTACAAAA
2453	TTTTAACCAAGAAGGTACAAAAT
2454	TTTAACCAAGAAGGTACAAAATT
2455	TTAACCAAGAAGGTACAAAATTG
2456	TAACCAAGAAGGTACAAAATTGG
2457	AACCAAGAAGGTACAAAATTGGT
2458	ACCAAGAAGGTACAAAATTGGTT
2459	CCAAGAAGGTACAAAATTGGTTG
2460	CAAGAAGGTACAAAATTGGTTGA
2461	AAGAAGGTACAAAATTGGTTGAA
2462	AGAAGGTACAAAATTGGTTGAAG
2463	GAAGGTACAAAATTGGTTGAAGA
2464	AAGGTACAAAATTGGTTGAAGAA
2465	AGGTACAAAATTGGTTGAAGAAT
2466	GGTACAAAATTGGTTGAAGAATC
2467	GTACAAAATTGGTTGAAGAATCT
2468	TACAAAATTGGTTGAAGAATCTG
2469	ACAAAATTGGTTGAAGAATCTGT
2470	CAAAATTGGTTGAAGAATCTGTG
2471	AAAATTGGTTGAAGAATCTGTGA
2472	AAATTGGTTGAAGAATCTGTGAA
2473	AATTGGTTGAAGAATCTGTGAAA
2474	ATTGGTTGAAGAATCTGTGAAAC
2475	TTGGTTGAAGAATCTGTGAAACA
2476	TGGTTGAAGAATCTGTGAAACAC
2477	GGTTGAAGAATCTGTGAAACACT
2478	GTTGAAGAATCTGTGAAACACTC
2479	TTGAAGAATCTGTGAAACACTCT
2480	TGAAGAATCTGTGAAACACTCTG
2481	GAAGAATCTGTGAAACACTCTGA
2482	AAGAATCTGTGAAACACTCTGAT
2483	AGAATCTGTGAAACACTCTGATA
2484	GAATCTGTGAAACACTCTGATAA
2485	AATCTGTGAAACACTCTGATAAA
2486	ATCTGTGAAACACTCTGATAAAC
2487	TCTGTGAAACACTCTGATAAACT
2488	CTGTGAAACACTCTGATAAACTC
2489	TGTGAAACACTCTGATAAACTCA
2490	GTGAAACACTCTGATAAACTCAA
2491	TGAAACACTCTGATAAACTCAAT

Fig. 27 cont'd (Sheet 43 of 84)

ID	SEQUENCE
2492	GAAACACTCTGATAAACTCAATG
2493	AAACACTCTGATAAACTCAATGG
2494	AACACTCTGATAAACTCAATGGC
2495	ACACTCTGATAAACTCAATGGCA
2496	CACTCTGATAAACTCAATGGCAA
2497	ACTCTGATAAACTCAATGGCAAC
2498	CTCTGATAAACTCAATGGCAACC
2499	TCTGATAAACTCAATGGCAACCT
2500	CTGATAAACTCAATGGCAACCTG
2501	TGATAAACTCAATGGCAACCTGG
2502	GATAAACTCAATGGCAACCTGGA
2503	ATAAACTCAATGGCAACCTGGAA
2504	TAAACTCAATGGCAACCTGGAAA
2505	AAACTCAATGGCAACCTGGAAAA
2506	AACTCAATGGCAACCTGGAAAAA
2507	ACTCAATGGCAACCTGGAAAAAA
2508	CTCAATGGCAACCTGGAAAAAAT
2509	TCAATGGCAACCTGGAAAAAATA
2510	CAATGGCAACCTGGAAAAAATAT
2511	AATGGCAACCTGGAAAAAATATC
2512	ATGGCAACCTGGAAAAAATATCT
2513	TGGCAACCTGGAAAAAATATCTC
2514	GGCAACCTGGAAAAAATATCTCA
2515	GCAACCTGGAAAAAATATCTCAA
2516	CAACCTGGAAAAAATATCTCAAG
2517	AACCTGGAAAAAATATCTCAAGA
2518	ACCTGGAAAAAATATCTCAAGAG
2519	CCTGGAAAAAATATCTCAAGAGA
2520	CTGGAAAAAATATCTCAAGAGAC
2521	TGGAAAAAATATCTCAAGAGACT
2522	GGAAAAAATATCTCAAGAGACTG
2523	GAAAAAATATCTCAAGAGACTGA
2524	AAAAAATATCTCAAGAGACTGAA
2525	AAAAATATCTCAAGAGACTGAAC
2526	AAAATATCTCAAGAGACTGAACA
2527	AAATATCTCAAGAGACTGAACAG
2528	AATATCTCAAGAGACTGAACAGA
2529	ATATCTCAAGAGACTGAACAGAG
2530	TATCTCAAGAGACTGAACAGAGA
2531	ATCTCAAGAGACTGAACAGAGAT
2532	TCTCAAGAGACTGAACAGAGATG
2533	CTCAAGAGACTGAACAGAGATGT
2534	TCAAGAGACTGAACAGAGATGTG
2535	CAAGAGACTGAACAGAGATGTGA
2536	AAGAGACTGAACAGAGATGTGAA
2537	AGAGACTGAACAGAGATGTGAAT
2538	GAGACTGAACAGAGATGTGAATC
2539	AGACTGAACAGAGATGTGAATCT
2540	GACTGAACAGAGATGTGAATCTC
2541	ACTGAACAGAGATGTGAATCTCT
2542	CTGAACAGAGATGTGAATCTCTG
2543	TGAACAGAGATGTGAATCTCTGA
2544	GAACAGAGATGTGAATCTCTGAA
2545	AACAGAGATGTGAATCTCTGAAC
2546	ACAGAGATGTGAATCTCTGAACA
2547	CAGAGATGTGAATCTCTGAACAC
2548	AGAGATGTGAATCTCTGAACACA
2549	GAGATGTGAATCTCTGAACACAA

Fig. 27 cont'd (Sheet 44 of 84)

ID	SEQUENCE
2550	AGATGTGAATCTCTGAACACAAG
2551	GATGTGAATCTCTGAACACAAGA
2552	ATGTGAATCTCTGAACACAAGAA
2553	TGTGAATCTCTGAACACAAGAAC
2554	GTGAATCTCTGAACACAAGAACA
2555	TGAATCTCTGAACACAAGAACAG
2556	GAATCTCTGAACACAAGAACAGT
2557	AATCTCTGAACACAAGAACAGTT
2558	ATCTCTGAACACAAGAACAGTTT
2559	TCTCTGAACACAAGAACAGTTTA
2560	CTCTGAACACAAGAACAGTTTAT
2561	TCTGAACACAAGAACAGTTTATT
2562	CTGAACACAAGAACAGTTTATTT
2563	TGAACACAAGAACAGTTTATTTT
2564	GAACACAAGAACAGTTTATTTTT
2565	AACACAAGAACAGTTTATTTTTC
2566	ACACAAGAACAGTTTATTTTTCT
2567	CACAAGAACAGTTTATTTTTCTG
2568	ACAAGAACAGTTTATTTTTCTGA
2569	CAAGAACAGTTTATTTTTCTGAA
2570	AAGAACAGTTTATTTTTCTGAAC
2571	AGAACAGTTTATTTTTCTGAACA
2572	GAACAGTTTATTTTTCTGAACAG
2573	AACAGTTTATTTTTCTGAACAGT
2574	ACAGTTTATTTTTCTGAACAGTG
2575	CAGTTTATTTTTCTGAACAGTGG
2576	AGTTTATTTTTCTGAACAGTGGG
2577	GTTTATTTTTCTGAACAGTGGGT
2578	TTTATTTTTCTGAACAGTGGGTA
2579	TTATTTTTCTGAACAGTGGGTAT
2580	TATTTTTCTGAACAGTGGGTATC
2581	ATTTTTCTGAACAGTGGGTATCT
2582	TTTTTCTGAACAGTGGGTATCTT
2583	TTTTCTGAACAGTGGGTATCTTC
2584	TTTCTGAACAGTGGGTATCTTCC
2585	TTCTGAACAGTGGGTATCTTCCT
2586	TCTGAACAGTGGGTATCTTCCTT
2587	CTGAACAGTGGGTATCTTCCTTA
2588	TGAACAGTGGGTATCTTCCTTAA
2589	GAACAGTGGGTATCTTCCTTAAA
2590	AACAGTGGGTATCTTCCTTAAAT
2591	ACAGTGGGTATCTTCCTTAAATG
2592	CAGTGGGTATCTTCCTTAAATGA
2593	AGTGGGTATCTTCCTTAAATGAA
2594	GTGGGTATCTTCCTTAAATGAAA
2595	TGGGTATCTTCCTTAAATGAAAG
2596	GGGTATCTTCCTTAAATGAAAGG
2597	GGTATCTTCCTTAAATGAAAGGG
2598	GTATCTTCCTTAAATGAAAGGGA
2599	TATCTTCCTTAAATGAAAGGGAA
2600	ATCTTCCTTAAATGAAAGGGAAC
2601	TCTTCCTTAAATGAAAGGGAACA
2602	CTTCCTTAAATGAAAGGGAACAG
2603	TTCCTTAAATGAAAGGGAACAGG
2604	TCCTTAAATGAAAGGGAACAGGA
2605	CCTTAAATGAAAGGGAACAGGAA
2606	CTTAAATGAAAGGGAACAGGAAC
2607	TTAAATGAAAGGGAACAGGAACT

Fig. 27 cont'd (Sheet 45 of 84)

ID	SEQUENCE
2608	TAAATGAAAGGGAACAGGAACTT
2609	AAATGAAAGGGAACAGGAACTTC
2610	AATGAAAGGGAACAGGAACTTCA
2611	ATGAAAGGGAACAGGAACTTCAC
2612	TGAAAGGGAACAGGAACTTCACA
2613	GAAAGGGAACAGGAACTTCACAA
2614	AAAGGGAACAGGAACTTCACAAC
2615	AAGGGAACAGGAACTTCACAACT
2616	AGGGAACAGGAACTTCACAACTT
2617	GGGAACAGGAACTTCACAACTTA
2618	GGAACAGGAACTTCACAACTTAT
2619	GAACAGGAACTTCACAACTTATT
2620	AACAGGAACTTCACAACTTATTG
2621	ACAGGAACTTCACAACTTATTGG
2622	CAGGAACTTCACAACTTATTGGA
2623	AGGAACTTCACAACTTATTGGAG
2624	GGAACTTCACAACTTATTGGAGG
2625	GAACTTCACAACTTATTGGAGGT
2626	AACTTCACAACTTATTGGAGGTT
2627	ACTTCACAACTTATTGGAGGTTG
2628	CTTCACAACTTATTGGAGGTTGT
2629	TTCACAACTTATTGGAGGTTGTA
2630	TCACAACTTATTGGAGGTTGTAA
2631	CACAACTTATTGGAGGTTGTAAG
2632	ACAACTTATTGGAGGTTGTAAGC
2633	CAACTTATTGGAGGTTGTAAGCC
2634	AACTTATTGGAGGTTGTAAGCCA
2635	ACTTATTGGAGGTTGTAAGCCAA
2636	CTTATTGGAGGTTGTAAGCCAAT
2637	TTATTGGAGGTTGTAAGCCAATG
2638	TATTGGAGGTTGTAAGCCAATGT
2639	ATTGGAGGTTGTAAGCCAATGTT
2640	TTGGAGGTTGTAAGCCAATGTTG
2641	TGGAGGTTGTAAGCCAATGTTGT
2642	GGAGGTTGTAAGCCAATGTTGTG
2643	GAGGTTGTAAGCCAATGTTGTGA
2644	AGGTTGTAAGCCAATGTTGTGAG
2645	GGTTGTAAGCCAATGTTGTGAGG
2646	GTTGTAAGCCAATGTTGTGAGGC
2647	TTGTAAGCCAATGTTGTGAGGCT
2648	TGTAAGCCAATGTTGTGAGGCTT
2649	GTAAGCCAATGTTGTGAGGCTTC
2650	TAAGCCAATGTTGTGAGGCTTCA
2651	AAGCCAATGTTGTGAGGCTTCAA
2652	AGCCAATGTTGTGAGGCTTCAAG
2653	GCCAATGTTGTGAGGCTTCAAGT
2654	CCAATGTTGTGAGGCTTCAAGTT
2655	CAATGTTGTGAGGCTTCAAGTTC
2656	AATGTTGTGAGGCTTCAAGTTCA
2657	ATGTTGTGAGGCTTCAAGTTCAG
2658	TGTTGTGAGGCTTCAAGTTCAGA
2659	GTTGTGAGGCTTCAAGTTCAGAC
2660	TTGTGAGGCTTCAAGTTCAGACA
2661	TGTGAGGCTTCAAGTTCAGACAT
2662	GTGAGGCTTCAAGTTCAGACATC
2663	TGAGGCTTCAAGTTCAGACATCA
2664	GAGGCTTCAAGTTCAGACATCAC
2665	AGGCTTCAAGTTCAGACATCACT

Fig. 27 cont'd (Sheet 46 of 84)

ID	SEQUENCE
2666	GGCTTCAAGTTCAGACATCACTG
2667	GCTTCAAGTTCAGACATCACTGA
2668	CTTCAAGTTCAGACATCACTGAG
2669	TTCAAGTTCAGACATCACTGAGA
2670	TCAAGTTCAGACATCACTGAGAA
2671	CAAGTTCAGACATCACTGAGAAA
2672	AAGTTCAGACATCACTGAGAAAT
2673	AGTTCAGACATCACTGAGAAATC
2674	GTTCAGACATCACTGAGAAATCA
2675	TTCAGACATCACTGAGAAATCAG
2676	TCAGACATCACTGAGAAATCAGA
2677	CAGACATCACTGAGAAATCAGAT
2678	AGACATCACTGAGAAATCAGATG
2679	GACATCACTGAGAAATCAGATGG
2680	ACATCACTGAGAAATCAGATGGA
2681	CATCACTGAGAAATCAGATGGAC
2682	ATCACTGAGAAATCAGATGGACG
2683	TCACTGAGAAATCAGATGGACGT
2684	CACTGAGAAATCAGATGGACGTA
2685	ACTGAGAAATCAGATGGACGTAA
2686	CTGAGAAATCAGATGGACGTAAG
2687	TGAGAAATCAGATGGACGTAAGG
2688	GAGAAATCAGATGGACGTAAGGC
2689	AGAAATCAGATGGACGTAAGGCA
2690	GAAATCAGATGGACGTAAGGCAG
2691	AAATCAGATGGACGTAAGGCAGC
2692	AATCAGATGGACGTAAGGCAGCT
2693	ATCAGATGGACGTAAGGCAGCTC
2694	TCAGATGGACGTAAGGCAGCTCA
2695	CAGATGGACGTAAGGCAGCTCAT
2696	AGATGGACGTAAGGCAGCTCATG
2697	GATGGACGTAAGGCAGCTCATGA
2698	ATGGACGTAAGGCAGCTCATGAG
2699	TGGACGTAAGGCAGCTCATGAGA
2700	GGACGTAAGGCAGCTCATGAGAA
2701	GACGTAAGGCAGCTCATGAGAAA
2702	ACGTAAGGCAGCTCATGAGAAAC
2703	CGTAAGGCAGCTCATGAGAAACA
2704	GTAAGGCAGCTCATGAGAAACAG
2705	TAAGGCAGCTCATGAGAAACAGC
2706	AAGGCAGCTCATGAGAAACAGCA
2707	AGGCAGCTCATGAGAAACAGCAT
2708	GGCAGCTCATGAGAAACAGCATA
2709	GCAGCTCATGAGAAACAGCATAA
2710	CAGCTCATGAGAAACAGCATAAC
2711	AGCTCATGAGAAACAGCATAACA
2712	GCTCATGAGAAACAGCATAACAT
2713	CTCATGAGAAACAGCATAACATT
2714	TCATGAGAAACAGCATAACATTT
2715	CATGAGAAACAGCATAACATTTT
2716	ATGAGAAACAGCATAACATTTTT
2717	TGAGAAACAGCATAACATTTTTC
2718	GAGAAACAGCATAACATTTTTCT
2719	AGAAACAGCATAACATTTTTCTT
2720	GAAACAGCATAACATTTTTCTTG
2721	AAACAGCATAACATTTTTCTTGA
2722	AACAGCATAACATTTTTCTTGAT
2723	ACAGCATAACATTTTTCTTGATC

Fig. 27 cont'd (Sheet 47 of 84)

ID	SEQUENCE
2724	CAGCATAACATTTTTCTTGATCA
2725	AGCATAACATTTTTCTTGATCAG
2726	GCATAACATTTTTCTTGATCAGA
2727	CATAACATTTTTCTTGATCAGAT
2728	ATAACATTTTTCTTGATCAGATG
2729	TAACATTTTTCTTGATCAGATGA
2730	AACATTTTTCTTGATCAGATGAC
2731	ACATTTTTCTTGATCAGATGACT
2732	CATTTTTCTTGATCAGATGACTA
2733	ATTTTTCTTGATCAGATGACTAT
2734	TTTTTCTTGATCAGATGACTATT
2735	TTTTCTTGATCAGATGACTATTG
2736	TTTCTTGATCAGATGACTATTGA
2737	TTCTTGATCAGATGACTATTGAT
2738	TCTTGATCAGATGACTATTGATG
2739	CTTGATCAGATGACTATTGATGA
2740	TTGATCAGATGACTATTGATGAA
2741	TGATCAGATGACTATTGATGAAG
2742	GATCAGATGACTATTGATGAAGA
2743	ATCAGATGACTATTGATGAAGAT
2744	TCAGATGACTATTGATGAAGATA
2745	CAGATGACTATTGATGAAGATAA
2746	AGATGACTATTGATGAAGATAAA
2747	GATGACTATTGATGAAGATAAAT
2748	ATGACTATTGATGAAGATAAATT
2749	TGACTATTGATGAAGATAAATTG
2750	GACTATTGATGAAGATAAATTGA
2751	ACTATTGATGAAGATAAATTGAT
2752	CTATTGATGAAGATAAATTGATA
2753	TATTGATGAAGATAAATTGATAG
2754	ATTGATGAAGATAAATTGATAGC
2755	TTGATGAAGATAAATTGATAGCA
2756	TGATGAAGATAAATTGATAGCAC
2757	GATGAAGATAAATTGATAGCACA
2758	ATGAAGATAAATTGATAGCACAA
2759	TGAAGATAAATTGATAGCACAAA
2760	GAAGATAAATTGATAGCACAAAA
2761	AAGATAAATTGATAGCACAAAAT
2762	AGATAAATTGATAGCACAAAATC
2763	GATAAATTGATAGCACAAAATCT
2764	ATAAATTGATAGCACAAAATCTA
2765	TAAATTGATAGCACAAAATCTAG
2766	AAATTGATAGCACAAAATCTAGA
2767	AATTGATAGCACAAAATCTAGAA
2768	ATTGATAGCACAAAATCTAGAAC
2769	TTGATAGCACAAAATCTAGAACT
2770	TGATAGCACAAAATCTAGAACTT
2771	GATAGCACAAAATCTAGAACTTA
2772	ATAGCACAAAATCTAGAACTTAA
2773	TAGCACAAAATCTAGAACTTAAT
2774	AGCACAAAATCTAGAACTTAATG
2775	GCACAAAATCTAGAACTTAATGA
2776	CACAAAATCTAGAACTTAATGAA
2777	ACAAAATCTAGAACTTAATGAAA
2778	CAAAATCTAGAACTTAATGAAAC
2779	AAAATCTAGAACTTAATGAAACC
2780	AAATCTAGAACTTAATGAAACCA
2781	AATCTAGAACTTAATGAAACCAT

Fig. 27 cont'd (Sheet 48 of 84)

ID	SEQUENCE
2782	ATCTAGAACTTAATGAAACCATA
2783	TCTAGAACTTAATGAAACCATAA
2784	CTAGAACTTAATGAAACCATAAA
2785	TAGAACTTAATGAAACCATAAAA
2786	AGAACTTAATGAAACCATAAAAA
2787	GAACTTAATGAAACCATAAAAAT
2788	AACTTAATGAAACCATAAAAATT
2789	ACTTAATGAAACCATAAAAATTG
2790	CTTAATGAAACCATAAAAATTGG
2791	TTAATGAAACCATAAAAATTGGT
2792	TAATGAAACCATAAAAATTGGTT
2793	AATGAAACCATAAAAATTGGTTT
2794	ATGAAACCATAAAAATTGGTTTG
2795	TGAAACCATAAAAATTGGTTTGA
2796	GAAACCATAAAAATTGGTTTGAC
2797	AAACCATAAAAATTGGTTTGACT
2798	AACCATAAAAATTGGTTTGACTA
2799	ACCATAAAAATTGGTTTGACTAA
2800	CCATAAAAATTGGTTTGACTAAG
2801	CATAAAAATTGGTTTGACTAAGC
2802	ATAAAAATTGGTTTGACTAAGCT
2803	TAAAAATTGGTTTGACTAAGCTT
2804	AAAAATTGGTTTGACTAAGCTTA
2805	AAAATTGGTTTGACTAAGCTTAA
2806	AAATTGGTTTGACTAAGCTTAAT
2807	AATTGGTTTGACTAAGCTTAATT
2808	ATTGGTTTGACTAAGCTTAATTG
2809	TTGGTTTGACTAAGCTTAATTGC
2810	TGGTTTGACTAAGCTTAATTGCT
2811	GGTTTGACTAAGCTTAATTGCTT
2812	GTTTGACTAAGCTTAATTGCTTT
2813	TTTGACTAAGCTTAATTGCTTTC
2814	TTGACTAAGCTTAATTGCTTTCT
2815	TGACTAAGCTTAATTGCTTTCTG
2816	GACTAAGCTTAATTGCTTTCTGG
2817	ACTAAGCTTAATTGCTTTCTGGA
2818	CTAAGCTTAATTGCTTTCTGGAA
2819	TAAGCTTAATTGCTTTCTGGAAC
2820	AAGCTTAATTGCTTTCTGGAACA
2821	AGCTTAATTGCTTTCTGGAACAG
2822	GCTTAATTGCTTTCTGGAACAGG
2823	CTTAATTGCTTTCTGGAACAGGA
2824	TTAATTGCTTTCTGGAACAGGAT
2825	TAATTGCTTTCTGGAACAGGATC
2826	AATTGCTTTCTGGAACAGGATCT
2827	ATTGCTTTCTGGAACAGGATCTG
2828	TTGCTTTCTGGAACAGGATCTGA
2829	TGCTTTCTGGAACAGGATCTGAA
2830	GCTTTCTGGAACAGGATCTGAAA
2831	CTTTCTGGAACAGGATCTGAAAC
2832	TTTCTGGAACAGGATCTGAAACT
2833	TTCTGGAACAGGATCTGAAACTG
2834	TCTGGAACAGGATCTGAAACTGG
2835	CTGGAACAGGATCTGAAACTGGA
2836	TGGAACAGGATCTGAAACTGGAT
2837	GGAACAGGATCTGAAACTGGATA
2838	GAACAGGATCTGAAACTGGATAT
2839	AACAGGATCTGAAACTGGATATC

Fig. 27 cont'd (Sheet 49 of 84)

ID	SEQUENCE
2840	ACAGGATCTGAAACTGGATATCC
2841	CAGGATCTGAAACTGGATATCCC
2842	AGGATCTGAAACTGGATATCCCA
2843	GGATCTGAAACTGGATATCCCAA
2844	GATCTGAAACTGGATATCCCAAC
2845	ATCTGAAACTGGATATCCCAACA
2846	TCTGAAACTGGATATCCCAACAG
2847	CTGAAACTGGATATCCCAACAGG
2848	TGAAACTGGATATCCCAACAGGT
2849	GAAACTGGATATCCCAACAGGTA
2850	AAACTGGATATCCCAACAGGTAC
2851	AACTGGATATCCCAACAGGTACG
2852	ACTGGATATCCCAACAGGTACGA
2853	CTGGATATCCCAACAGGTACGAC
2854	TGGATATCCCAACAGGTACGACA
2855	GGATATCCCAACAGGTACGACAC
2856	GATATCCCAACAGGTACGACACC
2857	ATATCCCAACAGGTACGACACCA
2858	TATCCCAACAGGTACGACACCAC
2859	ATCCCAACAGGTACGACACCACA
2860	TCCCAACAGGTACGACACCACAG
2861	CCCAACAGGTACGACACCACAGA
2862	CCAACAGGTACGACACCACAGAG
2863	CAACAGGTACGACACCACAGAGG
2864	AACAGGTACGACACCACAGAGGA
2865	ACAGGTACGACACCACAGAGGAA
2866	CAGGTACGACACCACAGAGGAAA
2867	AGGTACGACACCACAGAGGAAAA
2868	GGTACGACACCACAGAGGAAAAG
2869	GTACGACACCACAGAGGAAAAGT
2870	TACGACACCACAGAGGAAAAGTT
2871	ACGACACCACAGAGGAAAAGTTA
2872	CGACACCACAGAGGAAAAGTTAT
2873	GACACCACAGAGGAAAAGTTATT
2874	ACACCACAGAGGAAAAGTTATTT
2875	CACCACAGAGGAAAAGTTATTTA
2876	ACCACAGAGGAAAAGTTATTTAT
2877	CCACAGAGGAAAAGTTATTTATA
2878	CACAGAGGAAAAGTTATTTATAC
2879	ACAGAGGAAAAGTTATTTATACC
2880	CAGAGGAAAAGTTATTTATACCC
2881	AGAGGAAAAGTTATTTATACCCA
2882	GAGGAAAAGTTATTTATACCCAT
2883	AGGAAAAGTTATTTATACCCATC
2884	GGAAAAGTTATTTATACCCATCA
2885	GAAAAGTTATTTATACCCATCAA
2886	AAAAGTTATTTATACCCATCAAC
2887	AAAGTTATTTATACCCATCAACA
2888	AAGTTATTTATACCCATCAACAC
2889	AGTTATTTATACCCATCAACACT
2890	GTTATTTATACCCATCAACACTG
2891	TTATTTATACCCATCAACACTGG
2892	TATTTATACCCATCAACACTGGT
2893	ATTTATACCCATCAACACTGGTA
2894	TTTATACCCATCAACACTGGTAA
2895	TTATACCCATCAACACTGGTAAG
2896	TATACCCATCAACACTGGTAAGA
2897	ATACCCATCAACACTGGTAAGAA

Fig. 27 cont'd (Sheet 50 of 84)

ID	SEQUENCE
2898	TACCCATCAACACTGGTAAGAAC
2899	ACCCATCAACACTGGTAAGAACT
2900	CCCATCAACACTGGTAAGAACTG
2901	CCATCAACACTGGTAAGAACTGA
2902	CATCAACACTGGTAAGAACTGAA
2903	ATCAACACTGGTAAGAACTGAAC
2904	TCAACACTGGTAAGAACTGAACC
2905	CAACACTGGTAAGAACTGAACCA
2906	AACACTGGTAAGAACTGAACCAC
2907	ACACTGGTAAGAACTGAACCACG
2908	CACTGGTAAGAACTGAACCACGT
2909	ACTGGTAAGAACTGAACCACGTG
2910	CTGGTAAGAACTGAACCACGTGA
2911	TGGTAAGAACTGAACCACGTGAA
2912	GGTAAGAACTGAACCACGTGAAC
2913	GTAAGAACTGAACCACGTGAACA
2914	TAAGAACTGAACCACGTGAACAT
2915	AAGAACTGAACCACGTGAACATC
2916	AGAACTGAACCACGTGAACATCT
2917	GAACTGAACCACGTGAACATCTC
2918	AACTGAACCACGTGAACATCTCC
2919	ACTGAACCACGTGAACATCTCCT
2920	CTGAACCACGTGAACATCTCCTT
2921	TGAACCACGTGAACATCTCCTTG
2922	GAACCACGTGAACATCTCCTTGA
2923	AACCACGTGAACATCTCCTTGAT
2924	ACCACGTGAACATCTCCTTGATC
2925	CCACGTGAACATCTCCTTGATCA
2926	CACGTGAACATCTCCTTGATCAG
2927	ACGTGAACATCTCCTTGATCAGC
2928	CGTGAACATCTCCTTGATCAGCT
2929	GTGAACATCTCCTTGATCAGCTG
2930	TGAACATCTCCTTGATCAGCTGA
2931	GAACATCTCCTTGATCAGCTGAA
2932	AACATCTCCTTGATCAGCTGAAA
2933	ACATCTCCTTGATCAGCTGAAAA
2934	CATCTCCTTGATCAGCTGAAAAG
2935	ATCTCCTTGATCAGCTGAAAAGG
2936	TCTCCTTGATCAGCTGAAAAGGA
2937	CTCCTTGATCAGCTGAAAAGGAA
2938	TCCTTGATCAGCTGAAAAGGAAA
2939	CCTTGATCAGCTGAAAAGGAAAC
2940	CTTGATCAGCTGAAAAGGAAACA
2941	TTGATCAGCTGAAAAGGAAACAG
2942	TGATCAGCTGAAAAGGAAACAGC
2943	GATCAGCTGAAAAGGAAACAGCC
2944	ATCAGCTGAAAAGGAAACAGCCT
2945	TCAGCTGAAAAGGAAACAGCCTG
2946	CAGCTGAAAAGGAAACAGCCTGA
2947	AGCTGAAAAGGAAACAGCCTGAG
2948	GCTGAAAAGGAAACAGCCTGAGC
2949	CTGAAAAGGAAACAGCCTGAGCT
2950	TGAAAAGGAAACAGCCTGAGCTG
2951	GAAAAGGAAACAGCCTGAGCTGT
2952	AAAAGGAAACAGCCTGAGCTGTT
2953	AAAGGAAACAGCCTGAGCTGTTA
2954	AAGGAAACAGCCTGAGCTGTTAA
2955	AGGAAACAGCCTGAGCTGTTAAT

Fig. 27 cont'd (Sheet 51 of 84)

ID	SEQUENCE
2956	GGAAACAGCCTGAGCTGTTAATG
2957	GAAACAGCCTGAGCTGTTAATGA
2958	AAACAGCCTGAGCTGTTAATGAT
2959	AACAGCCTGAGCTGTTAATGATG
2960	ACAGCCTGAGCTGTTAATGATGC
2961	CAGCCTGAGCTGTTAATGATGCT
2962	AGCCTGAGCTGTTAATGATGCTA
2963	GCCTGAGCTGTTAATGATGCTAA
2964	CCTGAGCTGTTAATGATGCTAAA
2965	CTGAGCTGTTAATGATGCTAAAC
2966	TGAGCTGTTAATGATGCTAAACT
2967	GAGCTGTTAATGATGCTAAACTG
2968	AGCTGTTAATGATGCTAAACTGT
2969	GCTGTTAATGATGCTAAACTGTT
2970	CTGTTAATGATGCTAAACTGTTC
2971	TGTTAATGATGCTAAACTGTTCA
2972	GTTAATGATGCTAAACTGTTCAG
2973	TTAATGATGCTAAACTGTTCAGA
2974	TAATGATGCTAAACTGTTCAGAA
2975	AATGATGCTAAACTGTTCAGAAA
2976	ATGATGCTAAACTGTTCAGAAAA
2977	TGATGCTAAACTGTTCAGAAAAC
2978	GATGCTAAACTGTTCAGAAAACA
2979	ATGCTAAACTGTTCAGAAAACAA
2980	TGCTAAACTGTTCAGAAAACAAC
2981	GCTAAACTGTTCAGAAAACAACA
2982	CTAAACTGTTCAGAAAACAACAA
2983	TAAACTGTTCAGAAAACAACAAA
2984	AAACTGTTCAGAAAACAACAAAG
2985	AACTGTTCAGAAAACAACAAAGA
2986	ACTGTTCAGAAAACAACAAAGAA
2987	CTGTTCAGAAAACAACAAAGAAG
2988	TGTTCAGAAAACAACAAAGAAGA
2989	GTTCAGAAAACAACAAAGAAGAG
2990	TTCAGAAAACAACAAAGAAGAGA
2991	TCAGAAAACAACAAAGAAGAGAC
2992	CAGAAAACAACAAAGAAGAGACA
2993	AGAAAACAACAAAGAAGAGACAA
2994	GAAAACAACAAAGAAGAGACAAT
2995	AAAACAACAAAGAAGAGACAATT
2996	AAACAACAAAGAAGAGACAATTC
2997	AACAACAAAGAAGAGACAATTCC
2998	ACAACAAAGAAGAGACAATTCCG
2999	CAACAAAGAAGAGACAATTCCGG
3000	AACAAAGAAGAGACAATTCCGGA
3001	ACAAAGAAGAGACAATTCCGGAT
3002	CAAAGAAGAGACAATTCCGGATG
3003	AAAGAAGAGACAATTCCGGATGT
3004	AAGAAGAGACAATTCCGGATGTG
3005	AGAAGAGACAATTCCGGATGTGG
3006	GAAGAGACAATTCCGGATGTGGA
3007	AAGAGACAATTCCGGATGTGGAT
3008	AGAGACAATTCCGGATGTGGATG
3009	GAGACAATTCCGGATGTGGATGT
3010	AGACAATTCCGGATGTGGATGTA
3011	GACAATTCCGGATGTGGATGTAG
3012	ACAATTCCGGATGTGGATGTAGA
3013	CAATTCCGGATGTGGATGTAGAA

Fig. 27 cont'd (Sheet 52 of 84)

ID	SEQUENCE
3014	AATTCCGGATGTGGATGTAGAAG
3015	ATTCCGGATGTGGATGTAGAAGA
3016	TTCCGGATGTGGATGTAGAAGAG
3017	TCCGGATGTGGATGTAGAAGAGG
3018	CCGGATGTGGATGTAGAAGAGGC
3019	CGGATGTGGATGTAGAAGAGGCA
3020	GGATGTGGATGTAGAAGAGGCAG
3021	GATGTGGATGTAGAAGAGGCAGT
3022	ATGTGGATGTAGAAGAGGCAGTT
3023	TGTGGATGTAGAAGAGGCAGTTC
3024	GTGGATGTAGAAGAGGCAGTTCT
3025	TGGATGTAGAAGAGGCAGTTCTG
3026	GGATGTAGAAGAGGCAGTTCTGG
3027	GATGTAGAAGAGGCAGTTCTGGG
3028	ATGTAGAAGAGGCAGTTCTGGGG
3029	TGTAGAAGAGGCAGTTCTGGGGC
3030	GTAGAAGAGGCAGTTCTGGGGCA
3031	TAGAAGAGGCAGTTCTGGGGCAG
3032	AGAAGAGGCAGTTCTGGGGCAGT
3033	GAAGAGGCAGTTCTGGGGCAGTA
3034	AAGAGGCAGTTCTGGGGCAGTAT
3035	AGAGGCAGTTCTGGGGCAGTATA
3036	GAGGCAGTTCTGGGGCAGTATAC
3037	AGGCAGTTCTGGGGCAGTATACT
3038	GGCAGTTCTGGGGCAGTATACTG
3039	GCAGTTCTGGGGCAGTATACTGA
3040	CAGTTCTGGGGCAGTATACTGAA
3041	AGTTCTGGGGCAGTATACTGAAG
3042	GTTCTGGGGCAGTATACTGAAGA
3043	TTCTGGGGCAGTATACTGAAGAA
3044	TCTGGGGCAGTATACTGAAGAAC
3045	CTGGGGCAGTATACTGAAGAACC
3046	TGGGGCAGTATACTGAAGAACCT
3047	GGGGCAGTATACTGAAGAACCTC
3048	GGGCAGTATACTGAAGAACCTCT
3049	GGCAGTATACTGAAGAACCTCTA
3050	GCAGTATACTGAAGAACCTCTAA
3051	CAGTATACTGAAGAACCTCTAAG
3052	AGTATACTGAAGAACCTCTAAGT
3053	GTATACTGAAGAACCTCTAAGTC
3054	TATACTGAAGAACCTCTAAGTCA
3055	ATACTGAAGAACCTCTAAGTCAA
3056	TACTGAAGAACCTCTAAGTCAAG
3057	ACTGAAGAACCTCTAAGTCAAGA
3058	CTGAAGAACCTCTAAGTCAAGAG
3059	TGAAGAACCTCTAAGTCAAGAGC
3060	GAAGAACCTCTAAGTCAAGAGCC
3061	AAGAACCTCTAAGTCAAGAGCCA
3062	AGAACCTCTAAGTCAAGAGCCAT
3063	GAACCTCTAAGTCAAGAGCCATC
3064	AACCTCTAAGTCAAGAGCCATCT
3065	ACCTCTAAGTCAAGAGCCATCTG
3066	CCTCTAAGTCAAGAGCCATCTGT
3067	CTCTAAGTCAAGAGCCATCTGTA
3068	TCTAAGTCAAGAGCCATCTGTAG
3069	CTAAGTCAAGAGCCATCTGTAGA
3070	TAAGTCAAGAGCCATCTGTAGAT
3071	AAGTCAAGAGCCATCTGTAGATG

Fig. 27 cont'd (Sheet 53 of 84)

ID	SEQUENCE
3072	AGTCAAGAGCCATCTGTAGATGC
3073	GTCAAGAGCCATCTGTAGATGCT
3074	TCAAGAGCCATCTGTAGATGCTG
3075	CAAGAGCCATCTGTAGATGCTGG
3076	AAGAGCCATCTGTAGATGCTGGT
3077	AGAGCCATCTGTAGATGCTGGTG
3078	GAGCCATCTGTAGATGCTGGTGT
3079	AGCCATCTGTAGATGCTGGTGTG
3080	GCCATCTGTAGATGCTGGTGTGG
3081	CCATCTGTAGATGCTGGTGTGGA
3082	CATCTGTAGATGCTGGTGTGGAT
3083	ATCTGTAGATGCTGGTGTGGATT
3084	TCTGTAGATGCTGGTGTGGATTG
3085	CTGTAGATGCTGGTGTGGATTGT
3086	TGTAGATGCTGGTGTGGATTGTT
3087	GTAGATGCTGGTGTGGATTGTTC
3088	TAGATGCTGGTGTGGATTGTTCA
3089	AGATGCTGGTGTGGATTGTTCAT
3090	GATGCTGGTGTGGATTGTTCATC
3091	ATGCTGGTGTGGATTGTTCATCA
3092	TGCTGGTGTGGATTGTTCATCAA
3093	GCTGGTGTGGATTGTTCATCAAT
3094	CTGGTGTGGATTGTTCATCAATT
3095	TGGTGTGGATTGTTCATCAATTG
3096	GGTGTGGATTGTTCATCAATTGG
3097	GTGTGGATTGTTCATCAATTGGC
3098	TGTGGATTGTTCATCAATTGGCG
3099	GTGGATTGTTCATCAATTGGCGG
3100	TGGATTGTTCATCAATTGGCGGG
3101	GGATTGTTCATCAATTGGCGGGG
3102	GATTGTTCATCAATTGGCGGGGT
3103	ATTGTTCATCAATTGGCGGGGTT
3104	TTGTTCATCAATTGGCGGGGTTC
3105	TGTTCATCAATTGGCGGGGTTCC
3106	GTTCATCAATTGGCGGGGTTCCA
3107	TTCATCAATTGGCGGGGTTCCAT
3108	TCATCAATTGGCGGGGTTCCATT
3109	CATCAATTGGCGGGGTTCCATTT
3110	ATCAATTGGCGGGGTTCCATTTT
3111	TCAATTGGCGGGGTTCCATTTTT
3112	CAATTGGCGGGGTTCCATTTTTC
3113	AATTGGCGGGGTTCCATTTTTCC
3114	ATTGGCGGGGTTCCATTTTTCCA
3115	TTGGCGGGGTTCCATTTTTCCAG
3116	TGGCGGGGTTCCATTTTTCCAGC
3117	GGCGGGGTTCCATTTTTCCAGCA
3118	GCGGGGTTCCATTTTTCCAGCAT
3119	CGGGGTTCCATTTTTCCAGCATA
3120	GGGGTTCCATTTTTCCAGCATAA
3121	GGGTTCCATTTTTCCAGCATAAA
3122	GGTTCCATTTTTCCAGCATAAAA
3123	GTTCCATTTTTCCAGCATAAAAA
3124	TTCCATTTTTCCAGCATAAAAAA
3125	TCCATTTTTCCAGCATAAAAAAT
3126	CCATTTTTCCAGCATAAAAAATC
3127	CATTTTTCCAGCATAAAAAATCA
3128	ATTTTTCCAGCATAAAAAATCAC
3129	TTTTTCCAGCATAAAAAATCACA

Fig. 27 cont'd (Sheet 54 of 84)

ID	SEQUENCE
3130	TTTTCCAGCATAAAAAATCACAT
3131	TTTCCAGCATAAAAAATCACATG
3132	TTCCAGCATAAAAAATCACATGG
3133	TCCAGCATAAAAAATCACATGGA
3134	CCAGCATAAAAAATCACATGGAA
3135	CAGCATAAAAAATCACATGGAAA
3136	AGCATAAAAAATCACATGGAAAA
3137	GCATAAAAAATCACATGGAAAAG
3138	CATAAAAAATCACATGGAAAAGA
3139	ATAAAAAATCACATGGAAAAGAC
3140	TAAAAAATCACATGGAAAAGACA
3141	AAAAAATCACATGGAAAAGACAA
3142	AAAAATCACATGGAAAAGACAAA
3143	AAAATCACATGGAAAAGACAAAG
3144	AAATCACATGGAAAAGACAAAGA
3145	AATCACATGGAAAAGACAAAGAA
3146	ATCACATGGAAAAGACAAAGAAA
3147	TCACATGGAAAAGACAAAGAAAA
3148	CACATGGAAAAGACAAAGAAAAC
3149	ACATGGAAAAGACAAAGAAAACA
3150	CATGGAAAAGACAAAGAAAACAG
3151	ATGGAAAAGACAAAGAAAACAGA
3152	TGGAAAAGACAAAGAAAACAGAG
3153	GGAAAAGACAAAGAAAACAGAGG
3154	GAAAAGACAAAGAAAACAGAGGC
3155	AAAAGACAAAGAAAACAGAGGCA
3156	AAAGACAAAGAAAACAGAGGCAT
3157	AAGACAAAGAAAACAGAGGCATT
3158	AGACAAAGAAAACAGAGGCATTA
3159	GACAAAGAAAACAGAGGCATTAA
3160	ACAAAGAAAACAGAGGCATTAAC
3161	CAAAGAAAACAGAGGCATTAACA
3162	AAAGAAAACAGAGGCATTAACAC
3163	AAGAAAACAGAGGCATTAACACA
3164	AGAAAACAGAGGCATTAACACAC
3165	GAAAACAGAGGCATTAACACACT
3166	AAAACAGAGGCATTAACACACTG
3167	AAACAGAGGCATTAACACACTGG
3168	AACAGAGGCATTAACACACTGGA
3169	ACAGAGGCATTAACACACTGGAG
3170	CAGAGGCATTAACACACTGGAGA
3171	AGAGGCATTAACACACTGGAGAG
3172	GAGGCATTAACACACTGGAGAGG
3173	AGGCATTAACACACTGGAGAGGT
3174	GGCATTAACACACTGGAGAGGTC
3175	GCATTAACACACTGGAGAGGTCT
3176	CATTAACACACTGGAGAGGTCTA
3177	ATTAACACACTGGAGAGGTCTAA
3178	TTAACACACTGGAGAGGTCTAAA
3179	TAACACACTGGAGAGGTCTAAAG
3180	AACACACTGGAGAGGTCTAAAGT
3181	ACACACTGGAGAGGTCTAAAGTG
3182	CACACTGGAGAGGTCTAAAGTGG
3183	ACACTGGAGAGGTCTAAAGTGGA
3184	CACTGGAGAGGTCTAAAGTGGAA
3185	ACTGGAGAGGTCTAAAGTGGAAG
3186	CTGGAGAGGTCTAAAGTGGAAGA
3187	TGGAGAGGTCTAAAGTGGAAGAA

Fig. 27 cont'd (Sheet 55 of 84)

ID	SEQUENCE
3188	GGAGAGGTCTAAAGTGGAAGAAA
3189	GAGAGGTCTAAAGTGGAAGAAAC
3190	AGAGGTCTAAAGTGGAAGAAACT
3191	GAGGTCTAAAGTGGAAGAAACTA
3192	AGGTCTAAAGTGGAAGAAACTAC
3193	GGTCTAAAGTGGAAGAAACTACA
3194	GTCTAAAGTGGAAGAAACTACAG
3195	TCTAAAGTGGAAGAAACTACAGA
3196	CTAAAGTGGAAGAAACTACAGAG
3197	TAAAGTGGAAGAAACTACAGAGC
3198	AAAGTGGAAGAAACTACAGAGCA
3199	AAGTGGAAGAAACTACAGAGCAC
3200	AGTGGAAGAAACTACAGAGCACT
3201	GTGGAAGAAACTACAGAGCACTT
3202	TGGAAGAAACTACAGAGCACTTG
3203	GGAAGAAACTACAGAGCACTTGG
3204	GAAGAAACTACAGAGCACTTGGT
3205	AAGAAACTACAGAGCACTTGGTT
3206	AGAAACTACAGAGCACTTGGTTA
3207	GAAACTACAGAGCACTTGGTTAC
3208	AAACTACAGAGCACTTGGTTACA
3209	AACTACAGAGCACTTGGTTACAA
3210	ACTACAGAGCACTTGGTTACAAA
3211	CTACAGAGCACTTGGTTACAAAG
3212	TACAGAGCACTTGGTTACAAAGA
3213	ACAGAGCACTTGGTTACAAAGAG
3214	CAGAGCACTTGGTTACAAAGAGC
3215	AGAGCACTTGGTTACAAAGAGCA
3216	GAGCACTTGGTTACAAAGAGCAG
3217	AGCACTTGGTTACAAAGAGCAGA
3218	GCACTTGGTTACAAAGAGCAGAT
3219	CACTTGGTTACAAAGAGCAGATT
3220	ACTTGGTTACAAAGAGCAGATTA
3221	CTTGGTTACAAAGAGCAGATTAC
3222	TTGGTTACAAAGAGCAGATTACC
3223	TGGTTACAAAGAGCAGATTACCT
3224	GGTTACAAAGAGCAGATTACCTC
3225	GTTACAAAGAGCAGATTACCTCT
3226	TTACAAAGAGCAGATTACCTCTG
3227	TACAAAGAGCAGATTACCTCTGC
3228	ACAAAGAGCAGATTACCTCTGCG
3229	CAAAGAGCAGATTACCTCTGCGA
3230	AAAGAGCAGATTACCTCTGCGAG
3231	AAGAGCAGATTACCTCTGCGAGC
3232	AGAGCAGATTACCTCTGCGAGCC
3233	GAGCAGATTACCTCTGCGAGCCC
3234	AGCAGATTACCTCTGCGAGCCCA
3235	GCAGATTACCTCTGCGAGCCCAG
3236	CAGATTACCTCTGCGAGCCCAGA
3237	AGATTACCTCTGCGAGCCCAGAT
3238	GATTACCTCTGCGAGCCCAGATC
3239	ATTACCTCTGCGAGCCCAGATCA
3240	TTACCTCTGCGAGCCCAGATCAA
3241	TACCTCTGCGAGCCCAGATCAAC
3242	ACCTCTGCGAGCCCAGATCAACC
3243	CCTCTGCGAGCCCAGATCAACCT
3244	CTCTGCGAGCCCAGATCAACCTT
3245	TCTGCGAGCCCAGATCAACCTTT

Fig. 27 cont'd (Sheet 56 of 84)

ID	SEQUENCE
3246	CTGCGAGCCCAGATCAACCTTTA
3247	TTCACTTGGGGGTTGGCAATTTT
3248	TCACTTGGGGGTTGGCAATTTTA
3249	CACTTGGGGGTTGGCAATTTTAT
3250	ACTTGGGGGTTGGCAATTTTATT
3251	CTTGGGGGTTGGCAATTTTATTT
3252	TTGGGGGTTGGCAATTTTATTTT
3253	TGGGGGTTGGCAATTTTATTTTT
3254	GGGGGTTGGCAATTTTATTTTTA
3255	GGGGTTGGCAATTTTATTTTTAA
3256	GGGTTGGCAATTTTATTTTTAAA
3257	GGTTGGCAATTTTATTTTTAAAG
3258	GTTGGCAATTTTATTTTTAAAGA
3259	TTGGCAATTTTATTTTTAAAGAA
3260	TGGCAATTTTATTTTTAAAGAAA
3261	GGCAATTTTATTTTTAAAGAAAA
3262	GCAATTTTATTTTTAAAGAAAAC
3263	CAATTTTATTTTTAAAGAAAACT
3264	AATTTTATTTTTAAAGAAAACTT
3265	ATTTTATTTTTAAAGAAAACTTA
3266	TTTTATTTTTAAAGAAAACTTAA
3267	TTTATTTTTAAAGAAAACTTAAA
3268	TTATTTTTAAAGAAAACTTAAAA
3269	TATTTTTAAAGAAAACTTAAAAA
3270	ATTTTTAAAGAAAACTTAAAAAT
3271	TTTTTAAAGAAAACTTAAAAATA
3272	TTTTAAAGAAAACTTAAAAATAA
3273	TTTAAAGAAAACTTAAAAATAAA
3274	TTAAAGAAAACTTAAAAATAAAA
3275	TAAAGAAAACTTAAAAATAAAAC
3276	AAAGAAAACTTAAAAATAAAACC
3277	AAGAAAACTTAAAAATAAAACCT
3278	AGAAAACTTAAAAATAAAACCTG
3279	GAAAACTTAAAAATAAAACCTGA
3280	AAAACTTAAAAATAAAACCTGAA
3281	AAACTTAAAAATAAAACCTGAAA
3282	AACTTAAAAATAAAACCTGAAAC
3283	ACTTAAAAATAAAACCTGAAACC
3284	CTTAAAAATAAAACCTGAAACCC
3285	TTAAAAATAAAACCTGAAACCCC
3286	TAAAAATAAAACCTGAAACCCCA
3287	AAAAATAAAACCTGAAACCCCAG
3288	AAAATAAAACCTGAAACCCCAGA
3289	AAATAAAACCTGAAACCCCAGAA
3290	AATAAAACCTGAAACCCCAGAAC
3291	ATAAAACCTGAAACCCCAGAACT
3292	TAAAACCTGAAACCCCAGAACTT
3293	AAAACCTGAAACCCCAGAACTTG
3294	AAACCTGAAACCCCAGAACTTGA
3295	AACCTGAAACCCCAGAACTTGAG
3296	ACCTGAAACCCCAGAACTTGAGC
3297	CCTGAAACCCCAGAACTTGAGCC
3298	CTGAAACCCCAGAACTTGAGCCT
3299	TGAAACCCCAGAACTTGAGCCTT
3300	GAAACCCCAGAACTTGAGCCTTG
3301	AAACCCCAGAACTTGAGCCTTGT
3302	AACCCCAGAACTTGAGCCTTGTG
3303	ACCCCAGAACTTGAGCCTTGTGT

Fig. 27 cont'd (Sheet 57 of 84)

ID	SEQUENCE
3304	CCCCAGAACTTGAGCCTTGTGTA
3305	CCCAGAACTTGAGCCTTGTGTAT
3306	CCAGAACTTGAGCCTTGTGTATA
3307	CAGAACTTGAGCCTTGTGTATAG
3308	AGAACTTGAGCCTTGTGTATAGA
3309	GAACTTGAGCCTTGTGTATAGAT
3310	AACTTGAGCCTTGTGTATAGATT
3311	ACTTGAGCCTTGTGTATAGATTT
3312	CTTGAGCCTTGTGTATAGATTTT
3313	TTGAGCCTTGTGTATAGATTTTA
3314	TGAGCCTTGTGTATAGATTTTAA
3315	GAGCCTTGTGTATAGATTTTAAA
3316	AGCCTTGTGTATAGATTTTAAAA
3317	GCCTTGTGTATAGATTTTAAAAG
3318	CCTTGTGTATAGATTTTAAAAGA
3319	CTTGTGTATAGATTTTAAAAGAA
3320	TTGTGTATAGATTTTAAAAGAAT
3321	TGTGTATAGATTTTAAAAGAATA
3322	GTGTATAGATTTTAAAAGAATAT
3323	TGTATAGATTTTAAAAGAATATA
3324	GTATAGATTTTAAAAGAATATAT
3325	TATAGATTTTAAAAGAATATATA
3326	ATAGATTTTAAAAGAATATATAT
3327	TAGATTTTAAAAGAATATATATA
3328	AGATTTTAAAAGAATATATATAT
3329	GATTTTAAAAGAATATATATATC
3330	ATTTTAAAAGAATATATATATCA
3331	TTTTAAAAGAATATATATATCAG
3332	TTTAAAAGAATATATATATCAGC
3333	TTAAAAGAATATATATATCAGCC
3334	TAAAAGAATATATATATCAGCCG
3335	AAAAGAATATATATATCAGCCGG
3336	AAAGAATATATATATCAGCCGGG
3337	AAGAATATATATATCAGCCGGGC
3338	AGAATATATATATCAGCCGGGCG
3339	GGGCGCGGTGGCTCATGCCTGTA
3340	GGCGCGGTGGCTCATGCCTGTAA
3341	GCGCGGTGGCTCATGCCTGTAAT
3342	CGCGGTGGCTCATGCCTGTAATC
3343	GCGGTGGCTCATGCCTGTAATCC
3344	CGGTGGCTCATGCCTGTAATCCC
3345	GGTGGCTCATGCCTGTAATCCCA
3346	GTGGCTCATGCCTGTAATCCCAG
3347	TGGCTCATGCCTGTAATCCCAGC
3348	GGCTCATGCCTGTAATCCCAGCA
3349	GCTCATGCCTGTAATCCCAGCAC
3350	CTCATGCCTGTAATCCCAGCACT
3351	TCATGCCTGTAATCCCAGCACTT
3352	CATGCCTGTAATCCCAGCACTTT
3353	ATGCCTGTAATCCCAGCACTTTG
3354	TGCCTGTAATCCCAGCACTTTGG
3355	GCCTGTAATCCCAGCACTTTGGG
3356	CCTGTAATCCCAGCACTTTGGGA
3357	CTGTAATCCCAGCACTTTGGGAG
3358	TGTAATCCCAGCACTTTGGGAGG
3359	GTAATCCCAGCACTTTGGGAGGC
3360	TAATCCCAGCACTTTGGGAGGCT
3361	AATCCCAGCACTTTGGGAGGCTG

Fig. 27 cont'd (Sheet 58 of 84)

ID	SEQUENCE
3362	ATCCCAGCACTTTGGGAGGCTGA
3363	TCCCAGCACTTTGGGAGGCTGAG
3364	CCCAGCACTTTGGGAGGCTGAGG
3365	CCAGCACTTTGGGAGGCTGAGGC
3366	CAGCACTTTGGGAGGCTGAGGCG
3367	AGCACTTTGGGAGGCTGAGGCGG
3368	GCACTTTGGGAGGCTGAGGCGGG
3369	CACTTTGGGAGGCTGAGGCGGGT
3370	ACTTTGGGAGGCTGAGGCGGGTG
3371	CTTTGGGAGGCTGAGGCGGGTGG
3372	TTTGGGAGGCTGAGGCGGGTGGA
3373	TTGGGAGGCTGAGGCGGGTGGAT
3374	TGGGAGGCTGAGGCGGGTGGATT
3375	GGGAGGCTGAGGCGGGTGGATTG
3376	GGAGGCTGAGGCGGGTGGATTGC
3377	GAGGCTGAGGCGGGTGGATTGCT
3378	AGGCTGAGGCGGGTGGATTGCTT
3379	GGCTGAGGCGGGTGGATTGCTTG
3380	GCTGAGGCGGGTGGATTGCTTGA
3381	CTGAGGCGGGTGGATTGCTTGAG
3382	TGAGGCGGGTGGATTGCTTGAGC
3383	GAGGCGGGTGGATTGCTTGAGCC
3384	AGGCGGGTGGATTGCTTGAGCCC
3385	GGCGGGTGGATTGCTTGAGCCCA
3386	GCGGGTGGATTGCTTGAGCCCAG
3387	CGGGTGGATTGCTTGAGCCCAGG
3388	GGGTGGATTGCTTGAGCCCAGGA
3389	GGTGGATTGCTTGAGCCCAGGAG
3390	GTGGATTGCTTGAGCCCAGGAGT
3391	TGGATTGCTTGAGCCCAGGAGTT
3392	GGATTGCTTGAGCCCAGGAGTTT
3393	GATTGCTTGAGCCCAGGAGTTTG
3394	ATTGCTTGAGCCCAGGAGTTTGA
3395	TTGCTTGAGCCCAGGAGTTTGAG
3396	TGCTTGAGCCCAGGAGTTTGAGA
3397	GCTTGAGCCCAGGAGTTTGAGAC
3398	CTTGAGCCCAGGAGTTTGAGACC
3399	TTGAGCCCAGGAGTTTGAGACCA
3400	TGAGCCCAGGAGTTTGAGACCAG
3401	GAGCCCAGGAGTTTGAGACCAGC
3402	AGCCCAGGAGTTTGAGACCAGCC
3403	GCCCAGGAGTTTGAGACCAGCCT
3404	CCCAGGAGTTTGAGACCAGCCTG
3405	CCAGGAGTTTGAGACCAGCCTGG
3406	CAGGAGTTTGAGACCAGCCTGGC
3407	AGGAGTTTGAGACCAGCCTGGCC
3408	GGAGTTTGAGACCAGCCTGGCCA
3409	GAGTTTGAGACCAGCCTGGCCAA
3410	AGTTTGAGACCAGCCTGGCCAAC
3411	GTTTGAGACCAGCCTGGCCAACG
3412	TTTGAGACCAGCCTGGCCAACGT
3413	TTGAGACCAGCCTGGCCAACGTG
3414	TGAGACCAGCCTGGCCAACGTGG
3415	GAGACCAGCCTGGCCAACGTGGC
3416	AGACCAGCCTGGCCAACGTGGCA
3417	GACCAGCCTGGCCAACGTGGCAA
3418	ACCAGCCTGGCCAACGTGGCAAA
3419	CCAGCCTGGCCAACGTGGCAAAA

Fig. 27 cont'd (Sheet 59 of 84)

ID	SEQUENCE
3420	CAGCCTGGCCAACGTGGCAAAAC
3421	AGCCTGGCCAACGTGGCAAAACC
3422	GCCTGGCCAACGTGGCAAAACCT
3423	CCTGGCCAACGTGGCAAAACCTC
3424	CTGGCCAACGTGGCAAAACCTCG
3425	TGGCCAACGTGGCAAAACCTCGT
3426	GGCCAACGTGGCAAAACCTCGTC
3427	GCCAACGTGGCAAAACCTCGTCT
3428	CCAACGTGGCAAAACCTCGTCTC
3429	CAACGTGGCAAAACCTCGTCTCT
3430	AACGTGGCAAAACCTCGTCTCTG
3431	ACGTGGCAAAACCTCGTCTCTGT
3432	CGTGGCAAAACCTCGTCTCTGTT
3433	GTGGCAAAACCTCGTCTCTGTTA
3434	TGGCAAAACCTCGTCTCTGTTAA
3435	GGCAAAACCTCGTCTCTGTTAAA
3436	GCAAAACCTCGTCTCTGTTAAAA
3437	CAAAACCTCGTCTCTGTTAAAAA
3438	AAAACCTCGTCTCTGTTAAAAAT
3439	AAACCTCGTCTCTGTTAAAAATT
3440	AACCTCGTCTCTGTTAAAAATTA
3441	ACCTCGTCTCTGTTAAAAATTAG
3442	CCTCGTCTCTGTTAAAAATTAGC
3443	CTCGTCTCTGTTAAAAATTAGCC
3444	TCGTCTCTGTTAAAAATTAGCCG
3445	CGTCTCTGTTAAAAATTAGCCGG
3446	GTCTCTGTTAAAAATTAGCCGGG
3447	TCTCTGTTAAAAATTAGCCGGGC
3448	CTCTGTTAAAAATTAGCCGGGCG
3449	TCTGTTAAAAATTAGCCGGGCGT
3450	CTGTTAAAAATTAGCCGGGCGTG
3451	TGTTAAAAATTAGCCGGGCGTGG
3452	GTTAAAAATTAGCCGGGCGTGGT
3453	TTAAAAATTAGCCGGGCGTGGTG
3454	TAAAAATTAGCCGGGCGTGGTGG
3455	AAAAATTAGCCGGGCGTGGTGGC
3456	AAAATTAGCCGGGCGTGGTGGCA
3457	AAATTAGCCGGGCGTGGTGGCAC
3458	AATTAGCCGGGCGTGGTGGCACA
3459	ATTAGCCGGGCGTGGTGGCACAC
3460	TTAGCCGGGCGTGGTGGCACACT
3461	TAGCCGGGCGTGGTGGCACACTC
3462	AGCCGGGCGTGGTGGCACACTCC
3463	GCCGGGCGTGGTGGCACACTCCT
3464	CCGGGCGTGGTGGCACACTCCTG
3465	CGGGCGTGGTGGCACACTCCTGT
3466	GGGCGTGGTGGCACACTCCTGTA
3467	GGCGTGGTGGCACACTCCTGTAA
3468	GCGTGGTGGCACACTCCTGTAAT
3469	CGTGGTGGCACACTCCTGTAATC
3470	GTGGTGGCACACTCCTGTAATCC
3471	TGGTGGCACACTCCTGTAATCCC
3472	GGTGGCACACTCCTGTAATCCCA
3473	GTGGCACACTCCTGTAATCCCAG
3474	TGGCACACTCCTGTAATCCCAGC
3475	GGCACACTCCTGTAATCCCAGCT
3476	GCACACTCCTGTAATCCCAGCTA
3477	CACACTCCTGTAATCCCAGCTAC

Fig. 27 cont'd (Sheet 60 of 84)

ID	SEQUENCE
3478	ACACTCCTGTAATCCCAGCTACT
3479	CACTCCTGTAATCCCAGCTACTG
3480	ACTCCTGTAATCCCAGCTACTGG
3481	CTCCTGTAATCCCAGCTACTGGG
3482	TCCTGTAATCCCAGCTACTGGGG
3483	CCTGTAATCCCAGCTACTGGGGA
3484	CTGTAATCCCAGCTACTGGGGAG
3485	TGTAATCCCAGCTACTGGGGAGG
3486	GTAATCCCAGCTACTGGGGAGGC
3487	TAATCCCAGCTACTGGGGAGGCT
3488	AATCCCAGCTACTGGGGAGGCTG
3489	ATCCCAGCTACTGGGGAGGCTGA
3490	TCCCAGCTACTGGGGAGGCTGAG
3491	CCCAGCTACTGGGGAGGCTGAGG
3492	CCAGCTACTGGGGAGGCTGAGGC
3493	CAGCTACTGGGGAGGCTGAGGCA
3494	AGCTACTGGGGAGGCTGAGGCAC
3495	GCTACTGGGGAGGCTGAGGCACG
3496	CTACTGGGGAGGCTGAGGCACGA
3497	TACTGGGGAGGCTGAGGCACGAG
3498	ACTGGGGAGGCTGAGGCACGAGA
3499	CTGGGGAGGCTGAGGCACGAGAA
3500	TGGGGAGGCTGAGGCACGAGAAT
3501	GGGGAGGCTGAGGCACGAGAATC
3502	GGGAGGCTGAGGCACGAGAATCA
3503	GGAGGCTGAGGCACGAGAATCAC
3504	GAGGCTGAGGCACGAGAATCACT
3505	AGGCTGAGGCACGAGAATCACTT
3506	GGCTGAGGCACGAGAATCACTTG
3507	GCTGAGGCACGAGAATCACTTGA
3508	CTGAGGCACGAGAATCACTTGAA
3509	TGAGGCACGAGAATCACTTGAAC
3510	GAGGCACGAGAATCACTTGAACC
3511	AGGCACGAGAATCACTTGAACCC
3512	GGCACGAGAATCACTTGAACCCA
3513	GCACGAGAATCACTTGAACCCAG
3514	CACGAGAATCACTTGAACCCAGG
3515	ACGAGAATCACTTGAACCCAGGA
3516	CGAGAATCACTTGAACCCAGGAA
3517	GAGAATCACTTGAACCCAGGAAG
3518	AGAATCACTTGAACCCAGGAAGC
3519	GAATCACTTGAACCCAGGAAGCG
3520	AATCACTTGAACCCAGGAAGCGG
3521	ATCACTTGAACCCAGGAAGCGGG
3522	TCACTTGAACCCAGGAAGCGGGG
3523	CACTTGAACCCAGGAAGCGGGGT
3524	ACTTGAACCCAGGAAGCGGGGTT
3525	CTTGAACCCAGGAAGCGGGGTTG
3526	TTGAACCCAGGAAGCGGGGTTGC
3527	TGAACCCAGGAAGCGGGGTTGCA
3528	GAACCCAGGAAGCGGGGTTGCAG
3529	AACCCAGGAAGCGGGGTTGCAGT
3530	ACCCAGGAAGCGGGGTTGCAGTG
3531	CCCAGGAAGCGGGGTTGCAGTGA
3532	CCAGGAAGCGGGGTTGCAGTGAG
3533	CAGGAAGCGGGGTTGCAGTGAGC
3534	AGGAAGCGGGGTTGCAGTGAGCC
3535	GGAAGCGGGGTTGCAGTGAGCCA

Fig. 27 cont'd (Sheet 61 of 84)

ID	SEQUENCE
3536	GAAGCGGGGTTGCAGTGAGCCAA
3537	AAGCGGGGTTGCAGTGAGCCAAA
3538	AGCGGGGTTGCAGTGAGCCAAAG
3539	GCGGGGTTGCAGTGAGCCAAAGG
3540	CGGGGTTGCAGTGAGCCAAAGGT
3541	GGGGTTGCAGTGAGCCAAAGGTA
3542	GGGTTGCAGTGAGCCAAAGGTAC
3543	GGTTGCAGTGAGCCAAAGGTACA
3544	GTTGCAGTGAGCCAAAGGTACAC
3545	TTGCAGTGAGCCAAAGGTACACC
3546	TGCAGTGAGCCAAAGGTACACCA
3547	GCAGTGAGCCAAAGGTACACCAC
3548	CAGTGAGCCAAAGGTACACCACT
3549	AGTGAGCCAAAGGTACACCACTA
3550	GTGAGCCAAAGGTACACCACTAC
3551	TGAGCCAAAGGTACACCACTACA
3552	GAGCCAAAGGTACACCACTACAC
3553	AGCCAAAGGTACACCACTACACT
3554	GCCAAAGGTACACCACTACACTC
3555	CCAAAGGTACACCACTACACTCC
3556	CAAAGGTACACCACTACACTCCA
3557	AAAGGTACACCACTACACTCCAG
3558	AAGGTACACCACTACACTCCAGC
3559	AGGTACACCACTACACTCCAGCC
3560	GGTACACCACTACACTCCAGCCT
3561	GTACACCACTACACTCCAGCCTG
3562	TACACCACTACACTCCAGCCTGG
3563	ACACCACTACACTCCAGCCTGGG
3564	CACCACTACACTCCAGCCTGGGC
3565	ACCACTACACTCCAGCCTGGGCA
3566	CCACTACACTCCAGCCTGGGCAA
3567	CACTACACTCCAGCCTGGGCAAC
3568	ACTACACTCCAGCCTGGGCAACA
3569	CTACACTCCAGCCTGGGCAACAG
3570	TACACTCCAGCCTGGGCAACAGA
3571	ACACTCCAGCCTGGGCAACAGAG
3572	CACTCCAGCCTGGGCAACAGAGC
3573	ACTCCAGCCTGGGCAACAGAGCA
3574	CTCCAGCCTGGGCAACAGAGCAA
3575	TCCAGCCTGGGCAACAGAGCAAG
3576	CCAGCCTGGGCAACAGAGCAAGA
3577	CAGCCTGGGCAACAGAGCAAGAC
3578	AGCCTGGGCAACAGAGCAAGACT
3579	GCCTGGGCAACAGAGCAAGACTC
3580	CCTGGGCAACAGAGCAAGACTCG
3581	CTGGGCAACAGAGCAAGACTCGG
3582	TGGGCAACAGAGCAAGACTCGGT
3583	GGGCAACAGAGCAAGACTCGGTC
3584	GGCAACAGAGCAAGACTCGGTCT
3585	GCAACAGAGCAAGACTCGGTCTC
3586	CAACAGAGCAAGACTCGGTCTCA
3587	AACAGAGCAAGACTCGGTCTCAA
3588	ACAGAGCAAGACTCGGTCTCAAA
3589	CAGAGCAAGACTCGGTCTCAAAA
3590	AGAGCAAGACTCGGTCTCAAAAA
3591	GAGCAAGACTCGGTCTCAAAAAC
3592	AGCAAGACTCGGTCTCAAAAACA
3593	GCAAGACTCGGTCTCAAAAACAA

Fig. 27 cont'd (Sheet 62 of 84)

ID	SEQUENCE
3594	CAAGACTCGGTCTCAAAAACAAA
3595	AAGACTCGGTCTCAAAAACAAAA
3596	AGACTCGGTCTCAAAAACAAAAT
3597	GACTCGGTCTCAAAAACAAAATT
3598	ACTCGGTCTCAAAAACAAAATTT
3599	CTCGGTCTCAAAAACAAAATTTA
3600	TCGGTCTCAAAAACAAAATTTAA
3601	CGGTCTCAAAAACAAAATTTAAA
3602	GGTCTCAAAAACAAAATTTAAAA
3603	GTCTCAAAAACAAAATTTAAAAA
3604	TCTCAAAAACAAAATTTAAAAAA
3605	CTCAAAAACAAAATTTAAAAAAG
3606	TCAAAAACAAAATTTAAAAAAGA
3607	CAAAAACAAAATTTAAAAAAGAT
3608	AAAAACAAAATTTAAAAAAGATA
3609	AAAACAAAATTTAAAAAAGATAT
3610	AAACAAAATTTAAAAAAGATATA
3611	AACAAAATTTAAAAAAGATATAA
3612	ACAAAATTTAAAAAAGATATAAG
3613	CAAAATTTAAAAAAGATATAAGG
3614	AAAATTTAAAAAAGATATAAGGC
3615	AAATTTAAAAAAGATATAAGGCA
3616	AATTTAAAAAAGATATAAGGCAG
3617	ATTTAAAAAAGATATAAGGCAGT
3618	TTTAAAAAAGATATAAGGCAGTA
3619	TTAAAAAAGATATAAGGCAGTAC
3620	TAAAAAAGATATAAGGCAGTACT
3621	AAAAAAGATATAAGGCAGTACTG
3622	AAAAAGATATAAGGCAGTACTGT
3623	AAAAGATATAAGGCAGTACTGTA
3624	AAAGATATAAGGCAGTACTGTAA
3625	AAGATATAAGGCAGTACTGTAAA
3626	AGATATAAGGCAGTACTGTAAAT
3627	GATATAAGGCAGTACTGTAAATT
3628	ATATAAGGCAGTACTGTAAATTC
3629	TATAAGGCAGTACTGTAAATTCA
3630	ATAAGGCAGTACTGTAAATTCAG
3631	TAAGGCAGTACTGTAAATTCAGT
3632	AAGGCAGTACTGTAAATTCAGTT
3633	AGGCAGTACTGTAAATTCAGTTG
3634	GGCAGTACTGTAAATTCAGTTGA
3635	GCAGTACTGTAAATTCAGTTGAA
3636	CAGTACTGTAAATTCAGTTGAAT
3637	AGTACTGTAAATTCAGTTGAATT
3638	GTACTGTAAATTCAGTTGAATTT
3639	TACTGTAAATTCAGTTGAATTTT
3640	ACTGTAAATTCAGTTGAATTTTG
3641	CTGTAAATTCAGTTGAATTTTGA
3642	TGTAAATTCAGTTGAATTTTGAT
3643	GTAAATTCAGTTGAATTTTGATA
3644	TAAATTCAGTTGAATTTTGATAT
3645	AAATTCAGTTGAATTTTGATATC
3646	AATTCAGTTGAATTTTGATATCT
3647	ATTCAGTTGAATTTTGATATCTA
3648	TTCAGTTGAATTTTGATATCTAC
3649	TCAGTTGAATTTTGATATCTACC
3650	CAGTTGAATTTTGATATCTACCC
3651	AGTTGAATTTTGATATCTACCCA

Fig. 27 cont'd (Sheet 63 of 84)

ID	SEQUENCE
3652	GTTGAATTTTGATATCTACCCAT
3653	TTGAATTTTGATATCTACCCATT
3654	TGAATTTTGATATCTACCCATTT
3655	GAATTTTGATATCTACCCATTTT
3656	AATTTTGATATCTACCCATTTTT
3657	ATTTTGATATCTACCCATTTTTC
3658	TTTTGATATCTACCCATTTTTCT
3659	TTTGATATCTACCCATTTTTCTG
3660	TTGATATCTACCCATTTTTCTGT
3661	TGATATCTACCCATTTTTCTGTC
3662	GATATCTACCCATTTTTCTGTCA
3663	ATATCTACCCATTTTTCTGTCAT
3664	TATCTACCCATTTTTCTGTCATC
3665	ATCTACCCATTTTTCTGTCATCC
3666	TCTACCCATTTTTCTGTCATCCC
3667	CTACCCATTTTTCTGTCATCCCT
3668	TACCCATTTTTCTGTCATCCCTA
3669	ACCCATTTTTCTGTCATCCCTAT
3670	CCCATTTTTCTGTCATCCCTATA
3671	CCATTTTTCTGTCATCCCTATAG
3672	CATTTTTCTGTCATCCCTATAGT
3673	ATTTTTCTGTCATCCCTATAGTT
3674	TTTTTCTGTCATCCCTATAGTTC
3675	TTTTCTGTCATCCCTATAGTTCA
3676	TTTCTGTCATCCCTATAGTTCAC
3677	TTCTGTCATCCCTATAGTTCACT
3678	TCTGTCATCCCTATAGTTCACTT
3679	CTGTCATCCCTATAGTTCACTTT
3680	TGTCATCCCTATAGTTCACTTTG
3681	GTCATCCCTATAGTTCACTTTGT
3682	TCATCCCTATAGTTCACTTTGTA
3683	CATCCCTATAGTTCACTTTGTAT
3684	ATCCCTATAGTTCACTTTGTATT
3685	TCCCTATAGTTCACTTTGTATTA
3686	CCCTATAGTTCACTTTGTATTAA
3687	CCTATAGTTCACTTTGTATTAAA
3688	CTATAGTTCACTTTGTATTAAAT
3689	TATAGTTCACTTTGTATTAAATT
3690	ATAGTTCACTTTGTATTAAATTG
3691	TAGTTCACTTTGTATTAAATTGG
3692	AGTTCACTTTGTATTAAATTGGG
3693	GTTCACTTTGTATTAAATTGGGT
3694	TTCACTTTGTATTAAATTGGGTT
3695	TCACTTTGTATTAAATTGGGTTT
3696	CACTTTGTATTAAATTGGGTTTC
3697	ACTTTGTATTAAATTGGGTTTCA
3698	CTTTGTATTAAATTGGGTTTCAT
3699	TTTGTATTAAATTGGGTTTCATT
3700	TTGTATTAAATTGGGTTTCATTT
3701	TGTATTAAATTGGGTTTCATTTG
3702	GTATTAAATTGGGTTTCATTTGG
3703	TATTAAATTGGGTTTCATTTGGG
3704	ATTAAATTGGGTTTCATTTGGGA
3705	TTAAATTGGGTTTCATTTGGGAT
3706	TAAATTGGGTTTCATTTGGGATT
3707	AAATTGGGTTTCATTTGGGATTT
3708	AATTGGGTTTCATTTGGGATTTG
3709	ATTGGGTTTCATTTGGGATTTGC

Fig. 27 cont'd (Sheet 64 of 84)

ID	SEQUENCE
3710	TTGGGTTTCATTTGGGATTTGCA
3711	TGGGTTTCATTTGGGATTTGCAA
3712	GGGTTTCATTTGGGATTTGCAAT
3713	GGTTTCATTTGGGATTTGCAATG
3714	GTTTCATTTGGGATTTGCAATGT
3715	TTTCATTTGGGATTTGCAATGTA
3716	TTCATTTGGGATTTGCAATGTAA
3717	TCATTTGGGATTTGCAATGTAAA
3718	CATTTGGGATTTGCAATGTAAAT
3719	ATTTGGGATTTGCAATGTAAATA
3720	TTTGGGATTTGCAATGTAAATAC
3721	TTGGGATTTGCAATGTAAATACG
3722	TGGGATTTGCAATGTAAATACGT
3723	GGGATTTGCAATGTAAATACGTA
3724	GGATTTGCAATGTAAATACGTAT
3725	GATTTGCAATGTAAATACGTATT
3726	ATTTGCAATGTAAATACGTATTT
3727	TTTGCAATGTAAATACGTATTTC
3728	TTGCAATGTAAATACGTATTTCT
3729	TGCAATGTAAATACGTATTTCTA
3730	GCAATGTAAATACGTATTTCTAG
3731	CAATGTAAATACGTATTTCTAGT
3732	AATGTAAATACGTATTTCTAGTT
3733	ATGTAAATACGTATTTCTAGTTT
3734	TGTAAATACGTATTTCTAGTTTT
3735	GTAAATACGTATTTCTAGTTTTC
3736	TAAATACGTATTTCTAGTTTTCA
3737	AAATACGTATTTCTAGTTTTCAT
3738	AATACGTATTTCTAGTTTTCATA
3739	ATACGTATTTCTAGTTTTCATAT
3740	TACGTATTTCTAGTTTTCATATA
3741	ACGTATTTCTAGTTTTCATATAA
3742	CGTATTTCTAGTTTTCATATAAA
3743	GTATTTCTAGTTTTCATATAAAG
3744	TATTTCTAGTTTTCATATAAAGT
3745	ATTTCTAGTTTTCATATAAAGTA
3746	TTTCTAGTTTTCATATAAAGTAG
3747	TTCTAGTTTTCATATAAAGTAGT
3748	TCTAGTTTTCATATAAAGTAGTT
3749	CTAGTTTTCATATAAAGTAGTTC
3750	TAGTTTTCATATAAAGTAGTTCT
3751	AGTTTTCATATAAAGTAGTTCTT
3752	GTTTTCATATAAAGTAGTTCTTT
3753	TTTTCATATAAAGTAGTTCTTTT
3754	TTTCATATAAAGTAGTTCTTTTA
3755	TTCATATAAAGTAGTTCTTTTAT
3756	TCATATAAAGTAGTTCTTTTATA
3757	CATATAAAGTAGTTCTTTTATAA
3758	ATATAAAGTAGTTCTTTTATAAC
3759	TATAAAGTAGTTCTTTTATAACA
3760	ATAAAGTAGTTCTTTTATAACAA
3761	TAAAGTAGTTCTTTTATAACAAA
3762	AAAGTAGTTCTTTTATAACAAAT
3763	AAGTAGTTCTTTTATAACAAATG
3764	AGTAGTTCTTTTATAACAAATGA
3765	GTAGTTCTTTTATAACAAATGAA
3766	TAGTTCTTTTATAACAAATGAAA
3767	AGTTCTTTTATAACAAATGAAAA

Fig. 27 cont'd (Sheet 65 of 84)

ID	SEQUENCE
3768	GTTCTTTTATAACAAATGAAAAG
3769	TTCTTTTATAACAAATGAAAAGT
3770	TCTTTTATAACAAATGAAAAGTA
3771	CTTTTATAACAAATGAAAAGTAT
3772	TTTTATAACAAATGAAAAGTATT
3773	TTTATAACAAATGAAAAGTATTT
3774	TTATAACAAATGAAAAGTATTTT
3775	TATAACAAATGAAAAGTATTTTT
3776	ATAACAAATGAAAAGTATTTTTC
3777	TAACAAATGAAAAGTATTTTTCT
3778	AACAAATGAAAAGTATTTTTCTT
3779	ACAAATGAAAAGTATTTTTCTTG
3780	CAAATGAAAAGTATTTTTCTTGT
3781	AAATGAAAAGTATTTTTCTTGTA
3782	AATGAAAAGTATTTTTCTTGTAT
3783	ATGAAAAGTATTTTTCTTGTATA
3784	TGAAAAGTATTTTTCTTGTATAT
3785	GAAAAGTATTTTTCTTGTATATT
3786	AAAAGTATTTTTCTTGTATATTA
3787	AAAGTATTTTTCTTGTATATTAT
3788	AAGTATTTTTCTTGTATATTATT
3789	AGTATTTTTCTTGTATATTATTA
3790	GTATTTTTCTTGTATATTATTAA
3791	TATTTTTCTTGTATATTATTAAG
3792	ATTTTTCTTGTATATTATTAAGT
3793	TTTTTCTTGTATATTATTAAGTA
3794	TTTTCTTGTATATTATTAAGTAA
3795	TTTCTTGTATATTATTAAGTAAT
3796	TTCTTGTATATTATTAAGTAATG
3797	TCTTGTATATTATTAAGTAATGA
3798	CTTGTATATTATTAAGTAATGAA
3799	TTGTATATTATTAAGTAATGAAT
3800	TGTATATTATTAAGTAATGAATA
3801	GTATATTATTAAGTAATGAATAT
3802	TATATTATTAAGTAATGAATATA
3803	ATATTATTAAGTAATGAATATAT
3804	TATTATTAAGTAATGAATATATA
3805	ATTATTAAGTAATGAATATATAA
3806	TTATTAAGTAATGAATATATAAG
3807	TATTAAGTAATGAATATATAAGA
3808	ATTAAGTAATGAATATATAAGAA
3809	TTAAGTAATGAATATATAAGAAC
3810	TAAGTAATGAATATATAAGAACT
3811	AAGTAATGAATATATAAGAACTG
3812	AGTAATGAATATATAAGAACTGT
3813	GTAATGAATATATAAGAACTGTA
3814	TAATGAATATATAAGAACTGTAC
3815	AATGAATATATAAGAACTGTACT
3816	ATGAATATATAAGAACTGTACTC
3817	TGAATATATAAGAACTGTACTCT
3818	GAATATATAAGAACTGTACTCTT
3819	AATATATAAGAACTGTACTCTTC
3820	ATATATAAGAACTGTACTCTTCT
3821	TATATAAGAACTGTACTCTTCTC
3822	ATATAAGAACTGTACTCTTCTCA
3823	TATAAGAACTGTACTCTTCTCAG
3824	ATAAGAACTGTACTCTTCTCAGC
3825	TAAGAACTGTACTCTTCTCAGCT

Fig. 27 cont'd (Sheet 66 of 84)

ID	SEQUENCE
3826	AAGAACTGTACTCTTCTCAGCTT
3827	AGAACTGTACTCTTCTCAGCTTG
3828	GAACTGTACTCTTCTCAGCTTGA
3829	AACTGTACTCTTCTCAGCTTGAG
3830	ACTGTACTCTTCTCAGCTTGAGC
3831	CTGTACTCTTCTCAGCTTGAGCT
3832	TGTACTCTTCTCAGCTTGAGCTT
3833	GTACTCTTCTCAGCTTGAGCTTA
3834	TACTCTTCTCAGCTTGAGCTTAA
3835	ACTCTTCTCAGCTTGAGCTTAAC
3836	CTCTTCTCAGCTTGAGCTTAACA
3837	TCTTCTCAGCTTGAGCTTAACAT
3838	CTTCTCAGCTTGAGCTTAACATA
3839	TTCTCAGCTTGAGCTTAACATAG
3840	TCTCAGCTTGAGCTTAACATAGG
3841	CTCAGCTTGAGCTTAACATAGGT
3842	TCAGCTTGAGCTTAACATAGGTA
3843	CAGCTTGAGCTTAACATAGGTAA
3844	AGCTTGAGCTTAACATAGGTAAA
3845	GCTTGAGCTTAACATAGGTAAAT
3846	CTTGAGCTTAACATAGGTAAATA
3847	TTGAGCTTAACATAGGTAAATAT
3848	TGAGCTTAACATAGGTAAATATC
3849	GAGCTTAACATAGGTAAATATCA
3850	AGCTTAACATAGGTAAATATCAC
3851	GCTTAACATAGGTAAATATCACC
3852	CTTAACATAGGTAAATATCACCA
3853	TTAACATAGGTAAATATCACCAA
3854	TAACATAGGTAAATATCACCAAC
3855	AACATAGGTAAATATCACCAACA
3856	ACATAGGTAAATATCACCAACAT
3857	CATAGGTAAATATCACCAACATC
3858	ATAGGTAAATATCACCAACATCT
3859	TAGGTAAATATCACCAACATCTG
3860	AGGTAAATATCACCAACATCTGT
3861	GGTAAATATCACCAACATCTGTC
3862	GTAAATATCACCAACATCTGTCC
3863	TAAATATCACCAACATCTGTCCT
3864	AAATATCACCAACATCTGTCCTT
3865	AATATCACCAACATCTGTCCTTA
3866	ATATCACCAACATCTGTCCTTAG
3867	TATCACCAACATCTGTCCTTAGA
3868	ATCACCAACATCTGTCCTTAGAA
3869	TCACCAACATCTGTCCTTAGAAA
3870	CACCAACATCTGTCCTTAGAAAG
3871	ACCAACATCTGTCCTTAGAAAGG
3872	CCAACATCTGTCCTTAGAAAGGA
3873	CAACATCTGTCCTTAGAAAGGAC
3874	AACATCTGTCCTTAGAAAGGACC
3875	ACATCTGTCCTTAGAAAGGACCA
3876	CATCTGTCCTTAGAAAGGACCAT
3877	ATCTGTCCTTAGAAAGGACCATC
3878	TCTGTCCTTAGAAAGGACCATCT
3879	CTGTCCTTAGAAAGGACCATCTC
3880	TGTCCTTAGAAAGGACCATCTCA
3881	GTCCTTAGAAAGGACCATCTCAT
3882	TCCTTAGAAAGGACCATCTCATG
3883	CCTTAGAAAGGACCATCTCATGT

Fig. 27 cont'd (Sheet 67 of 84)

ID	SEQUENCE
3884	CTTAGAAAGGACCATCTCATGTT
3885	TTAGAAAGGACCATCTCATGTTT
3886	TAGAAAGGACCATCTCATGTTTT
3887	AGAAAGGACCATCTCATGTTTTT
3888	GAAAGGACCATCTCATGTTTTTT
3889	AAAGGACCATCTCATGTTTTTTT
3890	AAGGACCATCTCATGTTTTTTTT
3891	AGGACCATCTCATGTTTTTTTTC
3892	GGACCATCTCATGTTTTTTTTCT
3893	GACCATCTCATGTTTTTTTTCTT
3894	ACCATCTCATGTTTTTTTTCTTG
3895	CCATCTCATGTTTTTTTTCTTGC
3896	CATCTCATGTTTTTTTTCTTGCT
3897	ATCTCATGTTTTTTTTCTTGCTA
3898	TCTCATGTTTTTTTTCTTGCTAT
3899	CTCATGTTTTTTTTCTTGCTATG
3900	TCATGTTTTTTTTCTTGCTATGA
3901	CATGTTTTTTTTCTTGCTATGAC
3902	ATGTTTTTTTTCTTGCTATGACT
3903	TGTTTTTTTTCTTGCTATGACTT
3904	GTTTTTTTTCTTGCTATGACTTG
3905	TTTTTTTTCTTGCTATGACTTGT
3906	TTTTTTTCTTGCTATGACTTGTG
3907	TTTTTTCTTGCTATGACTTGTGT
3908	TTTTTCTTGCTATGACTTGTGTA
3909	TTTTCTTGCTATGACTTGTGTAT
3910	TTTCTTGCTATGACTTGTGTATT
3911	TTCTTGCTATGACTTGTGTATTT
3912	TCTTGCTATGACTTGTGTATTTT
3913	CTTGCTATGACTTGTGTATTTTC
3914	TTGCTATGACTTGTGTATTTTCT
3915	TGCTATGACTTGTGTATTTTCTT
3916	GCTATGACTTGTGTATTTTCTTG
3917	CTATGACTTGTGTATTTTCTTGC
3918	TATGACTTGTGTATTTTCTTGCA
3919	ATGACTTGTGTATTTTCTTGCAT
3920	TGACTTGTGTATTTTCTTGCATC
3921	GACTTGTGTATTTTCTTGCATCC
3922	ACTTGTGTATTTTCTTGCATCCT
3923	CTTGTGTATTTTCTTGCATCCTC
3924	TTGTGTATTTTCTTGCATCCTCC
3925	TGTGTATTTTCTTGCATCCTCCC
3926	GTGTATTTTCTTGCATCCTCCCT
3927	TGTATTTTCTTGCATCCTCCCTA
3928	GTATTTTCTTGCATCCTCCCTAG
3929	TATTTTCTTGCATCCTCCCTAGA
3930	ATTTTCTTGCATCCTCCCTAGAC
3931	TTTTCTTGCATCCTCCCTAGACT
3932	TTTCTTGCATCCTCCCTAGACTT
3933	TTCTTGCATCCTCCCTAGACTTC
3934	TCTTGCATCCTCCCTAGACTTCC
3935	CTTGCATCCTCCCTAGACTTCCC
3936	TTGCATCCTCCCTAGACTTCCCT
3937	TGCATCCTCCCTAGACTTCCCTA
3938	GCATCCTCCCTAGACTTCCCTAT
3939	CATCCTCCCTAGACTTCCCTATT
3940	ATCCTCCCTAGACTTCCCTATTT
3941	TCCTCCCTAGACTTCCCTATTTC

Fig. 27 cont'd (Sheet 68 of 84)

ID	SEQUENCE
3942	CCTCCCTAGACTTCCCTATTTCG
3943	CTCCCTAGACTTCCCTATTTCGC
3944	TCCCTAGACTTCCCTATTTCGCT
3945	CCCTAGACTTCCCTATTTCGCTT
3946	CCTAGACTTCCCTATTTCGCTTT
3947	CTAGACTTCCCTATTTCGCTTTC
3948	TAGACTTCCCTATTTCGCTTTCT
3949	AGACTTCCCTATTTCGCTTTCTC
3950	GACTTCCCTATTTCGCTTTCTCC
3951	ACTTCCCTATTTCGCTTTCTCCT
3952	CTTCCCTATTTCGCTTTCTCCTC
3953	TTCCCTATTTCGCTTTCTCCTCG
3954	TCCCTATTTCGCTTTCTCCTCGG
3955	CCCTATTTCGCTTTCTCCTCGGC
3956	CCTATTTCGCTTTCTCCTCGGCT
3957	CTATTTCGCTTTCTCCTCGGCTC
3958	TATTTCGCTTTCTCCTCGGCTCA
3959	ATTTCGCTTTCTCCTCGGCTCAC
3960	TTTCGCTTTCTCCTCGGCTCACT
3961	TTCGCTTTCTCCTCGGCTCACTT
3962	TCGCTTTCTCCTCGGCTCACTTT
3963	CGCTTTCTCCTCGGCTCACTTTC
3964	GCTTTCTCCTCGGCTCACTTTCT
3965	CTTTCTCCTCGGCTCACTTTCTC
3966	TTTCTCCTCGGCTCACTTTCTCC
3967	TTCTCCTCGGCTCACTTTCTCCC
3968	TCTCCTCGGCTCACTTTCTCCCT
3969	CTCCTCGGCTCACTTTCTCCCTT
3970	TCCTCGGCTCACTTTCTCCCTTT
3971	CCTCGGCTCACTTTCTCCCTTTT
3972	CTCGGCTCACTTTCTCCCTTTTT
3973	TCGGCTCACTTTCTCCCTTTTTA
3974	CGGCTCACTTTCTCCCTTTTTAT
3975	GGCTCACTTTCTCCCTTTTTATT
3976	GCTCACTTTCTCCCTTTTTATTT
3977	CTCACTTTCTCCCTTTTTATTTT
3978	TCACTTTCTCCCTTTTTATTTTT
3979	CACTTTCTCCCTTTTTATTTTTC
3980	ACTTTCTCCCTTTTTATTTTTCA
3981	CTTTCTCCCTTTTTATTTTTCAC
3982	TTTCTCCCTTTTTATTTTTCACC
3983	TTCTCCCTTTTTATTTTTCACCA
3984	TCTCCCTTTTTATTTTTCACCAA
3985	CTCCCTTTTTATTTTTCACCAAA
3986	TCCCTTTTTATTTTTCACCAAAC
3987	CCCTTTTTATTTTTCACCAAACC
3988	CCTTTTTATTTTTCACCAAACCA
3989	CTTTTTATTTTTCACCAAACCAT
3990	TTTTTATTTTTCACCAAACCATT
3991	TTTTATTTTTCACCAAACCATTT
3992	TTTATTTTTCACCAAACCATTTG
3993	TTATTTTTCACCAAACCATTTGT
3994	TATTTTTCACCAAACCATTTGTA
3995	ATTTTTCACCAAACCATTTGTAG
3996	TTTTTCACCAAACCATTTGTAGA
3997	TTTTCACCAAACCATTTGTAGAG
3998	TTTCACCAAACCATTTGTAGAGC
3999	TTCACCAAACCATTTGTAGAGCT

Fig. 27 cont'd (Sheet 69 of 84)

ID	SEQUENCE
4000	TCACCAAACCATTTGTAGAGCTA
4001	CACCAAACCATTTGTAGAGCTAC
4002	ACCAAACCATTTGTAGAGCTACA
4003	CCAAACCATTTGTAGAGCTACAA
4004	CAAACCATTTGTAGAGCTACAAA
4005	AAACCATTTGTAGAGCTACAAAA
4006	AACCATTTGTAGAGCTACAAAAC
4007	ACCATTTGTAGAGCTACAAAACC
4008	CCATTTGTAGAGCTACAAAACCT
4009	CATTTGTAGAGCTACAAAACCTA
4010	ATTTGTAGAGCTACAAAACCTAT
4011	TTTGTAGAGCTACAAAACCTATC
4012	TTGTAGAGCTACAAAACCTATCC
4013	TGTAGAGCTACAAAACCTATCCT
4014	GTAGAGCTACAAAACCTATCCTT
4015	TAGAGCTACAAAACCTATCCTTT
4016	AGAGCTACAAAACCTATCCTTTC
4017	GAGCTACAAAACCTATCCTTTCT
4018	AGCTACAAAACCTATCCTTTCTT
4019	GCTACAAAACCTATCCTTTCTTA
4020	CTACAAAACCTATCCTTTCTTAT
4021	TACAAAACCTATCCTTTCTTATT
4022	ACAAAACCTATCCTTTCTTATTT
4023	CAAAACCTATCCTTTCTTATTTT
4024	AAAACCTATCCTTTCTTATTTTC
4025	AAACCTATCCTTTCTTATTTTCA
4026	AACCTATCCTTTCTTATTTTCAG
4027	ACCTATCCTTTCTTATTTTCAGT
4028	CCTATCCTTTCTTATTTTCAGTA
4029	CTATCCTTTCTTATTTTCAGTAG
4030	TATCCTTTCTTATTTTCAGTAGT
4031	ATCCTTTCTTATTTTCAGTAGTC
4032	TCCTTTCTTATTTTCAGTAGTCA
4033	CCTTTCTTATTTTCAGTAGTCAG
4034	CTTTCTTATTTTCAGTAGTCAGA
4035	TTTCTTATTTTCAGTAGTCAGAA
4036	TTCTTATTTTCAGTAGTCAGAAT
4037	TCTTATTTTCAGTAGTCAGAATT
4038	CTTATTTTCAGTAGTCAGAATTT
4039	TTATTTTCAGTAGTCAGAATTTT
4040	TATTTTCAGTAGTCAGAATTTTA
4041	ATTTTCAGTAGTCAGAATTTTAT
4042	TTTTCAGTAGTCAGAATTTTATC
4043	TTTCAGTAGTCAGAATTTTATCT
4044	TTCAGTAGTCAGAATTTTATCTA
4045	TCAGTAGTCAGAATTTTATCTAG
4046	CAGTAGTCAGAATTTTATCTAGA
4047	AGTAGTCAGAATTTTATCTAGAA
4048	GTAGTCAGAATTTTATCTAGAAA
4049	TAGTCAGAATTTTATCTAGAAAT
4050	AGTCAGAATTTTATCTAGAAATC
4051	GTCAGAATTTTATCTAGAAATCT
4052	TCAGAATTTTATCTAGAAATCTT
4053	CAGAATTTTATCTAGAAATCTTT
4054	AGAATTTTATCTAGAAATCTTTT
4055	GAATTTTATCTAGAAATCTTTTA
4056	AATTTTATCTAGAAATCTTTTAA
4057	ATTTTATCTAGAAATCTTTTAAC

Fig. 27 cont'd (Sheet 70 of 84)

ID	SEQUENCE
4058	TTTTATCTAGAAATCTTTTAACA
4059	TTTATCTAGAAATCTTTTAACAC
4060	TTATCTAGAAATCTTTTAACACC
4061	TATCTAGAAATCTTTTAACACCT
4062	ATCTAGAAATCTTTTAACACCTT
4063	TCTAGAAATCTTTTAACACCTTT
4064	CTAGAAATCTTTTAACACCTTTT
4065	TAGAAATCTTTTAACACCTTTTT
4066	AGAAATCTTTTAACACCTTTTTA
4067	GAAATCTTTTAACACCTTTTTAG
4068	AAATCTTTTAACACCTTTTTAGT
4069	AATCTTTTAACACCTTTTTAGTG
4070	ATCTTTTAACACCTTTTTAGTGG
4071	TCTTTTAACACCTTTTTAGTGGT
4072	CTTTTAACACCTTTTTAGTGGTT
4073	TTTTAACACCTTTTTAGTGGTTA
4074	TTTAACACCTTTTTAGTGGTTAT
4075	TTAACACCTTTTTAGTGGTTATT
4076	TAACACCTTTTTAGTGGTTATTT
4077	AACACCTTTTTAGTGGTTATTTC
4078	ACACCTTTTTAGTGGTTATTTCT
4079	CACCTTTTTAGTGGTTATTTCTA
4080	ACCTTTTTAGTGGTTATTTCTAA
4081	CCTTTTTAGTGGTTATTTCTAAA
4082	CTTTTTAGTGGTTATTTCTAAAA
4083	TTTTTAGTGGTTATTTCTAAAAT
4084	TTTTAGTGGTTATTTCTAAAATC
4085	TTTAGTGGTTATTTCTAAAATCA
4086	TTAGTGGTTATTTCTAAAATCAC
4087	TAGTGGTTATTTCTAAAATCACT
4088	AGTGGTTATTTCTAAAATCACTG
4089	GTGGTTATTTCTAAAATCACTGT
4090	TGGTTATTTCTAAAATCACTGTC
4091	GGTTATTTCTAAAATCACTGTCA
4092	GTTATTTCTAAAATCACTGTCAA
4093	TTATTTCTAAAATCACTGTCAAC
4094	TATTTCTAAAATCACTGTCAACA
4095	ATTTCTAAAATCACTGTCAACAA
4096	TTTCTAAAATCACTGTCAACAAT
4097	TTCTAAAATCACTGTCAACAATA
4098	TCTAAAATCACTGTCAACAATAA
4099	CTAAAATCACTGTCAACAATAAA
4100	TAAAATCACTGTCAACAATAAAT
4101	AAAATCACTGTCAACAATAAATC
4102	AAATCACTGTCAACAATAAATCT
4103	AATCACTGTCAACAATAAATCTA
4104	ATCACTGTCAACAATAAATCTAA
4105	TCACTGTCAACAATAAATCTAAC
4106	CACTGTCAACAATAAATCTAACC
4107	ACTGTCAACAATAAATCTAACCC
4108	CTGTCAACAATAAATCTAACCCT
4109	TGTCAACAATAAATCTAACCCTA
4110	GTCAACAATAAATCTAACCCTAG
4111	TCAACAATAAATCTAACCCTAGT
4112	CAACAATAAATCTAACCCTAGTT
4113	AACAATAAATCTAACCCTAGTTG
4114	ACAATAAATCTAACCCTAGTTGT
4115	CAATAAATCTAACCCTAGTTGTA

Fig. 27 cont'd (Sheet 71 of 84)

ID	SEQUENCE
4116	AATAAATCTAACCCTAGTTGTAT
4117	ATAAATCTAACCCTAGTTGTATC
4118	TAAATCTAACCCTAGTTGTATCC
4119	AAATCTAACCCTAGTTGTATCCC
4120	AATCTAACCCTAGTTGTATCCCT
4121	ATCTAACCCTAGTTGTATCCCTC
4122	TCTAACCCTAGTTGTATCCCTCC
4123	CTAACCCTAGTTGTATCCCTCCT
4124	TAACCCTAGTTGTATCCCTCCTT
4125	AACCCTAGTTGTATCCCTCCTTT
4126	ACCCTAGTTGTATCCCTCCTTTA
4127	CCCTAGTTGTATCCCTCCTTTAA
4128	CCTAGTTGTATCCCTCCTTTAAG
4129	CTAGTTGTATCCCTCCTTTAAGT
4130	TAGTTGTATCCCTCCTTTAAGTA
4131	AGTTGTATCCCTCCTTTAAGTAT
4132	GTTGTATCCCTCCTTTAAGTATT
4133	TTGTATCCCTCCTTTAAGTATTT
4134	TGTATCCCTCCTTTAAGTATTTA
4135	GTATCCCTCCTTTAAGTATTTAA
4136	TATCCCTCCTTTAAGTATTTAAA
4137	ATCCCTCCTTTAAGTATTTAAAA
4138	TCCCTCCTTTAAGTATTTAAAAC
4139	CCCTCCTTTAAGTATTTAAAACT
4140	CCTCCTTTAAGTATTTAAAACTT
4141	CTCCTTTAAGTATTTAAAACTTG
4142	TCCTTTAAGTATTTAAAACTTGT
4143	CCTTTAAGTATTTAAAACTTGTT
4144	CTTTAAGTATTTAAAACTTGTTG
4145	TTTAAGTATTTAAAACTTGTTGC
4146	TTAAGTATTTAAAACTTGTTGCC
4147	TAAGTATTTAAAACTTGTTGCCC
4148	AAGTATTTAAAACTTGTTGCCCC
4149	AGTATTTAAAACTTGTTGCCCCA
4150	GTATTTAAAACTTGTTGCCCCAA
4151	TATTTAAAACTTGTTGCCCCAAA
4152	ATTTAAAACTTGTTGCCCCAAAT
4153	TTTAAAACTTGTTGCCCCAAATG
4154	TTAAAACTTGTTGCCCCAAATGT
4155	TAAAACTTGTTGCCCCAAATGTG
4156	AAAACTTGTTGCCCCAAATGTGA
4157	AAACTTGTTGCCCCAAATGTGAA
4158	AACTTGTTGCCCCAAATGTGAAA
4159	ACTTGTTGCCCCAAATGTGAAAG
4160	CTTGTTGCCCCAAATGTGAAAGC
4161	TTGTTGCCCCAAATGTGAAAGCA
4162	TGTTGCCCCAAATGTGAAAGCAT
4163	GTTGCCCCAAATGTGAAAGCATT
4164	TTGCCCCAAATGTGAAAGCATTT
4165	TGCCCCAAATGTGAAAGCATTTA
4166	GCCCCAAATGTGAAAGCATTTAA
4167	CCCCAAATGTGAAAGCATTTAAT
4168	CCCAAATGTGAAAGCATTTAATT
4169	CCAAATGTGAAAGCATTTAATTC
4170	CAAATGTGAAAGCATTTAATTCC
4171	AAATGTGAAAGCATTTAATTCCT
4172	AATGTGAAAGCATTTAATTCCTT
4173	ATGTGAAAGCATTTAATTCCTTT

Fig. 27 cont'd (Sheet 72 of 84)

ID	SEQUENCE
4174	TGTGAAAGCATTTAATTCCTTTA
4175	GTGAAAGCATTTAATTCCTTTAA
4176	TGAAAGCATTTAATTCCTTTAAG
4177	GAAAGCATTTAATTCCTTTAAGA
4178	AAAGCATTTAATTCCTTTAAGAG
4179	AAGCATTTAATTCCTTTAAGAGG
4180	AGCATTTAATTCCTTTAAGAGGC
4181	GCATTTAATTCCTTTAAGAGGCC
4182	CATTTAATTCCTTTAAGAGGCCT
4183	ATTTAATTCCTTTAAGAGGCCTA
4184	TTTAATTCCTTTAAGAGGCCTAA
4185	TTAATTCCTTTAAGAGGCCTAAC
4186	TAATTCCTTTAAGAGGCCTAACT
4187	AATTCCTTTAAGAGGCCTAACTC
4188	ATTCCTTTAAGAGGCCTAACTCA
4189	TTCCTTTAAGAGGCCTAACTCAT
4190	TCCTTTAAGAGGCCTAACTCATT
4191	CCTTTAAGAGGCCTAACTCATTC
4192	CTTTAAGAGGCCTAACTCATTCA
4193	TTTAAGAGGCCTAACTCATTCAC
4194	TTAAGAGGCCTAACTCATTCACC
4195	TAAGAGGCCTAACTCATTCACCC
4196	AAGAGGCCTAACTCATTCACCCT
4197	AGAGGCCTAACTCATTCACCCTG
4198	GAGGCCTAACTCATTCACCCTGA
4199	AGGCCTAACTCATTCACCCTGAC
4200	GGCCTAACTCATTCACCCTGACA
4201	GCCTAACTCATTCACCCTGACAG
4202	CCTAACTCATTCACCCTGACAGA
4203	CTAACTCATTCACCCTGACAGAG
4204	TAACTCATTCACCCTGACAGAGT
4205	AACTCATTCACCCTGACAGAGTT
4206	ACTCATTCACCCTGACAGAGTTC
4207	CTCATTCACCCTGACAGAGTTCA
4208	TCATTCACCCTGACAGAGTTCAC
4209	CATTCACCCTGACAGAGTTCACA
4210	ATTCACCCTGACAGAGTTCACAA
4211	TTCACCCTGACAGAGTTCACAAA
4212	TCACCCTGACAGAGTTCACAAAA
4213	CACCCTGACAGAGTTCACAAAAA
4214	ACCCTGACAGAGTTCACAAAAAG
4215	CCCTGACAGAGTTCACAAAAAGC
4216	CCTGACAGAGTTCACAAAAAGCC
4217	CTGACAGAGTTCACAAAAAGCCC
4218	TGACAGAGTTCACAAAAAGCCCA
4219	GACAGAGTTCACAAAAAGCCCAC
4220	ACAGAGTTCACAAAAAGCCCACT
4221	CAGAGTTCACAAAAAGCCCACTT
4222	AGAGTTCACAAAAAGCCCACTTT
4223	GAGTTCACAAAAAGCCCACTTTA
4224	AGTTCACAAAAAGCCCACTTTAG
4225	GTTCACAAAAAGCCCACTTTAGA
4226	TTCACAAAAAGCCCACTTTAGAG
4227	TCACAAAAAGCCCACTTTAGAGT
4228	CACAAAAAGCCCACTTTAGAGTA
4229	ACAAAAAGCCCACTTTAGAGTAT
4230	CAAAAAGCCCACTTTAGAGTATA
4231	AAAAAGCCCACTTTAGAGTATAC

Fig. 27 cont'd (Sheet 73 of 84)

ID	SEQUENCE
4232	AAAAGCCCACTTTAGAGTATACA
4233	AAAGCCCACTTTAGAGTATACAT
4234	AAGCCCACTTTAGAGTATACATT
4235	AGCCCACTTTAGAGTATACATTG
4236	GCCCACTTTAGAGTATACATTGC
4237	CCCACTTTAGAGTATACATTGCT
4238	CCACTTTAGAGTATACATTGCTA
4239	CACTTTAGAGTATACATTGCTAT
4240	ACTTTAGAGTATACATTGCTATT
4241	CTTTAGAGTATACATTGCTATTA
4242	TTTAGAGTATACATTGCTATTAT
4243	TTAGAGTATACATTGCTATTATG
4244	TAGAGTATACATTGCTATTATGG
4245	AGAGTATACATTGCTATTATGGG
4246	GAGTATACATTGCTATTATGGGA
4247	AGTATACATTGCTATTATGGGAG
4248	GTATACATTGCTATTATGGGAGA
4249	TATACATTGCTATTATGGGAGAC
4250	ATACATTGCTATTATGGGAGACC
4251	TACATTGCTATTATGGGAGACCA
4252	ACATTGCTATTATGGGAGACCAC
4253	CATTGCTATTATGGGAGACCACC
4254	ATTGCTATTATGGGAGACCACCC
4255	TTGCTATTATGGGAGACCACCCA
4256	TGCTATTATGGGAGACCACCCAG
4257	GCTATTATGGGAGACCACCCAGA
4258	CTATTATGGGAGACCACCCAGAC
4259	TATTATGGGAGACCACCCAGACA
4260	ATTATGGGAGACCACCCAGACAT
4261	TTATGGGAGACCACCCAGACATC
4262	TATGGGAGACCACCCAGACATCT
4263	ATGGGAGACCACCCAGACATCTG
4264	TGGGAGACCACCCAGACATCTGA
4265	GGGAGACCACCCAGACATCTGAC
4266	GGAGACCACCCAGACATCTGACT
4267	GAGACCACCCAGACATCTGACTA
4268	AGACCACCCAGACATCTGACTAA
4269	GACCACCCAGACATCTGACTAAT
4270	ACCACCCAGACATCTGACTAATG
4271	CCACCCAGACATCTGACTAATGG
4272	CACCCAGACATCTGACTAATGGC
4273	ACCCAGACATCTGACTAATGGCT
4274	CCCAGACATCTGACTAATGGCTC
4275	CCAGACATCTGACTAATGGCTCT
4276	CAGACATCTGACTAATGGCTCTG
4277	AGACATCTGACTAATGGCTCTGT
4278	GACATCTGACTAATGGCTCTGTG
4279	ACATCTGACTAATGGCTCTGTGC
4280	CATCTGACTAATGGCTCTGTGCC
4281	ATCTGACTAATGGCTCTGTGCCA
4282	TCTGACTAATGGCTCTGTGCCAC
4283	CTGACTAATGGCTCTGTGCCACA
4284	TGACTAATGGCTCTGTGCCACAC
4285	GACTAATGGCTCTGTGCCACACT
4286	ACTAATGGCTCTGTGCCACACTC
4287	CTAATGGCTCTGTGCCACACTCC
4288	TAATGGCTCTGTGCCACACTCCA
4289	AATGGCTCTGTGCCACACTCCAA

Fig. 27 cont'd (Sheet 74 of 84)

ID	SEQUENCE
4290	ATGGCTCTGTGCCACACTCCAAG
4291	TGGCTCTGTGCCACACTCCAAGA
4292	GGCTCTGTGCCACACTCCAAGAC
4293	GCTCTGTGCCACACTCCAAGACC
4294	CTCTGTGCCACACTCCAAGACCT
4295	TCTGTGCCACACTCCAAGACCTG
4296	CTGTGCCACACTCCAAGACCTGT
4297	TGTGCCACACTCCAAGACCTGTG
4298	GTGCCACACTCCAAGACCTGTGC
4299	TGCCACACTCCAAGACCTGTGCC
4300	GCCACACTCCAAGACCTGTGCCT
4301	CCACACTCCAAGACCTGTGCCTT
4302	CACACTCCAAGACCTGTGCCTTT
4303	ACACTCCAAGACCTGTGCCTTTT
4304	CACTCCAAGACCTGTGCCTTTTA
4305	ACTCCAAGACCTGTGCCTTTTAG
4306	CTCCAAGACCTGTGCCTTTTAGA
4307	TCCAAGACCTGTGCCTTTTAGAG
4308	CCAAGACCTGTGCCTTTTAGAGA
4309	CAAGACCTGTGCCTTTTAGAGAA
4310	AAGACCTGTGCCTTTTAGAGAAG
4311	AGACCTGTGCCTTTTAGAGAAGC
4312	GACCTGTGCCTTTTAGAGAAGCT
4313	ACCTGTGCCTTTTAGAGAAGCTC
4314	CCTGTGCCTTTTAGAGAAGCTCA
4315	CTGTGCCTTTTAGAGAAGCTCAC
4316	TGTGCCTTTTAGAGAAGCTCACA
4317	GTGCCTTTTAGAGAAGCTCACAA
4318	TGCCTTTTAGAGAAGCTCACAAT
4319	GCCTTTTAGAGAAGCTCACAATG
4320	CCTTTTAGAGAAGCTCACAATGA
4321	CTTTTAGAGAAGCTCACAATGAT
4322	TTTTAGAGAAGCTCACAATGATT
4323	TTTAGAGAAGCTCACAATGATTT
4324	TTAGAGAAGCTCACAATGATTTA
4325	TAGAGAAGCTCACAATGATTTAA
4326	AGAGAAGCTCACAATGATTTAAG
4327	GAGAAGCTCACAATGATTTAAGG
4328	AGAAGCTCACAATGATTTAAGGA
4329	GAAGCTCACAATGATTTAAGGAC
4330	AAGCTCACAATGATTTAAGGACT
4331	AGCTCACAATGATTTAAGGACTG
4332	GCTCACAATGATTTAAGGACTGT
4333	CTCACAATGATTTAAGGACTGTT
4334	TCACAATGATTTAAGGACTGTTT
4335	CACAATGATTTAAGGACTGTTTG
4336	ACAATGATTTAAGGACTGTTTGA
4337	CAATGATTTAAGGACTGTTTGAA
4338	AATGATTTAAGGACTGTTTGAAA
4339	ATGATTTAAGGACTGTTTGAAAC
4340	TGATTTAAGGACTGTTTGAAACT
4341	GATTTAAGGACTGTTTGAAACTT
4342	ATTTAAGGACTGTTTGAAACTTC
4343	TTTAAGGACTGTTTGAAACTTCC
4344	TTAAGGACTGTTTGAAACTTCCA
4345	TAAGGACTGTTTGAAACTTCCAA
4346	AAGGACTGTTTGAAACTTCCAAT
4347	AGGACTGTTTGAAACTTCCAATT

Fig. 27 cont'd (Sheet 75 of 84)

ID	SEQUENCE
4348	GGACTGTTTGAAACTTCCAATTA
4349	GACTGTTTGAAACTTCCAATTAT
4350	ACTGTTTGAAACTTCCAATTATG
4351	CTGTTTGAAACTTCCAATTATGT
4352	TGTTTGAAACTTCCAATTATGTC
4353	GTTTGAAACTTCCAATTATGTCT
4354	TTTGAAACTTCCAATTATGTCTA
4355	TTGAAACTTCCAATTATGTCTAT
4356	TGAAACTTCCAATTATGTCTATA
4357	GAAACTTCCAATTATGTCTATAA
4358	AAACTTCCAATTATGTCTATAAT
4359	AACTTCCAATTATGTCTATAATT
4360	ACTTCCAATTATGTCTATAATTT
4361	CTTCCAATTATGTCTATAATTTA
4362	TTCCAATTATGTCTATAATTTAT
4363	TCCAATTATGTCTATAATTTATA
4364	CCAATTATGTCTATAATTTATAT
4365	CAATTATGTCTATAATTTATATT
4366	AATTATGTCTATAATTTATATTC
4367	ATTATGTCTATAATTTATATTCT
4368	TTATGTCTATAATTTATATTCTT
4369	TATGTCTATAATTTATATTCTTT
4370	ATGTCTATAATTTATATTCTTTT
4371	TGTCTATAATTTATATTCTTTTG
4372	GTCTATAATTTATATTCTTTTGT
4373	TCTATAATTTATATTCTTTTGTT
4374	CTATAATTTATATTCTTTTGTTT
4375	TATAATTTATATTCTTTTGTTTA
4376	ATAATTTATATTCTTTTGTTTAC
4377	TAATTTATATTCTTTTGTTTACA
4378	AATTTATATTCTTTTGTTTACAT
4379	ATTTATATTCTTTTGTTTACATG
4380	TTTATATTCTTTTGTTTACATGA
4381	TTATATTCTTTTGTTTACATGAT
4382	TATATTCTTTTGTTTACATGATG
4383	ATATTCTTTTGTTTACATGATGA
4384	TATTCTTTTGTTTACATGATGAA
4385	ATTCTTTTGTTTACATGATGAAA
4386	TTCTTTTGTTTACATGATGAAAC
4387	TCTTTTGTTTACATGATGAAACT
4388	CTTTTGTTTACATGATGAAACTT
4389	TTTTGTTTACATGATGAAACTTT
4390	TTTGTTTACATGATGAAACTTTT
4391	TTGTTTACATGATGAAACTTTTT
4392	TGTTTACATGATGAAACTTTTTG
4393	GTTTACATGATGAAACTTTTTGT
4394	TTTACATGATGAAACTTTTTGTT
4395	TTACATGATGAAACTTTTTGTTG
4396	TACATGATGAAACTTTTTGTTGT
4397	ACATGATGAAACTTTTTGTTGTT
4398	CATGATGAAACTTTTTGTTGTTG
4399	ATGATGAAACTTTTTGTTGTTGC
4400	TGATGAAACTTTTTGTTGTTGCT
4401	GATGAAACTTTTTGTTGTTGCTT
4402	ATGAAACTTTTTGTTGTTGCTTG
4403	TGAAACTTTTTGTTGTTGCTTGT
4404	GAAACTTTTTGTTGTTGCTTGTT
4405	AAACTTTTTGTTGTTGCTTGTTT

Fig. 27 cont'd (Sheet 76 of 84)

ID	SEQUENCE
4406	AACTTTTTGTTGTTGCTTGTTTG
4407	ACTTTTTGTTGTTGCTTGTTTGT
4408	CTTTTTGTTGTTGCTTGTTTGTA
4409	TTTTTGTTGTTGCTTGTTTGTAT
4410	TTTTGTTGTTGCTTGTTTGTATA
4411	TTTGTTGTTGCTTGTTTGTATAT
4412	TTGTTGTTGCTTGTTTGTATATA
4413	TGTTGTTGCTTGTTTGTATATAA
4414	GTTGTTGCTTGTTTGTATATAAT
4415	TTGTTGCTTGTTTGTATATAATA
4416	TGTTGCTTGTTTGTATATAATAC
4417	GTTGCTTGTTTGTATATAATACA
4418	TTGCTTGTTTGTATATAATACAA
4419	TGCTTGTTTGTATATAATACAAT
4420	GCTTGTTTGTATATAATACAATG
4421	CTTGTTTGTATATAATACAATGT
4422	TTGTTTGTATATAATACAATGTG
4423	TGTTTGTATATAATACAATGTGT
4424	GTTTGTATATAATACAATGTGTA
4425	TTTGTATATAATACAATGTGTAC
4426	TTGTATATAATACAATGTGTACA
4427	TGTATATAATACAATGTGTACAT
4428	GTATATAATACAATGTGTACATG
4429	TATATAATACAATGTGTACATGT
4430	ATATAATACAATGTGTACATGTA
4431	TATAATACAATGTGTACATGTAT
4432	ATAATACAATGTGTACATGTATC
4433	TAATACAATGTGTACATGTATCT
4434	AATACAATGTGTACATGTATCTT
4435	ATACAATGTGTACATGTATCTTT
4436	TACAATGTGTACATGTATCTTTT
4437	ACAATGTGTACATGTATCTTTTT
4438	CAATGTGTACATGTATCTTTTTC
4439	AATGTGTACATGTATCTTTTTCT
4440	ATGTGTACATGTATCTTTTTCTC
4441	TGTGTACATGTATCTTTTTCTCG
4442	GTGTACATGTATCTTTTTCTCGA
4443	TGTACATGTATCTTTTTCTCGAT
4444	GTACATGTATCTTTTTCTCGATT
4445	TACATGTATCTTTTTCTCGATTC
4446	ACATGTATCTTTTTCTCGATTCA
4447	CATGTATCTTTTTCTCGATTCAA
4448	ATGTATCTTTTTCTCGATTCAAA
4449	TGTATCTTTTTCTCGATTCAAAT
4450	GTATCTTTTTCTCGATTCAAATC
4451	TATCTTTTTCTCGATTCAAATCT
4452	ATCTTTTTCTCGATTCAAATCTT
4453	TCTTTTTCTCGATTCAAATCTTA
4454	CTTTTTCTCGATTCAAATCTTAA
4455	TTTTTCTCGATTCAAATCTTAAC
4456	TTTTCTCGATTCAAATCTTAACC
4457	TTTCTCGATTCAAATCTTAACCC
4458	TTCTCGATTCAAATCTTAACCCT
4459	TCTCGATTCAAATCTTAACCCTT
4460	CTCGATTCAAATCTTAACCCTTA
4461	TCGATTCAAATCTTAACCCTTAG
4462	CGATTCAAATCTTAACCCTTAGG
4463	GATTCAAATCTTAACCCTTAGGA

Fig. 27 cont'd (Sheet 77 of 84)

ID	SEQUENCE
4464	ATTCAAATCTTAACCCTTAGGAC
4465	TTCAAATCTTAACCCTTAGGACT
4466	TCAAATCTTAACCCTTAGGACTC
4467	CAAATCTTAACCCTTAGGACTCT
4468	AAATCTTAACCCTTAGGACTCTG
4469	AATCTTAACCCTTAGGACTCTGG
4470	ATCTTAACCCTTAGGACTCTGGT
4471	TCTTAACCCTTAGGACTCTGGTA
4472	CTTAACCCTTAGGACTCTGGTAT
4473	TTAACCCTTAGGACTCTGGTATT
4474	TAACCCTTAGGACTCTGGTATTT
4475	AACCCTTAGGACTCTGGTATTTT
4476	ACCCTTAGGACTCTGGTATTTTT
4477	CCCTTAGGACTCTGGTATTTTTG
4478	CCTTAGGACTCTGGTATTTTTGA
4479	CTTAGGACTCTGGTATTTTTGAT
4480	TTAGGACTCTGGTATTTTTGATC
4481	TAGGACTCTGGTATTTTTGATCT
4482	AGGACTCTGGTATTTTTGATCTG
4483	GGACTCTGGTATTTTTGATCTGG
4484	GACTCTGGTATTTTTGATCTGGC
4485	ACTCTGGTATTTTTGATCTGGCA
4486	CTCTGGTATTTTTGATCTGGCAA
4487	TCTGGTATTTTTGATCTGGCAAC
4488	CTGGTATTTTTGATCTGGCAACC
4489	TGGTATTTTTGATCTGGCAACCA
4490	GGTATTTTTGATCTGGCAACCAT
4491	GTATTTTTGATCTGGCAACCATA
4492	TATTTTTGATCTGGCAACCATAT
4493	ATTTTTGATCTGGCAACCATATT
4494	TTTTTGATCTGGCAACCATATTT
4495	TTTTGATCTGGCAACCATATTTC
4496	TTTGATCTGGCAACCATATTTCT
4497	TTGATCTGGCAACCATATTTCTG
4498	TGATCTGGCAACCATATTTCTGG
4499	GATCTGGCAACCATATTTCTGGA
4500	ATCTGGCAACCATATTTCTGGAA
4501	TCTGGCAACCATATTTCTGGAAG
4502	CTGGCAACCATATTTCTGGAAGT
4503	TGGCAACCATATTTCTGGAAGTT
4504	GGCAACCATATTTCTGGAAGTTG
4505	GCAACCATATTTCTGGAAGTTGA
4506	CAACCATATTTCTGGAAGTTGAG
4507	AACCATATTTCTGGAAGTTGAGA
4508	ACCATATTTCTGGAAGTTGAGAT
4509	CCATATTTCTGGAAGTTGAGATG
4510	CATATTTCTGGAAGTTGAGATGT
4511	ATATTTCTGGAAGTTGAGATGTT
4512	TATTTCTGGAAGTTGAGATGTTT
4513	ATTTCTGGAAGTTGAGATGTTTC
4514	TTTCTGGAAGTTGAGATGTTTCA
4515	TTCTGGAAGTTGAGATGTTTCAG
4516	TCTGGAAGTTGAGATGTTTCAGC
4517	CTGGAAGTTGAGATGTTTCAGCT
4518	TGGAAGTTGAGATGTTTCAGCTT
4519	GGAAGTTGAGATGTTTCAGCTTG
4520	GAAGTTGAGATGTTTCAGCTTGA
4521	AAGTTGAGATGTTTCAGCTTGAA

Fig. 27 cont'd (Sheet 78 of 84)

ID	SEQUENCE
4522	AGTTGAGATGTTTCAGCTTGAAG
4523	GTTGAGATGTTTCAGCTTGAAGA
4524	TTGAGATGTTTCAGCTTGAAGAA
4525	TGAGATGTTTCAGCTTGAAGAAC
4526	GAGATGTTTCAGCTTGAAGAACC
4527	AGATGTTTCAGCTTGAAGAACCA
4528	GATGTTTCAGCTTGAAGAACCAA
4529	ATGTTTCAGCTTGAAGAACCAAA
4530	TGTTTCAGCTTGAAGAACCAAAA
4531	GTTTCAGCTTGAAGAACCAAAAC
4532	TTTCAGCTTGAAGAACCAAAACA
4533	TTCAGCTTGAAGAACCAAAACAG
4534	TCAGCTTGAAGAACCAAAACAGA
4535	CAGCTTGAAGAACCAAAACAGAA
4536	AGCTTGAAGAACCAAAACAGAAG
4537	GCTTGAAGAACCAAAACAGAAGG
4538	CTTGAAGAACCAAAACAGAAGGA
4539	TTGAAGAACCAAAACAGAAGGAA
4540	TGAAGAACCAAAACAGAAGGAAT
4541	GAAGAACCAAAACAGAAGGAATA
4542	AAGAACCAAAACAGAAGGAATAT
4543	AGAACCAAAACAGAAGGAATATG
4544	GAACCAAAACAGAAGGAATATGT
4545	AACCAAAACAGAAGGAATATGTA
4546	ACCAAAACAGAAGGAATATGTAC
4547	CCAAAACAGAAGGAATATGTACA
4548	CAAAACAGAAGGAATATGTACAA
4549	AAAACAGAAGGAATATGTACAAA
4550	AAACAGAAGGAATATGTACAAAG
4551	AACAGAAGGAATATGTACAAAGA
4552	ACAGAAGGAATATGTACAAAGAA
4553	CAGAAGGAATATGTACAAAGAAT
4554	AGAAGGAATATGTACAAAGAATA
4555	GAAGGAATATGTACAAAGAATAA
4556	AAGGAATATGTACAAAGAATAAA
4557	AGGAATATGTACAAAGAATAAAT
4558	GGAATATGTACAAAGAATAAATT
4559	GAATATGTACAAAGAATAAATTT
4560	AATATGTACAAAGAATAAATTTT
4561	ATATGTACAAAGAATAAATTTTC
4562	TATGTACAAAGAATAAATTTTCT
4563	ATGTACAAAGAATAAATTTTCTG
4564	TGTACAAAGAATAAATTTTCTGC
4565	GTACAAAGAATAAATTTTCTGCT
4566	TACAAAGAATAAATTTTCTGCTC
4567	ACAAAGAATAAATTTTCTGCTCA
4568	CAAAGAATAAATTTTCTGCTCAC
4569	AAAGAATAAATTTTCTGCTCACG
4570	AAGAATAAATTTTCTGCTCACGA
4571	AGAATAAATTTTCTGCTCACGAT
4572	GAATAAATTTTCTGCTCACGATG
4573	AATAAATTTTCTGCTCACGATGA
4574	ATAAATTTTCTGCTCACGATGAG
4575	TAAATTTTCTGCTCACGATGAGT
4576	AAATTTTCTGCTCACGATGAGTT
4577	AATTTTCTGCTCACGATGAGTTT
4578	ATTTTCTGCTCACGATGAGTTTA
4579	TTTTCTGCTCACGATGAGTTTAG

Fig. 27 cont'd (Sheet 79 of 84)

ID	SEQUENCE
4580	TTTCTGCTCACGATGAGTTTAGT
4581	TTCTGCTCACGATGAGTTTAGTG
4582	TCTGCTCACGATGAGTTTAGTGT
4583	CTGCTCACGATGAGTTTAGTGTG
4584	TGCTCACGATGAGTTTAGTGTGT
4585	GCTCACGATGAGTTTAGTGTGTA
4586	CTCACGATGAGTTTAGTGTGTAA
4587	TCACGATGAGTTTAGTGTGTAAA
4588	CACGATGAGTTTAGTGTGTAAAG
4589	ACGATGAGTTTAGTGTGTAAAGT
4590	CGATGAGTTTAGTGTGTAAAGTT
4591	GATGAGTTTAGTGTGTAAAGTTT
4592	ATGAGTTTAGTGTGTAAAGTTTA
4593	TGAGTTTAGTGTGTAAAGTTTAG
4594	GAGTTTAGTGTGTAAAGTTTAGA
4595	AGTTTAGTGTGTAAAGTTTAGAG
4596	GTTTAGTGTGTAAAGTTTAGAGA
4597	TTTAGTGTGTAAAGTTTAGAGAC
4598	TTAGTGTGTAAAGTTTAGAGACA
4599	TAGTGTGTAAAGTTTAGAGACAT
4600	AGTGTGTAAAGTTTAGAGACATC
4601	GTGTGTAAAGTTTAGAGACATCT
4602	TGTGTAAAGTTTAGAGACATCTG
4603	GTGTAAAGTTTAGAGACATCTGA
4604	TGTAAAGTTTAGAGACATCTGAC
4605	GTAAAGTTTAGAGACATCTGACT
4606	TAAAGTTTAGAGACATCTGACTT
4607	AAAGTTTAGAGACATCTGACTTT
4608	AAGTTTAGAGACATCTGACTTTG
4609	AGTTTAGAGACATCTGACTTTGA
4610	GTTTAGAGACATCTGACTTTGAT
4611	TTTAGAGACATCTGACTTTGATA
4612	TTAGAGACATCTGACTTTGATAG
4613	TAGAGACATCTGACTTTGATAGC
4614	AGAGACATCTGACTTTGATAGCT
4615	GAGACATCTGACTTTGATAGCTA
4616	AGACATCTGACTTTGATAGCTAA
4617	GACATCTGACTTTGATAGCTAAA
4618	ACATCTGACTTTGATAGCTAAAT
4619	CATCTGACTTTGATAGCTAAATT
4620	ATCTGACTTTGATAGCTAAATTA
4621	TCTGACTTTGATAGCTAAATTAA
4622	CTGACTTTGATAGCTAAATTAAA
4623	TGACTTTGATAGCTAAATTAAAC
4624	GACTTTGATAGCTAAATTAAACC
4625	ACTTTGATAGCTAAATTAAACCA
4626	CTTTGATAGCTAAATTAAACCAA
4627	TTTGATAGCTAAATTAAACCAAA
4628	TTGATAGCTAAATTAAACCAAAC
4629	TGATAGCTAAATTAAACCAAACC
4630	GATAGCTAAATTAAACCAAACCC
4631	ATAGCTAAATTAAACCAAACCCT
4632	TAGCTAAATTAAACCAAACCCTA
4633	AGCTAAATTAAACCAAACCCTAT
4634	GCTAAATTAAACCAAACCCTATT
4635	CTAAATTAAACCAAACCCTATTG
4636	TAAATTAAACCAAACCCTATTGA
4637	AAATTAAACCAAACCCTATTGAA

Fig. 27 cont'd (Sheet 80 of 84)

ID	SEQUENCE
4638	AATTAAACCAAACCCTATTGAAG
4639	ATTAAACCAAACCCTATTGAAGA
4640	TTAAACCAAACCCTATTGAAGAA
4641	TAAACCAAACCCTATTGAAGAAT
4642	AAACCAAACCCTATTGAAGAATT
4643	AACCAAACCCTATTGAAGAATTG
4644	ACCAAACCCTATTGAAGAATTGA
4645	CCAAACCCTATTGAAGAATTGAA
4646	CAAACCCTATTGAAGAATTGAAT
4647	AAACCCTATTGAAGAATTGAATA
4648	AACCCTATTGAAGAATTGAATAT
4649	ACCCTATTGAAGAATTGAATATA
4650	CCCTATTGAAGAATTGAATATAT
4651	CCTATTGAAGAATTGAATATATG
4652	CTATTGAAGAATTGAATATATGC
4653	TATTGAAGAATTGAATATATGCT
4654	ATTGAAGAATTGAATATATGCTA
4655	TTGAAGAATTGAATATATGCTAC
4656	TGAAGAATTGAATATATGCTACT
4657	GAAGAATTGAATATATGCTACTT
4658	AAGAATTGAATATATGCTACTTC
4659	AGAATTGAATATATGCTACTTCA
4660	GAATTGAATATATGCTACTTCAA
4661	AATTGAATATATGCTACTTCAAG
4662	ATTGAATATATGCTACTTCAAGA
4663	TTGAATATATGCTACTTCAAGAA
4664	TGAATATATGCTACTTCAAGAAA
4665	GAATATATGCTACTTCAAGAAAC
4666	AATATATGCTACTTCAAGAAACT
4667	ATATATGCTACTTCAAGAAACTA
4668	TATATGCTACTTCAAGAAACTAA
4669	ATATGCTACTTCAAGAAACTAAA
4670	TATGCTACTTCAAGAAACTAAAT
4671	ATGCTACTTCAAGAAACTAAATT
4672	TGCTACTTCAAGAAACTAAATTG
4673	GCTACTTCAAGAAACTAAATTGA
4674	CTACTTCAAGAAACTAAATTGAT
4675	TACTTCAAGAAACTAAATTGATC
4676	ACTTCAAGAAACTAAATTGATCT
4677	CTTCAAGAAACTAAATTGATCTC
4678	TTCAAGAAACTAAATTGATCTCG
4679	TCAAGAAACTAAATTGATCTCGT
4680	CAAGAAACTAAATTGATCTCGTA
4681	AAGAAACTAAATTGATCTCGTAG
4682	AGAAACTAAATTGATCTCGTAGA
4683	GAAACTAAATTGATCTCGTAGAA
4684	AAACTAAATTGATCTCGTAGAAT
4685	AACTAAATTGATCTCGTAGAATT
4686	ACTAAATTGATCTCGTAGAATTA
4687	CTAAATTGATCTCGTAGAATTAT
4688	TAAATTGATCTCGTAGAATTATC
4689	AAATTGATCTCGTAGAATTATCT
4690	AATTGATCTCGTAGAATTATCTT
4691	ATTGATCTCGTAGAATTATCTTA
4692	TTGATCTCGTAGAATTATCTTAA
4693	TGATCTCGTAGAATTATCTTAAT
4694	GATCTCGTAGAATTATCTTAATA
4695	ATCTCGTAGAATTATCTTAATAA

Fig. 27 cont'd (Sheet 81 of 84)

ID	SEQUENCE
4696	TCTCGTAGAATTATCTTAATAAA
4697	CTCGTAGAATTATCTTAATAAAA
4698	TCGTAGAATTATCTTAATAAAAT
4699	CGTAGAATTATCTTAATAAAATA
4700	GTAGAATTATCTTAATAAAATAA
4701	TAGAATTATCTTAATAAAATAAT
4702	AGAATTATCTTAATAAAATAATG
4703	GAATTATCTTAATAAAATAATGG
4704	AATTATCTTAATAAAATAATGGC
4705	ATTATCTTAATAAAATAATGGCT
4706	TTATCTTAATAAAATAATGGCTA
4707	TATCTTAATAAAATAATGGCTAT
4708	ATCTTAATAAAATAATGGCTATA
4709	TCTTAATAAAATAATGGCTATAA
4710	CTTAATAAAATAATGGCTATAAT
4711	TTAATAAAATAATGGCTATAATT
4712	TAATAAAATAATGGCTATAATTT
4713	AATAAAATAATGGCTATAATTTC
4714	ATAAAATAATGGCTATAATTTCT
4715	TAAAATAATGGCTATAATTTCTC
4716	AAAATAATGGCTATAATTTCTCT
4717	AAATAATGGCTATAATTTCTCTG
4718	AATAATGGCTATAATTTCTCTGC
4719	ATAATGGCTATAATTTCTCTGCA
4720	TAATGGCTATAATTTCTCTGCAA
4721	AATGGCTATAATTTCTCTGCAAA
4722	ATGGCTATAATTTCTCTGCAAAA
4723	TGGCTATAATTTCTCTGCAAAAT
4724	GGCTATAATTTCTCTGCAAAATC
4725	GCTATAATTTCTCTGCAAAATCA
4726	CTATAATTTCTCTGCAAAATCAG
4727	TATAATTTCTCTGCAAAATCAGA
4728	ATAATTTCTCTGCAAAATCAGAT
4729	TAATTTCTCTGCAAAATCAGATG
4730	AATTTCTCTGCAAAATCAGATGT
4731	ATTTCTCTGCAAAATCAGATGTC
4732	TTTCTCTGCAAAATCAGATGTCA
4733	TTCTCTGCAAAATCAGATGTCAG
4734	TCTCTGCAAAATCAGATGTCAGC
4735	CTCTGCAAAATCAGATGTCAGCA
4736	TCTGCAAAATCAGATGTCAGCAT
4737	CTGCAAAATCAGATGTCAGCATA
4738	TGCAAAATCAGATGTCAGCATAA
4739	GCAAAATCAGATGTCAGCATAAG
4740	CAAAATCAGATGTCAGCATAAGC
4741	AAAATCAGATGTCAGCATAAGCG
4742	AAATCAGATGTCAGCATAAGCGA
4743	AATCAGATGTCAGCATAAGCGAT
4744	ATCAGATGTCAGCATAAGCGATG
4745	TCAGATGTCAGCATAAGCGATGG
4746	CAGATGTCAGCATAAGCGATGGA
4747	AGATGTCAGCATAAGCGATGGAT
4748	GATGTCAGCATAAGCGATGGATA
4749	ATGTCAGCATAAGCGATGGATAA
4750	TGTCAGCATAAGCGATGGATAAT
4751	GTCAGCATAAGCGATGGATAATA
4752	TCAGCATAAGCGATGGATAATAC
4753	CAGCATAAGCGATGGATAATACC

Fig. 27 cont'd (Sheet 82 of 84)

ID	SEQUENCE
4754	AGCATAAGCGATGGATAATACCT
4755	GCATAAGCGATGGATAATACCTA
4756	CATAAGCGATGGATAATACCTAA
4757	ATAAGCGATGGATAATACCTAAT
4758	TAAGCGATGGATAATACCTAATA
4759	AAGCGATGGATAATACCTAATAA
4760	AGCGATGGATAATACCTAATAAA
4761	GCGATGGATAATACCTAATAAAC
4762	CGATGGATAATACCTAATAAACT
4763	GATGGATAATACCTAATAAACTG
4764	ATGGATAATACCTAATAAACTGC
4765	TGGATAATACCTAATAAACTGCC
4766	GGATAATACCTAATAAACTGCCC
4767	GATAATACCTAATAAACTGCCCT
4768	ATAATACCTAATAAACTGCCCTC
4769	TAATACCTAATAAACTGCCCTCA
4770	AATACCTAATAAACTGCCCTCAG
4771	ATACCTAATAAACTGCCCTCAGT
4772	TACCTAATAAACTGCCCTCAGTA
4773	ACCTAATAAACTGCCCTCAGTAA
4774	CCTAATAAACTGCCCTCAGTAAA
4775	CTAATAAACTGCCCTCAGTAAAT
4776	TAATAAACTGCCCTCAGTAAATC
4777	AATAAACTGCCCTCAGTAAATCC
4778	ATAAACTGCCCTCAGTAAATCCA
4779	TAAACTGCCCTCAGTAAATCCAT
4780	AAACTGCCCTCAGTAAATCCATG
4781	AACTGCCCTCAGTAAATCCATGG
4782	ACTGCCCTCAGTAAATCCATGGT
4783	CTGCCCTCAGTAAATCCATGGTT
4784	TGCCCTCAGTAAATCCATGGTTA
4785	GCCCTCAGTAAATCCATGGTTAA
4786	CCCTCAGTAAATCCATGGTTAAT
4787	CCTCAGTAAATCCATGGTTAATA
4788	CTCAGTAAATCCATGGTTAATAA
4789	TCAGTAAATCCATGGTTAATAAA
4790	CAGTAAATCCATGGTTAATAAAT
4791	AGTAAATCCATGGTTAATAAATG
4792	GTAAATCCATGGTTAATAAATGT
4793	TAAATCCATGGTTAATAAATGTG
4794	AAATCCATGGTTAATAAATGTGG
4795	AATCCATGGTTAATAAATGTGGT
4796	ATCCATGGTTAATAAATGTGGTT
4797	TCCATGGTTAATAAATGTGGTTT
4798	CCATGGTTAATAAATGTGGTTTC
4799	CATGGTTAATAAATGTGGTTTCT
4800	ATGGTTAATAAATGTGGTTTCTA
4801	TGGTTAATAAATGTGGTTTCTAC
4802	GGTTAATAAATGTGGTTTCTACA
4803	GTTAATAAATGTGGTTTCTACAT
4804	TTAATAAATGTGGTTTCTACATT

ID	SEQUENCE
1	GCGGCCGCAGCAGCCTCCGCCCC
2	CGGCCGCAGCAGCCTCCGCCCCC
3	CCCCCCGCACGGTGTGAGCGCCC
4	CCCCCGCACGGTGTGAGCGCCCG
5	CCCCGCACGGTGTGAGCGCCCGA
6	CCCGCACGGTGTGAGCGCCCGAC
7	CCGCACGGTGTGAGCGCCCGACG
8	CGCACGGTGTGAGCGCCCGACGC
9	GCACGGTGTGAGCGCCCGACGCG
10	CACGGTGTGAGCGCCCGACGCGG
11	ACGGTGTGAGCGCCCGACGCGGC
12	CGGTGTGAGCGCCCGACGCGGCC
13	GGTGTGAGCGCCCGACGCGGCCG
14	GTGTGAGCGCCCGACGCGGCCGA
15	TGTGAGCGCCCGACGCGGCCGAG
16	GTGAGCGCCCGACGCGGCCGAGG
17	TGAGCGCCCGACGCGGCCGAGGC
18	GAGCGCCCGACGCGGCCGAGGCG
19	AGCGCCCGACGCGGCCGAGGCGG
20	GCGCCCGACGCGGCCGAGGCGGC
21	CGCCCGACGCGGCCGAGGCGGCC
22	GCCCGACGCGGCCGAGGCGGCCG
23	GCGGCCGGAGTCCCGAGCTAGCC
24	CGGCCGGAGTCCCGAGCTAGCCC
25	GGCCGGAGTCCCGAGCTAGCCCC
26	GCCGGAGTCCCGAGCTAGCCCCG
27	CCGGAGTCCCGAGCTAGCCCCGG
28	CGGAGTCCCGAGCTAGCCCCGGC
29	CGCCGCCCAGACCGGACGACAGG
30	GCCGCCCAGACCGGACGACAGGC
31	CCGCCCAGACCGGACGACAGGCC
32	CGCCCAGACCGGACGACAGGCCA
33	GCCCAGACCGGACGACAGGCCAC
34	CCCAGACCGGACGACAGGCCACC
35	CCAGACCGGACGACAGGCCACCT
36	CAGACCGGACGACAGGCCACCTC
37	AGACCGGACGACAGGCCACCTCG
38	GACCGGACGACAGGCCACCTCGT
39	ACCGGACGACAGGCCACCTCGTC
40	CCGGACGACAGGCCACCTCGTCG
41	CGGACGACAGGCCACCTCGTCGG
42	GGACGACAGGCCACCTCGTCGGC
43	GACGACAGGCCACCTCGTCGGCG
44	ACGACAGGCCACCTCGTCGGCGT
45	CGACAGGCCACCTCGTCGGCGTC
46	GACAGGCCACCTCGTCGGCGTCC
47	ACAGGCCACCTCGTCGGCGTCCG
48	CAGGCCACCTCGTCGGCGTCCGC
49	AGGCCACCTCGTCGGCGTCCGCC
50	GGCCACCTCGTCGGCGTCCGCCC
51	GCCACCTCGTCGGCGTCCGCCCG
52	CCACCTCGTCGGCGTCCGCCCGA
53	CACCTCGTCGGCGTCCGCCCGAG
54	ACCTCGTCGGCGTCCGCCCGAGT
55	CCTCGTCGGCGTCCGCCCGAGTC
56	CTCGTCGGCGTCCGCCCGAGTCC
57	TCGTCGGCGTCCGCCCGAGTCCC
58	CGTCGGCGTCCGCCCGAGTCCCC

Fig. 28 (Sheet 1 of 93)

ID	SEQUENCE
59	GTCGGCGTCCGCCCGAGTCCCCG
60	TCGGCGTCCGCCCGAGTCCCCGC
61	CGGCGTCCGCCCGAGTCCCCGCC
62	GGCGTCCGCCCGAGTCCCCGCCT
63	GCGTCCGCCCGAGTCCCCGCCTC
64	CGTCCGCCCGAGTCCCCGCCTCG
65	GTCCGCCCGAGTCCCCGCCTCGC
66	TCCGCCCGAGTCCCCGCCTCGCC
67	CCGCCCGAGTCCCCGCCTCGCCG
68	CGCCCGAGTCCCCGCCTCGCCGC
69	GCCCGAGTCCCCGCCTCGCCGCC
70	CCCGAGTCCCCGCCTCGCCGCCA
71	CCGAGTCCCCGCCTCGCCGCCAA
72	CGAGTCCCCGCCTCGCCGCCAAC
73	GAGTCCCCGCCTCGCCGCCAACG
74	AGTCCCCGCCTCGCCGCCAACGC
75	GTCCCCGCCTCGCCGCCAACGCC
76	TCCCCGCCTCGCCGCCAACGCCA
77	CCCCGCCTCGCCGCCAACGCCAC
78	CCCGCCTCGCCGCCAACGCCACA
79	CCGCCTCGCCGCCAACGCCACAA
80	CGCCTCGCCGCCAACGCCACAAC
81	GCCTCGCCGCCAACGCCACAACC
82	CCTCGCCGCCAACGCCACAACCA
83	CTCGCCGCCAACGCCACAACCAC
84	TCGCCGCCAACGCCACAACCACC
85	CGCCGCCAACGCCACAACCACCG
86	GCCGCCAACGCCACAACCACCGC
87	CCGCCAACGCCACAACCACCGCG
88	CGCCAACGCCACAACCACCGCGC
89	GCCAACGCCACAACCACCGCGCA
90	CCAACGCCACAACCACCGCGCAC
91	CAACGCCACAACCACCGCGCACG
92	AACGCCACAACCACCGCGCACGG
93	ACGCCACAACCACCGCGCACGGC
94	CGCCACAACCACCGCGCACGGCC
95	GCCACAACCACCGCGCACGGCCC
96	CCACAACCACCGCGCACGGCCCC
97	CACAACCACCGCGCACGGCCCCC
98	ACAACCACCGCGCACGGCCCCCT
99	CAACCACCGCGCACGGCCCCCTG
100	AACCACCGCGCACGGCCCCCTGA
101	ACCACCGCGCACGGCCCCCTGAC
102	CCACCGCGCACGGCCCCCTGACT
103	CACCGCGCACGGCCCCCTGACTC
104	ACCGCGCACGGCCCCCTGACTCC
105	CCGCGCACGGCCCCCTGACTCCG
106	CGCGCACGGCCCCCTGACTCCGT
107	GCGCACGGCCCCCTGACTCCGTC
108	CGCACGGCCCCCTGACTCCGTCC
109	GCACGGCCCCCTGACTCCGTCCA
110	CACGGCCCCCTGACTCCGTCCAG
111	ACGGCCCCCTGACTCCGTCCAGT
112	CGGCCCCCTGACTCCGTCCAGTA
113	GGCCCCCTGACTCCGTCCAGTAT
114	GCCCCCTGACTCCGTCCAGTATT
115	CCCCCTGACTCCGTCCAGTATTG
116	CCCCTGACTCCGTCCAGTATTGA

Fig. 28 cont'd (Sheet 2 of 93)

ID	SEQUENCE
117	CCCTGACTCCGTCCAGTATTGAT
118	CCTGACTCCGTCCAGTATTGATC
119	CTGACTCCGTCCAGTATTGATCG
120	TGACTCCGTCCAGTATTGATCGG
121	GACTCCGTCCAGTATTGATCGGG
122	ACTCCGTCCAGTATTGATCGGGA
123	CTCCGTCCAGTATTGATCGGGAG
124	TCCGTCCAGTATTGATCGGGAGA
125	CCGTCCAGTATTGATCGGGAGAG
126	CGTCCAGTATTGATCGGGAGAGC
127	GTCCAGTATTGATCGGGAGAGCC
128	TCCAGTATTGATCGGGAGAGCCG
129	CCAGTATTGATCGGGAGAGCCGG
130	CAGTATTGATCGGGAGAGCCGGA
131	AGTATTGATCGGGAGAGCCGGAG
132	GTATTGATCGGGAGAGCCGGAGC
133	TATTGATCGGGAGAGCCGGAGCG
134	ATTGATCGGGAGAGCCGGAGCGA
135	TTGATCGGGAGAGCCGGAGCGAG
136	TGATCGGGAGAGCCGGAGCGAGC
137	GATCGGGAGAGCCGGAGCGAGCT
138	ATCGGGAGAGCCGGAGCGAGCTC
139	TCGGGAGAGCCGGAGCGAGCTCT
140	CGGGAGAGCCGGAGCGAGCTCTT
141	GGGAGAGCCGGAGCGAGCTCTTC
142	GGAGAGCCGGAGCGAGCTCTTCG
143	GAGAGCCGGAGCGAGCTCTTCGG
144	AGAGCCGGAGCGAGCTCTTCGGG
145	GAGCCGGAGCGAGCTCTTCGGGG
146	AGCCGGAGCGAGCTCTTCGGGGA
147	GCCGGAGCGAGCTCTTCGGGGAG
148	CCGGAGCGAGCTCTTCGGGGAGC
149	CGGAGCGAGCTCTTCGGGGAGCA
150	GGAGCGAGCTCTTCGGGGAGCAG
151	GAGCGAGCTCTTCGGGGAGCAGC
152	ATGCGACCCTCCGGGACGGCCGG
153	TGCGACCCTCCGGGACGGCCGGG
154	GCCGGGGCAGCGCTCCTGGCGCT
155	CCGGGGCAGCGCTCCTGGCGCTG
156	CGGGGCAGCGCTCCTGGCGCTGC
157	GGGGCAGCGCTCCTGGCGCTGCT
158	GGGCAGCGCTCCTGGCGCTGCTG
159	GGCAGCGCTCCTGGCGCTGCTGG
160	GCAGCGCTCCTGGCGCTGCTGGC
161	CAGCGCTCCTGGCGCTGCTGGCT
162	AGCGCTCCTGGCGCTGCTGGCTG
163	GCGCTCCTGGCGCTGCTGGCTGC
164	CGCTCCTGGCGCTGCTGGCTGCG
165	GCTCCTGGCGCTGCTGGCTGCGC
166	CTCCTGGCGCTGCTGGCTGCGCT
167	TCCTGGCGCTGCTGGCTGCGCTC
168	CCTGGCGCTGCTGGCTGCGCTCT
169	CTGGCGCTGCTGGCTGCGCTCTG
170	TGGCGCTGCTGGCTGCGCTCTGC
171	GGCGCTGCTGGCTGCGCTCTGCC
172	GCGCTGCTGGCTGCGCTCTGCCC
173	CGCTGCTGGCTGCGCTCTGCCCG
174	GCTGCTGGCTGCGCTCTGCCCGG

Fig. 28 cont'd (Sheet 3 of 93)

ID	SEQUENCE
175	CTGCTGGCTGCGCTCTGCCCGGC
176	TGCTGGCTGCGCTCTGCCCGGCG
177	GCTGGCTGCGCTCTGCCCGGCGA
178	CTGGCTGCGCTCTGCCCGGCGAG
179	TGGCTGCGCTCTGCCCGGCGAGT
180	GGCTGCGCTCTGCCCGGCGAGTC
181	GCTGCGCTCTGCCCGGCGAGTCG
182	CTGCGCTCTGCCCGGCGAGTCGG
183	TGCGCTCTGCCCGGCGAGTCGGG
184	GCGCTCTGCCCGGCGAGTCGGGC
185	CGCTCTGCCCGGCGAGTCGGGCT
186	GCTCTGCCCGGCGAGTCGGGCTC
187	CTCTGCCCGGCGAGTCGGGCTCT
188	TCTGCCCGGCGAGTCGGGCTCTG
189	CTGCCCGGCGAGTCGGGCTCTGG
190	TGCCCGGCGAGTCGGGCTCTGGA
191	GCCCGGCGAGTCGGGCTCTGGAG
192	CCCGGCGAGTCGGGCTCTGGAGG
193	CCGGCGAGTCGGGCTCTGGAGGA
194	CGGCGAGTCGGGCTCTGGAGGAA
195	GGCGAGTCGGGCTCTGGAGGAAA
196	GCGAGTCGGGCTCTGGAGGAAAA
197	CGAGTCGGGCTCTGGAGGAAAAG
198	GAGTCGGGCTCTGGAGGAAAAGA
199	AGTCGGGCTCTGGAGGAAAAGAA
200	GTCGGGCTCTGGAGGAAAAGAAA
201	TCGGGCTCTGGAGGAAAAGAAAG
202	CGGGCTCTGGAGGAAAAGAAAGT
203	GGGCTCTGGAGGAAAAGAAAGTT
204	GGCTCTGGAGGAAAAGAAAGTTT
205	GCTCTGGAGGAAAAGAAAGTTTG
206	CTCTGGAGGAAAAGAAAGTTTGC
207	TCTGGAGGAAAAGAAAGTTTGCC
208	CTGGAGGAAAAGAAAGTTTGCCA
209	TGGAGGAAAAGAAAGTTTGCCAA
210	GGAGGAAAAGAAAGTTTGCCAAG
211	GAGGAAAAGAAAGTTTGCCAAGG
212	AGGAAAAGAAAGTTTGCCAAGGC
213	GGAAAAGAAAGTTTGCCAAGGCA
214	GAAAAGAAAGTTTGCCAAGGCAC
215	AAAAGAAAGTTTGCCAAGGCACG
216	AAAGAAAGTTTGCCAAGGCACGA
217	AAGAAAGTTTGCCAAGGCACGAG
218	AGAAAGTTTGCCAAGGCACGAGT
219	GAAAGTTTGCCAAGGCACGAGTA
220	AAAGTTTGCCAAGGCACGAGTAA
221	AAGTTTGCCAAGGCACGAGTAAC
222	AGTTTGCCAAGGCACGAGTAACA
223	GTTTGCCAAGGCACGAGTAACAA
224	TTTGCCAAGGCACGAGTAACAAG
225	TTGCCAAGGCACGAGTAACAAGC
226	TGCCAAGGCACGAGTAACAAGCT
227	GCCAAGGCACGAGTAACAAGCTC
228	CCAAGGCACGAGTAACAAGCTCA
229	CAAGGCACGAGTAACAAGCTCAC
230	AAGGCACGAGTAACAAGCTCACG
231	AGGCACGAGTAACAAGCTCACGC
232	GGCACGAGTAACAAGCTCACGCA

Fig. 28 cont'd (Sheet 4 of 93)

ID	SEQUENCE
233	GCACGAGTAACAAGCTCACGCAG
234	CACGAGTAACAAGCTCACGCAGT
235	ACGAGTAACAAGCTCACGCAGTT
236	CGAGTAACAAGCTCACGCAGTTG
237	GAGTAACAAGCTCACGCAGTTGG
238	AGTAACAAGCTCACGCAGTTGGG
239	GTAACAAGCTCACGCAGTTGGGC
240	TAACAAGCTCACGCAGTTGGGCA
241	AACAAGCTCACGCAGTTGGGCAC
242	ACAAGCTCACGCAGTTGGGCACT
243	CAAGCTCACGCAGTTGGGCACTT
244	AAGCTCACGCAGTTGGGCACTTT
245	AGCTCACGCAGTTGGGCACTTTT
246	GCTCACGCAGTTGGGCACTTTTG
247	CTCACGCAGTTGGGCACTTTTGA
248	TCACGCAGTTGGGCACTTTTGAA
249	CACGCAGTTGGGCACTTTTGAAG
250	ACGCAGTTGGGCACTTTTGAAGA
251	CGCAGTTGGGCACTTTTGAAGAT
252	GCAGTTGGGCACTTTTGAAGATC
253	CAGTTGGGCACTTTTGAAGATCA
254	AGTTGGGCACTTTTGAAGATCAT
255	GTTGGGCACTTTTGAAGATCATT
256	TTGGGCACTTTTGAAGATCATTT
257	TGGGCACTTTTGAAGATCATTTT
258	GGGCACTTTTGAAGATCATTTTC
259	GGCACTTTTGAAGATCATTTTCT
260	GCACTTTTGAAGATCATTTTCTC
261	CACTTTTGAAGATCATTTTCTCA
262	ACTTTTGAAGATCATTTTCTCAG
263	CTTTTGAAGATCATTTTCTCAGC
264	TTTTGAAGATCATTTTCTCAGCC
265	TTTGAAGATCATTTTCTCAGCCT
266	TTGAAGATCATTTTCTCAGCCTC
267	TGAAGATCATTTTCTCAGCCTCC
268	GAAGATCATTTTCTCAGCCTCCA
269	AAGATCATTTTCTCAGCCTCCAG
270	AGATCATTTTCTCAGCCTCCAGA
271	GATCATTTTCTCAGCCTCCAGAG
272	ATCATTTTCTCAGCCTCCAGAGG
273	TCATTTTCTCAGCCTCCAGAGGA
274	CATTTTCTCAGCCTCCAGAGGAT
275	ATTTTCTCAGCCTCCAGAGGATG
276	TTTTCTCAGCCTCCAGAGGATGT
277	TTTCTCAGCCTCCAGAGGATGTT
278	TTCTCAGCCTCCAGAGGATGTTC
279	TCTCAGCCTCCAGAGGATGTTCA
280	CTCAGCCTCCAGAGGATGTTCAA
281	TCAGCCTCCAGAGGATGTTCAAT
282	CAGCCTCCAGAGGATGTTCAATA
283	AGCCTCCAGAGGATGTTCAATAA
284	GCCTCCAGAGGATGTTCAATAAC
285	CCTCCAGAGGATGTTCAATAACT
286	CTCCAGAGGATGTTCAATAACTG
287	TCCAGAGGATGTTCAATAACTGT
288	CCAGAGGATGTTCAATAACTGTG
289	CAGAGGATGTTCAATAACTGTGA
290	AGAGGATGTTCAATAACTGTGAG

Fig. 28 cont'd (Sheet 5 of 93)

ID	SEQUENCE
291	GAGGATGTTCAATAACTGTGAGG
292	AGGATGTTCAATAACTGTGAGGT
293	GGATGTTCAATAACTGTGAGGTG
294	GATGTTCAATAACTGTGAGGTGG
295	ATGTTCAATAACTGTGAGGTGGT
296	TGTTCAATAACTGTGAGGTGGTC
297	GTTCAATAACTGTGAGGTGGTCC
298	TTCAATAACTGTGAGGTGGTCCT
299	TCAATAACTGTGAGGTGGTCCTT
300	CAATAACTGTGAGGTGGTCCTTG
301	AATAACTGTGAGGTGGTCCTTGG
302	ATAACTGTGAGGTGGTCCTTGGG
303	TAACTGTGAGGTGGTCCTTGGGA
304	AACTGTGAGGTGGTCCTTGGGAA
305	ACTGTGAGGTGGTCCTTGGGAAT
306	CTGTGAGGTGGTCCTTGGGAATT
307	TGTGAGGTGGTCCTTGGGAATTT
308	GTGAGGTGGTCCTTGGGAATTTG
309	TGAGGTGGTCCTTGGGAATTTGG
310	GAGGTGGTCCTTGGGAATTTGGA
311	AGGTGGTCCTTGGGAATTTGGAA
312	GGTGGTCCTTGGGAATTTGGAAA
313	GTGGTCCTTGGGAATTTGGAAAT
314	TGGTCCTTGGGAATTTGGAAATT
315	GGTCCTTGGGAATTTGGAAATTA
316	GTCCTTGGGAATTTGGAAATTAC
317	TCCTTGGGAATTTGGAAATTACC
318	CCTTGGGAATTTGGAAATTACCT
319	CTTGGGAATTTGGAAATTACCTA
320	TTGGGAATTTGGAAATTACCTAT
321	TGGGAATTTGGAAATTACCTATG
322	GGGAATTTGGAAATTACCTATGT
323	GGAATTTGGAAATTACCTATGTG
324	GAATTTGGAAATTACCTATGTGC
325	AATTTGGAAATTACCTATGTGCA
326	ATTTGGAAATTACCTATGTGCAG
327	TTTGGAAATTACCTATGTGCAGA
328	TTGGAAATTACCTATGTGCAGAG
329	TGGAAATTACCTATGTGCAGAGG
330	GGAAATTACCTATGTGCAGAGGA
331	GAAATTACCTATGTGCAGAGGAA
332	AAATTACCTATGTGCAGAGGAAT
333	AATTACCTATGTGCAGAGGAATT
334	ATTACCTATGTGCAGAGGAATTA
335	TTACCTATGTGCAGAGGAATTAT
336	TACCTATGTGCAGAGGAATTATG
337	ACCTATGTGCAGAGGAATTATGA
338	CCTATGTGCAGAGGAATTATGAT
339	CTATGTGCAGAGGAATTATGATC
340	TATGTGCAGAGGAATTATGATCT
341	ATGTGCAGAGGAATTATGATCTT
342	TGTGCAGAGGAATTATGATCTTT
343	GTGCAGAGGAATTATGATCTTTC
344	TGCAGAGGAATTATGATCTTTCC
345	GCAGAGGAATTATGATCTTTCCT
346	CAGAGGAATTATGATCTTTCCTT
347	AGAGGAATTATGATCTTTCCTTC
348	GAGGAATTATGATCTTTCCTTCT

Fig. 28 cont'd (Sheet 6 of 93)

ID	SEQUENCE
349	AGGAATTATGATCTTTCCTTCTT
350	GGAATTATGATCTTTCCTTCTTA
351	GAATTATGATCTTTCCTTCTTAA
352	AATTATGATCTTTCCTTCTTAAA
353	ATTATGATCTTTCCTTCTTAAAG
354	TTATGATCTTTCCTTCTTAAAGA
355	TATGATCTTTCCTTCTTAAAGAC
356	ATGATCTTTCCTTCTTAAAGACC
357	TGATCTTTCCTTCTTAAAGACCA
358	GATCTTTCCTTCTTAAAGACCAT
359	ATCTTTCCTTCTTAAAGACCATC
360	TCTTTCCTTCTTAAAGACCATCC
361	CTTTCCTTCTTAAAGACCATCCA
362	TTTCCTTCTTAAAGACCATCCAG
363	TTCCTTCTTAAAGACCATCCAGG
364	TCCTTCTTAAAGACCATCCAGGA
365	CCTTCTTAAAGACCATCCAGGAG
366	CTTCTTAAAGACCATCCAGGAGG
367	TTCTTAAAGACCATCCAGGAGGT
368	TCTTAAAGACCATCCAGGAGGTG
369	CTTAAAGACCATCCAGGAGGTGG
370	TTAAAGACCATCCAGGAGGTGGC
371	TAAAGACCATCCAGGAGGTGGCT
372	AAAGACCATCCAGGAGGTGGCTG
373	AAGACCATCCAGGAGGTGGCTGG
374	AGACCATCCAGGAGGTGGCTGGT
375	GACCATCCAGGAGGTGGCTGGTT
376	ACCATCCAGGAGGTGGCTGGTTA
377	CCATCCAGGAGGTGGCTGGTTAT
378	CATCCAGGAGGTGGCTGGTTATG
379	ATCCAGGAGGTGGCTGGTTATGT
380	TCCAGGAGGTGGCTGGTTATGTC
381	CCAGGAGGTGGCTGGTTATGTCC
382	CAGGAGGTGGCTGGTTATGTCCT
383	AGGAGGTGGCTGGTTATGTCCTC
384	GGAGGTGGCTGGTTATGTCCTCA
385	GAGGTGGCTGGTTATGTCCTCAT
386	AGGTGGCTGGTTATGTCCTCATT
387	GGTGGCTGGTTATGTCCTCATTG
388	GTGGCTGGTTATGTCCTCATTGC
389	TGGCTGGTTATGTCCTCATTGCC
390	GGCTGGTTATGTCCTCATTGCCC
391	GCTGGTTATGTCCTCATTGCCCT
392	CTGGTTATGTCCTCATTGCCCTC
393	TGGTTATGTCCTCATTGCCCTCA
394	GGTTATGTCCTCATTGCCCTCAA
395	GTTATGTCCTCATTGCCCTCAAC
396	TTATGTCCTCATTGCCCTCAACA
397	TATGTCCTCATTGCCCTCAACAC
398	ATGTCCTCATTGCCCTCAACACA
399	TGTCCTCATTGCCCTCAACACAG
400	GTCCTCATTGCCCTCAACACAGT
401	TCCTCATTGCCCTCAACACAGTG
402	CCTCATTGCCCTCAACACAGTGG
403	CTCATTGCCCTCAACACAGTGGA
404	TCATTGCCCTCAACACAGTGGAG
405	CATTGCCCTCAACACAGTGGAGC
406	ATTGCCCTCAACACAGTGGAGCG

Fig. 28 cont'd (Sheet 7 of 93)

ID	SEQUENCE
407	TTGCCCTCAACACAGTGGAGCGA
408	TGCCCTCAACACAGTGGAGCGAA
409	GCCCTCAACACAGTGGAGCGAAT
410	CCCTCAACACAGTGGAGCGAATT
411	CCTCAACACAGTGGAGCGAATTC
412	CTCAACACAGTGGAGCGAATTCC
413	TCAACACAGTGGAGCGAATTCCT
414	CAACACAGTGGAGCGAATTCCTT
415	AACACAGTGGAGCGAATTCCTTT
416	ACACAGTGGAGCGAATTCCTTTG
417	CACAGTGGAGCGAATTCCTTTGG
418	ACAGTGGAGCGAATTCCTTTGGA
419	CAGTGGAGCGAATTCCTTTGGAA
420	AGTGGAGCGAATTCCTTTGGAAA
421	GTGGAGCGAATTCCTTTGGAAAA
422	TGGAGCGAATTCCTTTGGAAAAC
423	GGAGCGAATTCCTTTGGAAAACC
424	GAGCGAATTCCTTTGGAAAACCT
425	AGCGAATTCCTTTGGAAAACCTG
426	GCGAATTCCTTTGGAAAACCTGC
427	CGAATTCCTTTGGAAAACCTGCA
428	GAATTCCTTTGGAAAACCTGCAG
429	AATTCCTTTGGAAAACCTGCAGA
430	ATTCCTTTGGAAAACCTGCAGAT
431	TTCCTTTGGAAAACCTGCAGATC
432	TCCTTTGGAAAACCTGCAGATCA
433	CCTTTGGAAAACCTGCAGATCAT
434	CTTTGGAAAACCTGCAGATCATC
435	TTTGGAAAACCTGCAGATCATCA
436	TTGGAAAACCTGCAGATCATCAG
437	TGGAAAACCTGCAGATCATCAGA
438	GGAAAACCTGCAGATCATCAGAG
439	GAAAACCTGCAGATCATCAGAGG
440	AAAACCTGCAGATCATCAGAGGA
441	AAACCTGCAGATCATCAGAGGAA
442	AACCTGCAGATCATCAGAGGAAA
443	ACCTGCAGATCATCAGAGGAAAT
444	CCTGCAGATCATCAGAGGAAATA
445	CTGCAGATCATCAGAGGAAATAT
446	TGCAGATCATCAGAGGAAATATG
447	GCAGATCATCAGAGGAAATATGT
448	CAGATCATCAGAGGAAATATGTA
449	AGATCATCAGAGGAAATATGTAC
450	GATCATCAGAGGAAATATGTACT
451	ATCATCAGAGGAAATATGTACTA
452	TCATCAGAGGAAATATGTACTAC
453	CATCAGAGGAAATATGTACTACG
454	ATCAGAGGAAATATGTACTACGA
455	TCAGAGGAAATATGTACTACGAA
456	CAGAGGAAATATGTACTACGAAA
457	AGAGGAAATATGTACTACGAAAA
458	GAGGAAATATGTACTACGAAAAT
459	AGGAAATATGTACTACGAAAATT
460	GGAAATATGTACTACGAAAATTC
461	GAAATATGTACTACGAAAATTCC
462	AAATATGTACTACGAAAATTCCT
463	AATATGTACTACGAAAATTCCTA
464	ATATGTACTACGAAAATTCCTAT

Fig. 28 cont'd (Sheet 8 of 93)

ID	SEQUENCE
465	TATGTACTACGAAAATTCCTATG
466	ATGTACTACGAAAATTCCTATGC
467	TGTACTACGAAAATTCCTATGCC
468	GTACTACGAAAATTCCTATGCCT
469	TACTACGAAAATTCCTATGCCTT
470	ACTACGAAAATTCCTATGCCTTA
471	CTACGAAAATTCCTATGCCTTAG
472	TACGAAAATTCCTATGCCTTAGC
473	ACGAAAATTCCTATGCCTTAGCA
474	CGAAAATTCCTATGCCTTAGCAG
475	GAAAATTCCTATGCCTTAGCAGT
476	AAAATTCCTATGCCTTAGCAGTC
477	AAATTCCTATGCCTTAGCAGTCT
478	AATTCCTATGCCTTAGCAGTCTT
479	ATTCCTATGCCTTAGCAGTCTTA
480	TTCCTATGCCTTAGCAGTCTTAT
481	TCCTATGCCTTAGCAGTCTTATC
482	CCTATGCCTTAGCAGTCTTATCT
483	CTATGCCTTAGCAGTCTTATCTA
484	TATGCCTTAGCAGTCTTATCTAA
485	ATGCCTTAGCAGTCTTATCTAAC
486	TGCCTTAGCAGTCTTATCTAACT
487	GCCTTAGCAGTCTTATCTAACTA
488	CCTTAGCAGTCTTATCTAACTAT
489	CTTAGCAGTCTTATCTAACTATG
490	TTAGCAGTCTTATCTAACTATGA
491	TAGCAGTCTTATCTAACTATGAT
492	AGCAGTCTTATCTAACTATGATG
493	GCAGTCTTATCTAACTATGATGC
494	CAGTCTTATCTAACTATGATGCA
495	AGTCTTATCTAACTATGATGCAA
496	GTCTTATCTAACTATGATGCAAA
497	TCTTATCTAACTATGATGCAAAT
498	CTTATCTAACTATGATGCAAATA
499	TTATCTAACTATGATGCAAATAA
500	TATCTAACTATGATGCAAATAAA
501	ATCTAACTATGATGCAAATAAAA
502	TCTAACTATGATGCAAATAAAAC
503	CTAACTATGATGCAAATAAAACC
504	TAACTATGATGCAAATAAAACCG
505	AACTATGATGCAAATAAAACCGG
506	ACTATGATGCAAATAAAACCGGA
507	CTATGATGCAAATAAAACCGGAC
508	TATGATGCAAATAAAACCGGACT
509	ATGATGCAAATAAAACCGGACTG
510	TGATGCAAATAAAACCGGACTGA
511	GATGCAAATAAAACCGGACTGAA
512	ATGCAAATAAAACCGGACTGAAG
513	TGCAAATAAAACCGGACTGAAGG
514	GCAAATAAAACCGGACTGAAGGA
515	CAAATAAAACCGGACTGAAGGAG
516	AAATAAAACCGGACTGAAGGAGC
517	AATAAAACCGGACTGAAGGAGCT
518	ATAAAACCGGACTGAAGGAGCTG
519	TAAAACCGGACTGAAGGAGCTGC
520	AAAACCGGACTGAAGGAGCTGCC
521	AAACCGGACTGAAGGAGCTGCCC
522	AACCGGACTGAAGGAGCTGCCCA

Fig. 28 cont'd (Sheet 9 of 93)

ID	SEQUENCE
523	ACCGGACTGAAGGAGCTGCCCAT
524	CCGGACTGAAGGAGCTGCCCATG
525	CGGACTGAAGGAGCTGCCCATGA
526	GGACTGAAGGAGCTGCCCATGAG
527	GACTGAAGGAGCTGCCCATGAGA
528	ACTGAAGGAGCTGCCCATGAGAA
529	CTGAAGGAGCTGCCCATGAGAAA
530	TGAAGGAGCTGCCCATGAGAAAT
531	GAAGGAGCTGCCCATGAGAAATT
532	AAGGAGCTGCCCATGAGAAATTT
533	AGGAGCTGCCCATGAGAAATTTA
534	GGAGCTGCCCATGAGAAATTTAC
535	GAGCTGCCCATGAGAAATTTACA
536	AGCTGCCCATGAGAAATTTACAG
537	GCTGCCCATGAGAAATTTACAGG
538	CTGCCCATGAGAAATTTACAGGA
539	TGCCCATGAGAAATTTACAGGAA
540	GCCCATGAGAAATTTACAGGAAA
541	CCCATGAGAAATTTACAGGAAAT
542	CCATGAGAAATTTACAGGAAATC
543	CATGAGAAATTTACAGGAAATCC
544	ATGAGAAATTTACAGGAAATCCT
545	TGAGAAATTTACAGGAAATCCTG
546	GAGAAATTTACAGGAAATCCTGC
547	AGAAATTTACAGGAAATCCTGCA
548	GAAATTTACAGGAAATCCTGCAT
549	AAATTTACAGGAAATCCTGCATG
550	AATTTACAGGAAATCCTGCATGG
551	ATTTACAGGAAATCCTGCATGGC
552	TTTACAGGAAATCCTGCATGGCG
553	TTACAGGAAATCCTGCATGGCGC
554	TACAGGAAATCCTGCATGGCGCC
555	ACAGGAAATCCTGCATGGCGCCG
556	CAGGAAATCCTGCATGGCGCCGT
557	AGGAAATCCTGCATGGCGCCGTG
558	GGAAATCCTGCATGGCGCCGTGC
559	GAAATCCTGCATGGCGCCGTGCG
560	AAATCCTGCATGGCGCCGTGCGG
561	AATCCTGCATGGCGCCGTGCGGT
562	ATCCTGCATGGCGCCGTGCGGTT
563	TCCTGCATGGCGCCGTGCGGTTC
564	CCTGCATGGCGCCGTGCGGTTCA
565	CTGCATGGCGCCGTGCGGTTCAG
566	TGCATGGCGCCGTGCGGTTCAGC
567	GCATGGCGCCGTGCGGTTCAGCA
568	CATGGCGCCGTGCGGTTCAGCAA
569	ATGGCGCCGTGCGGTTCAGCAAC
570	TGGCGCCGTGCGGTTCAGCAACA
571	GGCGCCGTGCGGTTCAGCAACAA
572	GCGCCGTGCGGTTCAGCAACAAC
573	CGCCGTGCGGTTCAGCAACAACC
574	GCCGTGCGGTTCAGCAACAACCC
575	CCGTGCGGTTCAGCAACAACCCT
576	CGTGCGGTTCAGCAACAACCCTG
577	GTGCGGTTCAGCAACAACCCTGC
578	TGCGGTTCAGCAACAACCCTGCC
579	GCGGTTCAGCAACAACCCTGCCC
580	CGGTTCAGCAACAACCCTGCCCT

Fig. 28 cont'd (Sheet 10 of 93)

ID	SEQUENCE
581	GGTTCAGCAACAACCCTGCCCTG
582	GTTCAGCAACAACCCTGCCCTGT
583	TTCAGCAACAACCCTGCCCTGTG
584	TCAGCAACAACCCTGCCCTGTGC
585	CAGCAACAACCCTGCCCTGTGCA
586	AGCAACAACCCTGCCCTGTGCAA
587	GCAACAACCCTGCCCTGTGCAAC
588	CAACAACCCTGCCCTGTGCAACG
589	AACAACCCTGCCCTGTGCAACGT
590	ACAACCCTGCCCTGTGCAACGTG
591	CAACCCTGCCCTGTGCAACGTGG
592	AACCCTGCCCTGTGCAACGTGGA
593	ACCCTGCCCTGTGCAACGTGGAG
594	CCCTGCCCTGTGCAACGTGGAGA
595	CCTGCCCTGTGCAACGTGGAGAG
596	CTGCCCTGTGCAACGTGGAGAGC
597	TGCCCTGTGCAACGTGGAGAGCA
598	GCCCTGTGCAACGTGGAGAGCAT
599	CCCTGTGCAACGTGGAGAGCATC
600	CCTGTGCAACGTGGAGAGCATCC
601	CTGTGCAACGTGGAGAGCATCCA
602	TGTGCAACGTGGAGAGCATCCAG
603	GTGCAACGTGGAGAGCATCCAGT
604	TGCAACGTGGAGAGCATCCAGTG
605	GCAACGTGGAGAGCATCCAGTGG
606	CAACGTGGAGAGCATCCAGTGGC
607	AACGTGGAGAGCATCCAGTGGCG
608	ACGTGGAGAGCATCCAGTGGCGG
609	CGTGGAGAGCATCCAGTGGCGGG
610	GTGGAGAGCATCCAGTGGCGGGA
611	TGGAGAGCATCCAGTGGCGGGAC
612	GGAGAGCATCCAGTGGCGGGACA
613	GAGAGCATCCAGTGGCGGGACAT
614	AGAGCATCCAGTGGCGGGACATA
615	GAGCATCCAGTGGCGGGACATAG
616	AGCATCCAGTGGCGGGACATAGT
617	GCATCCAGTGGCGGGACATAGTC
618	CATCCAGTGGCGGGACATAGTCA
619	ATCCAGTGGCGGGACATAGTCAG
620	TCCAGTGGCGGGACATAGTCAGC
621	CCAGTGGCGGGACATAGTCAGCA
622	CAGTGGCGGGACATAGTCAGCAG
623	AGTGGCGGGACATAGTCAGCAGT
624	GTGGCGGGACATAGTCAGCAGTG
625	TGGCGGGACATAGTCAGCAGTGA
626	GGCGGGACATAGTCAGCAGTGAC
627	GCGGGACATAGTCAGCAGTGACT
628	CGGGACATAGTCAGCAGTGACTT
629	GGGACATAGTCAGCAGTGACTTT
630	GGACATAGTCAGCAGTGACTTTC
631	GACATAGTCAGCAGTGACTTTCT
632	ACATAGTCAGCAGTGACTTTCTC
633	CATAGTCAGCAGTGACTTTCTCA
634	ATAGTCAGCAGTGACTTTCTCAG
635	TAGTCAGCAGTGACTTTCTCAGC
636	AGTCAGCAGTGACTTTCTCAGCA
637	GTCAGCAGTGACTTTCTCAGCAA
638	TCAGCAGTGACTTTCTCAGCAAC

Fig. 28 cont'd (Sheet 11 of 93)

ID	SEQUENCE
639	CAGCAGTGACTTTCTCAGCAACA
640	AGCAGTGACTTTCTCAGCAACAT
641	GCAGTGACTTTCTCAGCAACATG
642	CAGTGACTTTCTCAGCAACATGT
643	AGTGACTTTCTCAGCAACATGTC
644	GTGACTTTCTCAGCAACATGTCG
645	TGACTTTCTCAGCAACATGTCGA
646	GACTTTCTCAGCAACATGTCGAT
647	ACTTTCTCAGCAACATGTCGATG
648	CTTTCTCAGCAACATGTCGATGG
649	TTTCTCAGCAACATGTCGATGGA
650	TTCTCAGCAACATGTCGATGGAC
651	TCTCAGCAACATGTCGATGGACT
652	CTCAGCAACATGTCGATGGACTT
653	TCAGCAACATGTCGATGGACTTC
654	CAGCAACATGTCGATGGACTTCC
655	AGCAACATGTCGATGGACTTCCA
656	GCAACATGTCGATGGACTTCCAG
657	CAACATGTCGATGGACTTCCAGA
658	AACATGTCGATGGACTTCCAGAA
659	ACATGTCGATGGACTTCCAGAAC
660	CATGTCGATGGACTTCCAGAACC
661	ATGTCGATGGACTTCCAGAACCA
662	TGTCGATGGACTTCCAGAACCAC
663	GTCGATGGACTTCCAGAACCACC
664	TCGATGGACTTCCAGAACCACCT
665	CGATGGACTTCCAGAACCACCTG
666	GATGGACTTCCAGAACCACCTGG
667	ATGGACTTCCAGAACCACCTGGG
668	TGGACTTCCAGAACCACCTGGGC
669	GGACTTCCAGAACCACCTGGGCA
670	GACTTCCAGAACCACCTGGGCAG
671	ACTTCCAGAACCACCTGGGCAGC
672	CTTCCAGAACCACCTGGGCAGCT
673	TTCCAGAACCACCTGGGCAGCTG
674	TCCAGAACCACCTGGGCAGCTGC
675	CCAGAACCACCTGGGCAGCTGCC
676	CAGAACCACCTGGGCAGCTGCCA
677	AGAACCACCTGGGCAGCTGCCAA
678	GAACCACCTGGGCAGCTGCCAAA
679	AACCACCTGGGCAGCTGCCAAAA
680	ACCACCTGGGCAGCTGCCAAAAG
681	CCACCTGGGCAGCTGCCAAAAGT
682	CACCTGGGCAGCTGCCAAAAGTG
683	ACCTGGGCAGCTGCCAAAAGTGT
684	CCTGGGCAGCTGCCAAAAGTGTG
685	CTGGGCAGCTGCCAAAAGTGTGA
686	TGGGCAGCTGCCAAAAGTGTGAT
687	GGGCAGCTGCCAAAAGTGTGATC
688	GGCAGCTGCCAAAAGTGTGATCC
689	GCAGCTGCCAAAAGTGTGATCCA
690	CAGCTGCCAAAAGTGTGATCCAA
691	AGCTGCCAAAAGTGTGATCCAAG
692	GCTGCCAAAAGTGTGATCCAAGC
693	CTGCCAAAAGTGTGATCCAAGCT
694	TGCCAAAAGTGTGATCCAAGCTG
695	GCCAAAAGTGTGATCCAAGCTGT
696	CCAAAAGTGTGATCCAAGCTGTC

Fig. 28 cont'd (Sheet 12 of 93)

ID	SEQUENCE
697	CAAAAGTGTGATCCAAGCTGTCC
698	AAAAGTGTGATCCAAGCTGTCCC
699	AAAGTGTGATCCAAGCTGTCCCA
700	AAGTGTGATCCAAGCTGTCCCAA
701	AGTGTGATCCAAGCTGTCCCAAT
702	GTGTGATCCAAGCTGTCCCAATG
703	TGTGATCCAAGCTGTCCCAATGG
704	GTGATCCAAGCTGTCCCAATGGG
705	TGATCCAAGCTGTCCCAATGGGA
706	GATCCAAGCTGTCCCAATGGGAG
707	ATCCAAGCTGTCCCAATGGGAGC
708	TCCAAGCTGTCCCAATGGGAGCT
709	CCAAGCTGTCCCAATGGGAGCTG
710	CAAGCTGTCCCAATGGGAGCTGC
711	AAGCTGTCCCAATGGGAGCTGCT
712	AGCTGTCCCAATGGGAGCTGCTG
713	GCTGTCCCAATGGGAGCTGCTGG
714	CTGTCCCAATGGGAGCTGCTGGG
715	TGTCCCAATGGGAGCTGCTGGGG
716	GTCCCAATGGGAGCTGCTGGGGT
717	TCCCAATGGGAGCTGCTGGGGTG
718	CCCAATGGGAGCTGCTGGGGTGC
719	CCAATGGGAGCTGCTGGGGTGCA
720	CAATGGGAGCTGCTGGGGTGCAG
721	AATGGGAGCTGCTGGGGTGCAGG
722	ATGGGAGCTGCTGGGGTGCAGGA
723	TGGGAGCTGCTGGGGTGCAGGAG
724	GGGAGCTGCTGGGGTGCAGGAGA
725	GGAGCTGCTGGGGTGCAGGAGAG
726	GAGCTGCTGGGGTGCAGGAGAGG
727	AGCTGCTGGGGTGCAGGAGAGGA
728	GCTGCTGGGGTGCAGGAGAGGAG
729	CTGCTGGGGTGCAGGAGAGGAGA
730	TGCTGGGGTGCAGGAGAGGAGAA
731	GCTGGGGTGCAGGAGAGGAGAAC
732	CTGGGGTGCAGGAGAGGAGAACT
733	TGGGGTGCAGGAGAGGAGAACTG
734	GGGGTGCAGGAGAGGAGAACTGC
735	GGGTGCAGGAGAGGAGAACTGCC
736	GGTGCAGGAGAGGAGAACTGCCA
737	GTGCAGGAGAGGAGAACTGCCAG
738	TGCAGGAGAGGAGAACTGCCAGA
739	GCAGGAGAGGAGAACTGCCAGAA
740	CAGGAGAGGAGAACTGCCAGAAA
741	AGGAGAGGAGAACTGCCAGAAAC
742	GGAGAGGAGAACTGCCAGAAACT
743	GAGAGGAGAACTGCCAGAAACTG
744	AGAGGAGAACTGCCAGAAACTGA
745	GAGGAGAACTGCCAGAAACTGAC
746	AGGAGAACTGCCAGAAACTGACC
747	GGAGAACTGCCAGAAACTGACCA
748	GAGAACTGCCAGAAACTGACCAA
749	AGAACTGCCAGAAACTGACCAAA
750	GAACTGCCAGAAACTGACCAAAA
751	AACTGCCAGAAACTGACCAAAAT
752	ACTGCCAGAAACTGACCAAAATC
753	CTGCCAGAAACTGACCAAAATCA
754	TGCCAGAAACTGACCAAAATCAT

Fig. 28 cont'd (Sheet 13 of 93)

ID	SEQUENCE
755	GCCAGAAACTGACCAAAATCATC
756	CCAGAAACTGACCAAAATCATCT
757	CAGAAACTGACCAAAATCATCTG
758	AGAAACTGACCAAAATCATCTGT
759	GAAACTGACCAAAATCATCTGTG
760	AAACTGACCAAAATCATCTGTGC
761	AACTGACCAAAATCATCTGTGCC
762	ACTGACCAAAATCATCTGTGCCC
763	CTGACCAAAATCATCTGTGCCCA
764	TGACCAAAATCATCTGTGCCCAG
765	GACCAAAATCATCTGTGCCCAGC
766	ACCAAAATCATCTGTGCCCAGCA
767	CCAAAATCATCTGTGCCCAGCAG
768	CAAAATCATCTGTGCCCAGCAGT
769	AAAATCATCTGTGCCCAGCAGTG
770	AAATCATCTGTGCCCAGCAGTGC
771	AATCATCTGTGCCCAGCAGTGCT
772	ATCATCTGTGCCCAGCAGTGCTC
773	TCATCTGTGCCCAGCAGTGCTCC
774	CATCTGTGCCCAGCAGTGCTCCG
775	ATCTGTGCCCAGCAGTGCTCCGG
776	TCTGTGCCCAGCAGTGCTCCGGG
777	CTGTGCCCAGCAGTGCTCCGGGC
778	TGTGCCCAGCAGTGCTCCGGGCG
779	GTGCCCAGCAGTGCTCCGGGCGC
780	TGCCCAGCAGTGCTCCGGGCGCT
781	GCCCAGCAGTGCTCCGGGCGCTG
782	CCCAGCAGTGCTCCGGGCGCTGC
783	CCAGCAGTGCTCCGGGCGCTGCC
784	CAGCAGTGCTCCGGGCGCTGCCG
785	AGCAGTGCTCCGGGCGCTGCCGT
786	GCAGTGCTCCGGGCGCTGCCGTG
787	CAGTGCTCCGGGCGCTGCCGTGG
788	AGTGCTCCGGGCGCTGCCGTGGC
789	GTGCTCCGGGCGCTGCCGTGGCA
790	TGCTCCGGGCGCTGCCGTGGCAA
791	GCTCCGGGCGCTGCCGTGGCAAG
792	CTCCGGGCGCTGCCGTGGCAAGT
793	TCCGGGCGCTGCCGTGGCAAGTC
794	CCGGGCGCTGCCGTGGCAAGTCC
795	CGGGCGCTGCCGTGGCAAGTCCC
796	GGGCGCTGCCGTGGCAAGTCCCC
797	GGCGCTGCCGTGGCAAGTCCCCC
798	GCGCTGCCGTGGCAAGTCCCCCA
799	CGCTGCCGTGGCAAGTCCCCCAG
800	GCTGCCGTGGCAAGTCCCCCAGT
801	CTGCCGTGGCAAGTCCCCCAGTG
802	TGCCGTGGCAAGTCCCCCAGTGA
803	GCCGTGGCAAGTCCCCCAGTGAC
804	CCGTGGCAAGTCCCCCAGTGACT
805	CGTGGCAAGTCCCCCAGTGACTG
806	GTGGCAAGTCCCCCAGTGACTGC
807	TGGCAAGTCCCCCAGTGACTGCT
808	GGCAAGTCCCCCAGTGACTGCTG
809	GCAAGTCCCCCAGTGACTGCTGC
810	CAAGTCCCCCAGTGACTGCTGCC
811	AAGTCCCCCAGTGACTGCTGCCA
812	AGTCCCCCAGTGACTGCTGCCAC

Fig. 28 cont'd (Sheet 14 of 93)

ID	SEQUENCE
813	GTCCCCCAGTGACTGCTGCCACA
814	TCCCCCAGTGACTGCTGCCACAA
815	CCCCCAGTGACTGCTGCCACAAC
816	CCCCAGTGACTGCTGCCACAACC
817	CCCAGTGACTGCTGCCACAACCA
818	CCAGTGACTGCTGCCACAACCAG
819	CAGTGACTGCTGCCACAACCAGT
820	AGTGACTGCTGCCACAACCAGTG
821	GTGACTGCTGCCACAACCAGTGT
822	TGACTGCTGCCACAACCAGTGTG
823	GACTGCTGCCACAACCAGTGTGC
824	ACTGCTGCCACAACCAGTGTGCT
825	CTGCTGCCACAACCAGTGTGCTG
826	TGCTGCCACAACCAGTGTGCTGC
827	GCTGCCACAACCAGTGTGCTGCA
828	CTGCCACAACCAGTGTGCTGCAG
829	TGCCACAACCAGTGTGCTGCAGG
830	GCCACAACCAGTGTGCTGCAGGC
831	CCACAACCAGTGTGCTGCAGGCT
832	CACAACCAGTGTGCTGCAGGCTG
833	ACAACCAGTGTGCTGCAGGCTGC
834	CAACCAGTGTGCTGCAGGCTGCA
835	AACCAGTGTGCTGCAGGCTGCAC
836	ACCAGTGTGCTGCAGGCTGCACA
837	CCAGTGTGCTGCAGGCTGCACAG
838	CAGTGTGCTGCAGGCTGCACAGG
839	AGTGTGCTGCAGGCTGCACAGGC
840	GTGTGCTGCAGGCTGCACAGGCC
841	TGTGCTGCAGGCTGCACAGGCCC
842	GTGCTGCAGGCTGCACAGGCCCC
843	TGCTGCAGGCTGCACAGGCCCCC
844	GCTGCAGGCTGCACAGGCCCCCG
845	CCCCCGGGAGAGCGACTGCCTGG
846	CCCCGGGAGAGCGACTGCCTGGT
847	CCCGGGAGAGCGACTGCCTGGTC
848	CCGGGAGAGCGACTGCCTGGTCT
849	CGGGAGAGCGACTGCCTGGTCTG
850	GGGAGAGCGACTGCCTGGTCTGC
851	GGAGAGCGACTGCCTGGTCTGCC
852	GAGAGCGACTGCCTGGTCTGCCG
853	AGAGCGACTGCCTGGTCTGCCGC
854	GAGCGACTGCCTGGTCTGCCGCA
855	AGCGACTGCCTGGTCTGCCGCAA
856	GCGACTGCCTGGTCTGCCGCAAA
857	CGACTGCCTGGTCTGCCGCAAAT
858	GACTGCCTGGTCTGCCGCAAATT
859	ACTGCCTGGTCTGCCGCAAATTC
860	CTGCCTGGTCTGCCGCAAATTCC
861	TGCCTGGTCTGCCGCAAATTCCG
862	GCCTGGTCTGCCGCAAATTCCGA
863	CCTGGTCTGCCGCAAATTCCGAG
864	CTGGTCTGCCGCAAATTCCGAGA
865	TGGTCTGCCGCAAATTCCGAGAC
866	GGTCTGCCGCAAATTCCGAGACG
867	GTCTGCCGCAAATTCCGAGACGA
868	TCTGCCGCAAATTCCGAGACGAA
869	CTGCCGCAAATTCCGAGACGAAG
870	TGCCGCAAATTCCGAGACGAAGC

Fig. 28 cont'd (Sheet 15 of 93)

ID	SEQUENCE
871	GCCGCAAATTCCGAGACGAAGCC
872	CCGCAAATTCCGAGACGAAGCCA
873	CGCAAATTCCGAGACGAAGCCAC
874	GCAAATTCCGAGACGAAGCCACG
875	CAAATTCCGAGACGAAGCCACGT
876	AAATTCCGAGACGAAGCCACGTG
877	AATTCCGAGACGAAGCCACGTGC
878	ATTCCGAGACGAAGCCACGTGCA
879	TTCCGAGACGAAGCCACGTGCAA
880	TCCGAGACGAAGCCACGTGCAAG
881	CCGAGACGAAGCCACGTGCAAGG
882	CGAGACGAAGCCACGTGCAAGGA
883	GAGACGAAGCCACGTGCAAGGAC
884	AGACGAAGCCACGTGCAAGGACA
885	GACGAAGCCACGTGCAAGGACAC
886	ACGAAGCCACGTGCAAGGACACC
887	CGAAGCCACGTGCAAGGACACCT
888	GAAGCCACGTGCAAGGACACCTG
889	AAGCCACGTGCAAGGACACCTGC
890	AGCCACGTGCAAGGACACCTGCC
891	GCCACGTGCAAGGACACCTGCCC
892	CCACGTGCAAGGACACCTGCCCC
893	CACGTGCAAGGACACCTGCCCCC
894	ACGTGCAAGGACACCTGCCCCCC
895	CGTGCAAGGACACCTGCCCCCCA
896	GTGCAAGGACACCTGCCCCCCAC
897	TGCAAGGACACCTGCCCCCCACT
898	GCAAGGACACCTGCCCCCCACTC
899	CAAGGACACCTGCCCCCCACTCA
900	AAGGACACCTGCCCCCCACTCAT
901	AGGACACCTGCCCCCCACTCATG
902	GGACACCTGCCCCCCACTCATGC
903	GACACCTGCCCCCCACTCATGCT
904	ACACCTGCCCCCCACTCATGCTC
905	CACCTGCCCCCCACTCATGCTCT
906	ACCTGCCCCCCACTCATGCTCTA
907	CCTGCCCCCCACTCATGCTCTAC
908	CTGCCCCCCACTCATGCTCTACA
909	TGCCCCCCACTCATGCTCTACAA
910	GCCCCCCACTCATGCTCTACAAC
911	CCCCCCACTCATGCTCTACAACC
912	CCCCCACTCATGCTCTACAACCC
913	CCCCACTCATGCTCTACAACCCC
914	CCCACTCATGCTCTACAACCCCA
915	CCACTCATGCTCTACAACCCCAC
916	CACTCATGCTCTACAACCCCACC
917	ACTCATGCTCTACAACCCCACCA
918	CTCATGCTCTACAACCCCACCAC
919	TCATGCTCTACAACCCCACCACG
920	CATGCTCTACAACCCCACCACGT
921	ATGCTCTACAACCCCACCACGTA
922	TGCTCTACAACCCCACCACGTAC
923	GCTCTACAACCCCACCACGTACC
924	CTCTACAACCCCACCACGTACCA
925	TCTACAACCCCACCACGTACCAG
926	CTACAACCCCACCACGTACCAGA
927	TACAACCCCACCACGTACCAGAT
928	ACAACCCCACCACGTACCAGATG

Fig. 28 cont'd (Sheet 16 of 93)

ID	SEQUENCE
929	CAACCCCACCACGTACCAGATGG
930	AACCCCACCACGTACCAGATGGA
931	ACCCCACCACGTACCAGATGGAT
932	CCCCACCACGTACCAGATGGATG
933	CCCACCACGTACCAGATGGATGT
934	CCACCACGTACCAGATGGATGTG
935	CACCACGTACCAGATGGATGTGA
936	ACCACGTACCAGATGGATGTGAA
937	CCACGTACCAGATGGATGTGAAC
938	CACGTACCAGATGGATGTGAACC
939	ACGTACCAGATGGATGTGAACCC
940	CGTACCAGATGGATGTGAACCCC
941	GTACCAGATGGATGTGAACCCCG
942	TACCAGATGGATGTGAACCCCGA
943	ACCAGATGGATGTGAACCCCGAG
944	CCAGATGGATGTGAACCCCGAGG
945	CAGATGGATGTGAACCCCGAGGG
946	AGATGGATGTGAACCCCGAGGGC
947	GATGGATGTGAACCCCGAGGGCA
948	ATGGATGTGAACCCCGAGGGCAA
949	TGGATGTGAACCCCGAGGGCAAA
950	GGATGTGAACCCCGAGGGCAAAT
951	GATGTGAACCCCGAGGGCAAATA
952	ATGTGAACCCCGAGGGCAAATAC
953	TGTGAACCCCGAGGGCAAATACA
954	GTGAACCCCGAGGGCAAATACAG
955	TGAACCCCGAGGGCAAATACAGC
956	GAACCCCGAGGGCAAATACAGCT
957	AACCCCGAGGGCAAATACAGCTT
958	ACCCCGAGGGCAAATACAGCTTT
959	CCCCGAGGGCAAATACAGCTTTG
960	CCCGAGGGCAAATACAGCTTTGG
961	CCGAGGGCAAATACAGCTTTGGT
962	CGAGGGCAAATACAGCTTTGGTG
963	GAGGGCAAATACAGCTTTGGTGC
964	AGGGCAAATACAGCTTTGGTGCC
965	GGGCAAATACAGCTTTGGTGCCA
966	GGCAAATACAGCTTTGGTGCCAC
967	GCAAATACAGCTTTGGTGCCACC
968	CAAATACAGCTTTGGTGCCACCT
969	AAATACAGCTTTGGTGCCACCTG
970	AATACAGCTTTGGTGCCACCTGC
971	ATACAGCTTTGGTGCCACCTGCG
972	TACAGCTTTGGTGCCACCTGCGT
973	ACAGCTTTGGTGCCACCTGCGTG
974	CAGCTTTGGTGCCACCTGCGTGA
975	AGCTTTGGTGCCACCTGCGTGAA
976	GCTTTGGTGCCACCTGCGTGAAG
977	CTTTGGTGCCACCTGCGTGAAGA
978	TTTGGTGCCACCTGCGTGAAGAA
979	TTGGTGCCACCTGCGTGAAGAAG
980	TGGTGCCACCTGCGTGAAGAAGT
981	GGTGCCACCTGCGTGAAGAAGTG
982	GTGCCACCTGCGTGAAGAAGTGT
983	TGCCACCTGCGTGAAGAAGTGTC
984	GCCACCTGCGTGAAGAAGTGTCC
985	CCACCTGCGTGAAGAAGTGTCCC
986	CACCTGCGTGAAGAAGTGTCCCC

Fig. 28 cont'd (Sheet 17 of 93)

ID	SEQUENCE
987	ACCTGCGTGAAGAAGTGTCCCCG
988	CCTGCGTGAAGAAGTGTCCCCGT
989	CTGCGTGAAGAAGTGTCCCCGTA
990	TGCGTGAAGAAGTGTCCCCGTAA
991	GCGTGAAGAAGTGTCCCCGTAAT
992	CGTGAAGAAGTGTCCCCGTAATT
993	GTGAAGAAGTGTCCCCGTAATTA
994	TGAAGAAGTGTCCCCGTAATTAT
995	GAAGAAGTGTCCCCGTAATTATG
996	AAGAAGTGTCCCCGTAATTATGT
997	AGAAGTGTCCCCGTAATTATGTG
998	GAAGTGTCCCCGTAATTATGTGG
999	AAGTGTCCCCGTAATTATGTGGT
1000	AGTGTCCCCGTAATTATGTGGTG
1001	GTGTCCCCGTAATTATGTGGTGA
1002	TGTCCCCGTAATTATGTGGTGAC
1003	GTCCCCGTAATTATGTGGTGACA
1004	TCCCCGTAATTATGTGGTGACAG
1005	CCCCGTAATTATGTGGTGACAGA
1006	CCCGTAATTATGTGGTGACAGAT
1007	CCGTAATTATGTGGTGACAGATC
1008	CGTAATTATGTGGTGACAGATCA
1009	GTAATTATGTGGTGACAGATCAC
1010	TAATTATGTGGTGACAGATCACG
1011	AATTATGTGGTGACAGATCACGG
1012	ATTATGTGGTGACAGATCACGGC
1013	TTATGTGGTGACAGATCACGGCT
1014	TATGTGGTGACAGATCACGGCTC
1015	ATGTGGTGACAGATCACGGCTCG
1016	TGTGGTGACAGATCACGGCTCGT
1017	GTGGTGACAGATCACGGCTCGTG
1018	TGGTGACAGATCACGGCTCGTGC
1019	GGTGACAGATCACGGCTCGTGCG
1020	GTGACAGATCACGGCTCGTGCGT
1021	TGACAGATCACGGCTCGTGCGTC
1022	GACAGATCACGGCTCGTGCGTCC
1023	ACAGATCACGGCTCGTGCGTCCG
1024	CAGATCACGGCTCGTGCGTCCGA
1025	AGATCACGGCTCGTGCGTCCGAG
1026	GATCACGGCTCGTGCGTCCGAGC
1027	ATCACGGCTCGTGCGTCCGAGCC
1028	TCACGGCTCGTGCGTCCGAGCCT
1029	CACGGCTCGTGCGTCCGAGCCTG
1030	ACGGCTCGTGCGTCCGAGCCTGT
1031	CGGCTCGTGCGTCCGAGCCTGTG
1032	GGCTCGTGCGTCCGAGCCTGTGG
1033	GCTCGTGCGTCCGAGCCTGTGGG
1034	CTCGTGCGTCCGAGCCTGTGGGG
1035	TCGTGCGTCCGAGCCTGTGGGGC
1036	CGTGCGTCCGAGCCTGTGGGGCC
1037	GTGCGTCCGAGCCTGTGGGGCCG
1038	TGCGTCCGAGCCTGTGGGGCCGA
1039	GCGTCCGAGCCTGTGGGGCCGAC
1040	CGTCCGAGCCTGTGGGGCCGACA
1041	GTCCGAGCCTGTGGGGCCGACAG
1042	TCCGAGCCTGTGGGGCCGACAGC
1043	CCGAGCCTGTGGGGCCGACAGCT
1044	CGAGCCTGTGGGGCCGACAGCTA

Fig. 28 cont'd (Sheet 18 of 93)

ID	SEQUENCE
1045	GAGCCTGTGGGGCCGACAGCTAT
1046	AGCCTGTGGGGCCGACAGCTATG
1047	GCCTGTGGGGCCGACAGCTATGA
1048	CCTGTGGGGCCGACAGCTATGAG
1049	CTGTGGGGCCGACAGCTATGAGA
1050	TGTGGGGCCGACAGCTATGAGAT
1051	GTGGGGCCGACAGCTATGAGATG
1052	TGGGGCCGACAGCTATGAGATGG
1053	GGGGCCGACAGCTATGAGATGGA
1054	GGGCCGACAGCTATGAGATGGAG
1055	GGCCGACAGCTATGAGATGGAGG
1056	GCCGACAGCTATGAGATGGAGGA
1057	CCGACAGCTATGAGATGGAGGAA
1058	CGACAGCTATGAGATGGAGGAAG
1059	GACAGCTATGAGATGGAGGAAGA
1060	ACAGCTATGAGATGGAGGAAGAC
1061	CAGCTATGAGATGGAGGAAGACG
1062	AGCTATGAGATGGAGGAAGACGG
1063	GCTATGAGATGGAGGAAGACGGC
1064	CTATGAGATGGAGGAAGACGGCG
1065	TATGAGATGGAGGAAGACGGCGT
1066	ATGAGATGGAGGAAGACGGCGTC
1067	TGAGATGGAGGAAGACGGCGTCC
1068	GAGATGGAGGAAGACGGCGTCCG
1069	AGATGGAGGAAGACGGCGTCCGC
1070	GATGGAGGAAGACGGCGTCCGCA
1071	ATGGAGGAAGACGGCGTCCGCAA
1072	TGGAGGAAGACGGCGTCCGCAAG
1073	GGAGGAAGACGGCGTCCGCAAGT
1074	GAGGAAGACGGCGTCCGCAAGTG
1075	AGGAAGACGGCGTCCGCAAGTGT
1076	GGAAGACGGCGTCCGCAAGTGTA
1077	GAAGACGGCGTCCGCAAGTGTAA
1078	AAGACGGCGTCCGCAAGTGTAAG
1079	AGACGGCGTCCGCAAGTGTAAGA
1080	GACGGCGTCCGCAAGTGTAAGAA
1081	ACGGCGTCCGCAAGTGTAAGAAG
1082	CGGCGTCCGCAAGTGTAAGAAGT
1083	GGCGTCCGCAAGTGTAAGAAGTG
1084	GCGTCCGCAAGTGTAAGAAGTGC
1085	CGTCCGCAAGTGTAAGAAGTGCG
1086	GTCCGCAAGTGTAAGAAGTGCGA
1087	TCCGCAAGTGTAAGAAGTGCGAA
1088	CCGCAAGTGTAAGAAGTGCGAAG
1089	CGCAAGTGTAAGAAGTGCGAAGG
1090	GCAAGTGTAAGAAGTGCGAAGGG
1091	CAAGTGTAAGAAGTGCGAAGGGC
1092	AAGTGTAAGAAGTGCGAAGGGCC
1093	AGTGTAAGAAGTGCGAAGGGCCT
1094	GTGTAAGAAGTGCGAAGGGCCTT
1095	TGTAAGAAGTGCGAAGGGCCTTG
1096	GTAAGAAGTGCGAAGGGCCTTGC
1097	TAAGAAGTGCGAAGGGCCTTGCC
1098	AAGAAGTGCGAAGGGCCTTGCCG
1099	AGAAGTGCGAAGGGCCTTGCCGC
1100	GAAGTGCGAAGGGCCTTGCCGCA
1101	AAGTGCGAAGGGCCTTGCCGCAA
1102	AGTGCGAAGGGCCTTGCCGCAAA

Fig. 28 cont'd (Sheet 19 of 93)

ID	SEQUENCE
1103	GTGCGAAGGGCCTTGCCGCAAAG
1104	TGCGAAGGGCCTTGCCGCAAAGT
1105	GCGAAGGGCCTTGCCGCAAAGTG
1106	CGAAGGGCCTTGCCGCAAAGTGT
1107	GAAGGGCCTTGCCGCAAAGTGTG
1108	AAGGGCCTTGCCGCAAAGTGTGT
1109	AGGGCCTTGCCGCAAAGTGTGTA
1110	GGGCCTTGCCGCAAAGTGTGTAA
1111	GGCCTTGCCGCAAAGTGTGTAAC
1112	GCCTTGCCGCAAAGTGTGTAACG
1113	CCTTGCCGCAAAGTGTGTAACGG
1114	CTTGCCGCAAAGTGTGTAACGGA
1115	TTGCCGCAAAGTGTGTAACGGAA
1116	TGCCGCAAAGTGTGTAACGGAAT
1117	GCCGCAAAGTGTGTAACGGAATA
1118	CCGCAAAGTGTGTAACGGAATAG
1119	CGCAAAGTGTGTAACGGAATAGG
1120	GCAAAGTGTGTAACGGAATAGGT
1121	CAAAGTGTGTAACGGAATAGGTA
1122	AAAGTGTGTAACGGAATAGGTAT
1123	AAGTGTGTAACGGAATAGGTATT
1124	AGTGTGTAACGGAATAGGTATTG
1125	GTGTGTAACGGAATAGGTATTGG
1126	TGTGTAACGGAATAGGTATTGGT
1127	GTGTAACGGAATAGGTATTGGTG
1128	TGTAACGGAATAGGTATTGGTGA
1129	GTAACGGAATAGGTATTGGTGAA
1130	TAACGGAATAGGTATTGGTGAAT
1131	AACGGAATAGGTATTGGTGAATT
1132	ACGGAATAGGTATTGGTGAATTT
1133	CGGAATAGGTATTGGTGAATTTA
1134	GGAATAGGTATTGGTGAATTTAA
1135	GAATAGGTATTGGTGAATTTAAA
1136	AATAGGTATTGGTGAATTTAAAG
1137	ATAGGTATTGGTGAATTTAAAGA
1138	TAGGTATTGGTGAATTTAAAGAC
1139	AGGTATTGGTGAATTTAAAGACT
1140	GGTATTGGTGAATTTAAAGACTC
1141	GTATTGGTGAATTTAAAGACTCA
1142	TATTGGTGAATTTAAAGACTCAC
1143	ATTGGTGAATTTAAAGACTCACT
1144	TTGGTGAATTTAAAGACTCACTC
1145	TGGTGAATTTAAAGACTCACTCT
1146	GGTGAATTTAAAGACTCACTCTC
1147	GTGAATTTAAAGACTCACTCTCC
1148	TGAATTTAAAGACTCACTCTCCA
1149	GAATTTAAAGACTCACTCTCCAT
1150	AATTTAAAGACTCACTCTCCATA
1151	ATTTAAAGACTCACTCTCCATAA
1152	TTTAAAGACTCACTCTCCATAAA
1153	TTAAAGACTCACTCTCCATAAAT
1154	TAAAGACTCACTCTCCATAAATG
1155	AAAGACTCACTCTCCATAAATGC
1156	AAGACTCACTCTCCATAAATGCT
1157	AGACTCACTCTCCATAAATGCTA
1158	GACTCACTCTCCATAAATGCTAC
1159	ACTCACTCTCCATAAATGCTACG
1160	CTCACTCTCCATAAATGCTACGA

Fig. 28 cont'd (Sheet 20 of 93)

ID	SEQUENCE
1161	TCACTCTCCATAAATGCTACGAA
1162	CACTCTCCATAAATGCTACGAAT
1163	ACTCTCCATAAATGCTACGAATA
1164	CTCTCCATAAATGCTACGAATAT
1165	TCTCCATAAATGCTACGAATATT
1166	CTCCATAAATGCTACGAATATTA
1167	TCCATAAATGCTACGAATATTAA
1168	CCATAAATGCTACGAATATTAAA
1169	CATAAATGCTACGAATATTAAAC
1170	ATAAATGCTACGAATATTAAACA
1171	TAAATGCTACGAATATTAAACAC
1172	AAATGCTACGAATATTAAACACT
1173	AATGCTACGAATATTAAACACTT
1174	ATGCTACGAATATTAAACACTTC
1175	TGCTACGAATATTAAACACTTCA
1176	GCTACGAATATTAAACACTTCAA
1177	CTACGAATATTAAACACTTCAAA
1178	TACGAATATTAAACACTTCAAAA
1179	ACGAATATTAAACACTTCAAAAA
1180	CGAATATTAAACACTTCAAAAAC
1181	GAATATTAAACACTTCAAAAACT
1182	AATATTAAACACTTCAAAAACTG
1183	ATATTAAACACTTCAAAAACTGC
1184	TATTAAACACTTCAAAAACTGCA
1185	ATTAAACACTTCAAAAACTGCAC
1186	TTAAACACTTCAAAAACTGCACC
1187	TAAACACTTCAAAAACTGCACCT
1188	AAACACTTCAAAAACTGCACCTC
1189	AACACTTCAAAAACTGCACCTCC
1190	ACACTTCAAAAACTGCACCTCCA
1191	CACTTCAAAAACTGCACCTCCAT
1192	ACTTCAAAAACTGCACCTCCATC
1193	CTTCAAAAACTGCACCTCCATCA
1194	TTCAAAAACTGCACCTCCATCAG
1195	TCAAAAACTGCACCTCCATCAGT
1196	CAAAAACTGCACCTCCATCAGTG
1197	AAAAACTGCACCTCCATCAGTGG
1198	AAAACTGCACCTCCATCAGTGGC
1199	AAACTGCACCTCCATCAGTGGCG
1200	AACTGCACCTCCATCAGTGGCGA
1201	ACTGCACCTCCATCAGTGGCGAT
1202	CTGCACCTCCATCAGTGGCGATC
1203	TGCACCTCCATCAGTGGCGATCT
1204	GCACCTCCATCAGTGGCGATCTC
1205	CACCTCCATCAGTGGCGATCTCC
1206	ACCTCCATCAGTGGCGATCTCCA
1207	CCTCCATCAGTGGCGATCTCCAC
1208	CTCCATCAGTGGCGATCTCCACA
1209	TCCATCAGTGGCGATCTCCACAT
1210	CCATCAGTGGCGATCTCCACATC
1211	CATCAGTGGCGATCTCCACATCC
1212	ATCAGTGGCGATCTCCACATCCT
1213	TCAGTGGCGATCTCCACATCCTG
1214	CAGTGGCGATCTCCACATCCTGC
1215	AGTGGCGATCTCCACATCCTGCC
1216	GTGGCGATCTCCACATCCTGCCG
1217	TGGCGATCTCCACATCCTGCCGG
1218	GGCGATCTCCACATCCTGCCGGT

Fig. 28 cont'd (Sheet 21 of 93)

ID	SEQUENCE
1219	GCGATCTCCACATCCTGCCGGTG
1220	CGATCTCCACATCCTGCCGGTGG
1221	GATCTCCACATCCTGCCGGTGGC
1222	ATCTCCACATCCTGCCGGTGGCA
1223	TCTCCACATCCTGCCGGTGGCAT
1224	CTCCACATCCTGCCGGTGGCATT
1225	TCCACATCCTGCCGGTGGCATTT
1226	CCACATCCTGCCGGTGGCATTTA
1227	CACATCCTGCCGGTGGCATTTAG
1228	ACATCCTGCCGGTGGCATTTAGG
1229	CATCCTGCCGGTGGCATTTAGGG
1230	ATCCTGCCGGTGGCATTTAGGGG
1231	TCCTGCCGGTGGCATTTAGGGGT
1232	CCTGCCGGTGGCATTTAGGGGTG
1233	CTGCCGGTGGCATTTAGGGGTGA
1234	TGCCGGTGGCATTTAGGGGTGAC
1235	GCCGGTGGCATTTAGGGGTGACT
1236	CCGGTGGCATTTAGGGGTGACTC
1237	CGGTGGCATTTAGGGGTGACTCC
1238	GGTGGCATTTAGGGGTGACTCCT
1239	GTGGCATTTAGGGGTGACTCCTT
1240	TGGCATTTAGGGGTGACTCCTTC
1241	GGCATTTAGGGGTGACTCCTTCA
1242	GCATTTAGGGGTGACTCCTTCAC
1243	CATTTAGGGGTGACTCCTTCACA
1244	ATTTAGGGGTGACTCCTTCACAC
1245	TTTAGGGGTGACTCCTTCACACA
1246	TTAGGGGTGACTCCTTCACACAT
1247	TAGGGGTGACTCCTTCACACATA
1248	AGGGGTGACTCCTTCACACATAC
1249	GGGGTGACTCCTTCACACATACT
1250	GGGTGACTCCTTCACACATACTC
1251	GGTGACTCCTTCACACATACTCC
1252	GTGACTCCTTCACACATACTCCT
1253	TGACTCCTTCACACATACTCCTC
1254	GACTCCTTCACACATACTCCTCC
1255	ACTCCTTCACACATACTCCTCCT
1256	CTCCTTCACACATACTCCTCCTC
1257	TCCTTCACACATACTCCTCCTCT
1258	CCTTCACACATACTCCTCCTCTG
1259	CTTCACACATACTCCTCCTCTGG
1260	TTCACACATACTCCTCCTCTGGA
1261	TCACACATACTCCTCCTCTGGAT
1262	CACACATACTCCTCCTCTGGATC
1263	ACACATACTCCTCCTCTGGATCC
1264	CACATACTCCTCCTCTGGATCCA
1265	ACATACTCCTCCTCTGGATCCAC
1266	CATACTCCTCCTCTGGATCCACA
1267	ATACTCCTCCTCTGGATCCACAG
1268	TACTCCTCCTCTGGATCCACAGG
1269	ACTCCTCCTCTGGATCCACAGGA
1270	CTCCTCCTCTGGATCCACAGGAA
1271	TCCTCCTCTGGATCCACAGGAAC
1272	CCTCCTCTGGATCCACAGGAACT
1273	CTCCTCTGGATCCACAGGAACTG
1274	TCCTCTGGATCCACAGGAACTGG
1275	CCTCTGGATCCACAGGAACTGGA
1276	CTCTGGATCCACAGGAACTGGAT

Fig. 28 cont'd (Sheet 22 of 93)

ID	SEQUENCE
1277	TCTGGATCCACAGGAACTGGATA
1278	CTGGATCCACAGGAACTGGATAT
1279	TGGATCCACAGGAACTGGATATT
1280	GGATCCACAGGAACTGGATATTC
1281	GATCCACAGGAACTGGATATTCT
1282	ATCCACAGGAACTGGATATTCTG
1283	TCCACAGGAACTGGATATTCTGA
1284	CCACAGGAACTGGATATTCTGAA
1285	CACAGGAACTGGATATTCTGAAA
1286	ACAGGAACTGGATATTCTGAAAA
1287	CAGGAACTGGATATTCTGAAAAC
1288	AGGAACTGGATATTCTGAAAACC
1289	GGAACTGGATATTCTGAAAACCG
1290	GAACTGGATATTCTGAAAACCGT
1291	AACTGGATATTCTGAAAACCGTA
1292	ACTGGATATTCTGAAAACCGTAA
1293	CTGGATATTCTGAAAACCGTAAA
1294	TGGATATTCTGAAAACCGTAAAG
1295	GGATATTCTGAAAACCGTAAAGG
1296	GATATTCTGAAAACCGTAAAGGA
1297	ATATTCTGAAAACCGTAAAGGAA
1298	TATTCTGAAAACCGTAAAGGAAA
1299	ATTCTGAAAACCGTAAAGGAAAT
1300	TTCTGAAAACCGTAAAGGAAATC
1301	TCTGAAAACCGTAAAGGAAATCA
1302	CTGAAAACCGTAAAGGAAATCAC
1303	TGAAAACCGTAAAGGAAATCACA
1304	GAAAACCGTAAAGGAAATCACAG
1305	AAAACCGTAAAGGAAATCACAGG
1306	AAACCGTAAAGGAAATCACAGGG
1307	AACCGTAAAGGAAATCACAGGGT
1308	ACCGTAAAGGAAATCACAGGGTT
1309	CCGTAAAGGAAATCACAGGGTTT
1310	CGTAAAGGAAATCACAGGGTTTT
1311	GTAAAGGAAATCACAGGGTTTTT
1312	TAAAGGAAATCACAGGGTTTTTG
1313	AAAGGAAATCACAGGGTTTTTGC
1314	AAGGAAATCACAGGGTTTTTGCT
1315	AGGAAATCACAGGGTTTTTGCTG
1316	GGAAATCACAGGGTTTTTGCTGA
1317	GAAATCACAGGGTTTTTGCTGAT
1318	AAATCACAGGGTTTTTGCTGATT
1319	AATCACAGGGTTTTTGCTGATTC
1320	ATCACAGGGTTTTTGCTGATTCA
1321	TCACAGGGTTTTTGCTGATTCAG
1322	CACAGGGTTTTTGCTGATTCAGG
1323	ACAGGGTTTTTGCTGATTCAGGC
1324	CAGGGTTTTTGCTGATTCAGGCT
1325	AGGGTTTTTGCTGATTCAGGCTT
1326	GGGTTTTTGCTGATTCAGGCTTG
1327	GGTTTTTGCTGATTCAGGCTTGG
1328	GTTTTTGCTGATTCAGGCTTGGC
1329	TTTTTGCTGATTCAGGCTTGGCC
1330	TTTTGCTGATTCAGGCTTGGCCT
1331	TTTGCTGATTCAGGCTTGGCCTG
1332	TTGCTGATTCAGGCTTGGCCTGA
1333	TGCTGATTCAGGCTTGGCCTGAA
1334	GCTGATTCAGGCTTGGCCTGAAA

Fig. 28 cont'd (Sheet 23 of 93)

ID	SEQUENCE
1335	CTGATTCAGGCTTGGCCTGAAAA
1336	TGATTCAGGCTTGGCCTGAAAAC
1337	GATTCAGGCTTGGCCTGAAAACA
1338	ATTCAGGCTTGGCCTGAAAACAG
1339	TTCAGGCTTGGCCTGAAAACAGG
1340	TCAGGCTTGGCCTGAAAACAGGA
1341	CAGGCTTGGCCTGAAAACAGGAC
1342	AGGCTTGGCCTGAAAACAGGACG
1343	GGCTTGGCCTGAAAACAGGACGG
1344	GCTTGGCCTGAAAACAGGACGGA
1345	CTTGGCCTGAAAACAGGACGGAC
1346	TTGGCCTGAAAACAGGACGGACC
1347	TGGCCTGAAAACAGGACGGACCT
1348	GGCCTGAAAACAGGACGGACCTC
1349	GCCTGAAAACAGGACGGACCTCC
1350	CCTGAAAACAGGACGGACCTCCA
1351	CTGAAAACAGGACGGACCTCCAT
1352	TGAAAACAGGACGGACCTCCATG
1353	GAAAACAGGACGGACCTCCATGC
1354	AAAACAGGACGGACCTCCATGCC
1355	AAACAGGACGGACCTCCATGCCT
1356	AACAGGACGGACCTCCATGCCTT
1357	ACAGGACGGACCTCCATGCCTTT
1358	CAGGACGGACCTCCATGCCTTTG
1359	AGGACGGACCTCCATGCCTTTGA
1360	GGACGGACCTCCATGCCTTTGAG
1361	GACGGACCTCCATGCCTTTGAGA
1362	ACGGACCTCCATGCCTTTGAGAA
1363	CGGACCTCCATGCCTTTGAGAAC
1364	GGACCTCCATGCCTTTGAGAACC
1365	GACCTCCATGCCTTTGAGAACCT
1366	ACCTCCATGCCTTTGAGAACCTA
1367	CCTCCATGCCTTTGAGAACCTAG
1368	CTCCATGCCTTTGAGAACCTAGA
1369	TCCATGCCTTTGAGAACCTAGAA
1370	CCATGCCTTTGAGAACCTAGAAA
1371	CATGCCTTTGAGAACCTAGAAAT
1372	ATGCCTTTGAGAACCTAGAAATC
1373	TGCCTTTGAGAACCTAGAAATCA
1374	GCCTTTGAGAACCTAGAAATCAT
1375	CCTTTGAGAACCTAGAAATCATA
1376	CTTTGAGAACCTAGAAATCATAC
1377	TTTGAGAACCTAGAAATCATACG
1378	TTGAGAACCTAGAAATCATACGC
1379	TGAGAACCTAGAAATCATACGCG
1380	GAGAACCTAGAAATCATACGCGG
1381	AGAACCTAGAAATCATACGCGGC
1382	GAACCTAGAAATCATACGCGGCA
1383	AACCTAGAAATCATACGCGGCAG
1384	ACCTAGAAATCATACGCGGCAGG
1385	CCTAGAAATCATACGCGGCAGGA
1386	CTAGAAATCATACGCGGCAGGAC
1387	TAGAAATCATACGCGGCAGGACC
1388	AGAAATCATACGCGGCAGGACCA
1389	GAAATCATACGCGGCAGGACCAA
1390	AAATCATACGCGGCAGGACCAAG
1391	AATCATACGCGGCAGGACCAAGC
1392	ATCATACGCGGCAGGACCAAGCA

Fig. 28 cont'd (Sheet 24 of 93)

ID	SEQUENCE
1393	TCATACGCGGCAGGACCAAGCAA
1394	CATACGCGGCAGGACCAAGCAAC
1395	ATACGCGGCAGGACCAAGCAACA
1396	TACGCGGCAGGACCAAGCAACAT
1397	ACGCGGCAGGACCAAGCAACATG
1398	CGCGGCAGGACCAAGCAACATGG
1399	GCGGCAGGACCAAGCAACATGGT
1400	CGGCAGGACCAAGCAACATGGTC
1401	GGCAGGACCAAGCAACATGGTCA
1402	GCAGGACCAAGCAACATGGTCAG
1403	CAGGACCAAGCAACATGGTCAGT
1404	AGGACCAAGCAACATGGTCAGTT
1405	GGACCAAGCAACATGGTCAGTTT
1406	GACCAAGCAACATGGTCAGTTTT
1407	ACCAAGCAACATGGTCAGTTTTC
1408	CCAAGCAACATGGTCAGTTTTCT
1409	CAAGCAACATGGTCAGTTTTCTC
1410	AAGCAACATGGTCAGTTTTCTCT
1411	AGCAACATGGTCAGTTTTCTCTT
1412	GCAACATGGTCAGTTTTCTCTTG
1413	CAACATGGTCAGTTTTCTCTTGC
1414	AACATGGTCAGTTTTCTCTTGCA
1415	ACATGGTCAGTTTTCTCTTGCAG
1416	CATGGTCAGTTTTCTCTTGCAGT
1417	ATGGTCAGTTTTCTCTTGCAGTC
1418	TGGTCAGTTTTCTCTTGCAGTCG
1419	GGTCAGTTTTCTCTTGCAGTCGT
1420	GTCAGTTTTCTCTTGCAGTCGTC
1421	TCAGTTTTCTCTTGCAGTCGTCA
1422	CAGTTTTCTCTTGCAGTCGTCAG
1423	AGTTTTCTCTTGCAGTCGTCAGC
1424	GTTTTCTCTTGCAGTCGTCAGCC
1425	TTTTCTCTTGCAGTCGTCAGCCT
1426	TTTCTCTTGCAGTCGTCAGCCTG
1427	TTCTCTTGCAGTCGTCAGCCTGA
1428	TCTCTTGCAGTCGTCAGCCTGAA
1429	CTCTTGCAGTCGTCAGCCTGAAC
1430	TCTTGCAGTCGTCAGCCTGAACA
1431	CTTGCAGTCGTCAGCCTGAACAT
1432	TTGCAGTCGTCAGCCTGAACATA
1433	TGCAGTCGTCAGCCTGAACATAA
1434	GCAGTCGTCAGCCTGAACATAAC
1435	CAGTCGTCAGCCTGAACATAACA
1436	AGTCGTCAGCCTGAACATAACAT
1437	GTCGTCAGCCTGAACATAACATC
1438	TCGTCAGCCTGAACATAACATCC
1439	CGTCAGCCTGAACATAACATCCT
1440	GTCAGCCTGAACATAACATCCTT
1441	TCAGCCTGAACATAACATCCTTG
1442	CAGCCTGAACATAACATCCTTGG
1443	AGCCTGAACATAACATCCTTGGG
1444	GCCTGAACATAACATCCTTGGGA
1445	CCTGAACATAACATCCTTGGGAT
1446	CTGAACATAACATCCTTGGGATT
1447	TGAACATAACATCCTTGGGATTA
1448	GAACATAACATCCTTGGGATTAC
1449	AACATAACATCCTTGGGATTACG
1450	ACATAACATCCTTGGGATTACGC

Fig. 28 cont'd (Sheet 25 of 93)

ID	SEQUENCE
1451	CATAACATCCTTGGGATTACGCT
1452	ATAACATCCTTGGGATTACGCTC
1453	TAACATCCTTGGGATTACGCTCC
1454	AACATCCTTGGGATTACGCTCCC
1455	ACATCCTTGGGATTACGCTCCCT
1456	CATCCTTGGGATTACGCTCCCTC
1457	ATCCTTGGGATTACGCTCCCTCA
1458	TCCTTGGGATTACGCTCCCTCAA
1459	CCTTGGGATTACGCTCCCTCAAG
1460	CTTGGGATTACGCTCCCTCAAGG
1461	TTGGGATTACGCTCCCTCAAGGA
1462	TGGGATTACGCTCCCTCAAGGAG
1463	GGGATTACGCTCCCTCAAGGAGA
1464	GGATTACGCTCCCTCAAGGAGAT
1465	GATTACGCTCCCTCAAGGAGATA
1466	ATTACGCTCCCTCAAGGAGATAA
1467	TTACGCTCCCTCAAGGAGATAAG
1468	TACGCTCCCTCAAGGAGATAAGT
1469	ACGCTCCCTCAAGGAGATAAGTG
1470	CGCTCCCTCAAGGAGATAAGTGA
1471	GCTCCCTCAAGGAGATAAGTGAT
1472	CTCCCTCAAGGAGATAAGTGATG
1473	TCCCTCAAGGAGATAAGTGATGG
1474	CCCTCAAGGAGATAAGTGATGGA
1475	CCTCAAGGAGATAAGTGATGGAG
1476	CTCAAGGAGATAAGTGATGGAGA
1477	TCAAGGAGATAAGTGATGGAGAT
1478	CAAGGAGATAAGTGATGGAGATG
1479	AAGGAGATAAGTGATGGAGATGT
1480	AGGAGATAAGTGATGGAGATGTG
1481	GGAGATAAGTGATGGAGATGTGA
1482	GAGATAAGTGATGGAGATGTGAT
1483	AGATAAGTGATGGAGATGTGATA
1484	GATAAGTGATGGAGATGTGATAA
1485	ATAAGTGATGGAGATGTGATAAT
1486	TAAGTGATGGAGATGTGATAATT
1487	AAGTGATGGAGATGTGATAATTT
1488	AGTGATGGAGATGTGATAATTTC
1489	GTGATGGAGATGTGATAATTTCA
1490	TGATGGAGATGTGATAATTTCAG
1491	GATGGAGATGTGATAATTTCAGG
1492	ATGGAGATGTGATAATTTCAGGA
1493	TGGAGATGTGATAATTTCAGGAA
1494	GGAGATGTGATAATTTCAGGAAA
1495	GAGATGTGATAATTTCAGGAAAC
1496	AGATGTGATAATTTCAGGAAACA
1497	GATGTGATAATTTCAGGAAACAA
1498	ATGTGATAATTTCAGGAAACAAA
1499	TGTGATAATTTCAGGAAACAAAA
1500	GTGATAATTTCAGGAAACAAAAA
1501	TGATAATTTCAGGAAACAAAAAT
1502	GATAATTTCAGGAAACAAAAATT
1503	ATAATTTCAGGAAACAAAAATTT
1504	TAATTTCAGGAAACAAAAATTTG
1505	AATTTCAGGAAACAAAAATTTGT
1506	ATTTCAGGAAACAAAAATTTGTG
1507	TTTCAGGAAACAAAAATTTGTGC
1508	TTCAGGAAACAAAAATTTGTGCT

Fig. 28 cont'd (Sheet 26 of 93)

ID	SEQUENCE
1509	TCAGGAAACAAAAATTTGTGCTA
1510	CAGGAAACAAAAATTTGTGCTAT
1511	AGGAAACAAAAATTTGTGCTATG
1512	GGAAACAAAAATTTGTGCTATGC
1513	GAAACAAAAATTTGTGCTATGCA
1514	AAACAAAAATTTGTGCTATGCAA
1515	AACAAAAATTTGTGCTATGCAAA
1516	ACAAAAATTTGTGCTATGCAAAT
1517	CAAAAATTTGTGCTATGCAAATA
1518	AAAAATTTGTGCTATGCAAATAC
1519	AAAATTTGTGCTATGCAAATACA
1520	AAATTTGTGCTATGCAAATACAA
1521	AATTTGTGCTATGCAAATACAAT
1522	ATTTGTGCTATGCAAATACAATA
1523	TTTGTGCTATGCAAATACAATAA
1524	TTGTGCTATGCAAATACAATAAA
1525	TGTGCTATGCAAATACAATAAAC
1526	GTGCTATGCAAATACAATAAACT
1527	TGCTATGCAAATACAATAAACTG
1528	GCTATGCAAATACAATAAACTGG
1529	CTATGCAAATACAATAAACTGGA
1530	TATGCAAATACAATAAACTGGAA
1531	ATGCAAATACAATAAACTGGAAA
1532	TGCAAATACAATAAACTGGAAAA
1533	GCAAATACAATAAACTGGAAAAA
1534	CAAATACAATAAACTGGAAAAAA
1535	AAATACAATAAACTGGAAAAAAC
1536	AATACAATAAACTGGAAAAAACT
1537	ATACAATAAACTGGAAAAAACTG
1538	TACAATAAACTGGAAAAAACTGT
1539	ACAATAAACTGGAAAAAACTGTT
1540	CAATAAACTGGAAAAAACTGTTT
1541	AATAAACTGGAAAAAACTGTTTG
1542	ATAAACTGGAAAAAACTGTTTGG
1543	TAAACTGGAAAAAACTGTTTGGG
1544	AAACTGGAAAAAACTGTTTGGGA
1545	AACTGGAAAAAACTGTTTGGGAC
1546	ACTGGAAAAAACTGTTTGGGACC
1547	CTGGAAAAAACTGTTTGGGACCT
1548	TGGAAAAAACTGTTTGGGACCTC
1549	GGAAAAAACTGTTTGGGACCTCC
1550	GAAAAAACTGTTTGGGACCTCCG
1551	AAAAAACTGTTTGGGACCTCCGG
1552	AAAAACTGTTTGGGACCTCCGGT
1553	AAAACTGTTTGGGACCTCCGGTC
1554	AAACTGTTTGGGACCTCCGGTCA
1555	AACTGTTTGGGACCTCCGGTCAG
1556	ACTGTTTGGGACCTCCGGTCAGA
1557	CTGTTTGGGACCTCCGGTCAGAA
1558	TGTTTGGGACCTCCGGTCAGAAA
1559	GTTTGGGACCTCCGGTCAGAAAA
1560	TTTGGGACCTCCGGTCAGAAAAC
1561	TTGGGACCTCCGGTCAGAAAACC
1562	TGGGACCTCCGGTCAGAAAACCA
1563	GGGACCTCCGGTCAGAAAACCAA
1564	GGACCTCCGGTCAGAAAACCAAA
1565	GACCTCCGGTCAGAAAACCAAAA
1566	ACCTCCGGTCAGAAAACCAAAAT

Fig. 28 cont'd (Sheet 27 of 93)

ID	SEQUENCE
1567	CCTCCGGTCAGAAAACCAAAATT
1568	CTCCGGTCAGAAAACCAAAATTA
1569	TCCGGTCAGAAAACCAAAATTAT
1570	CCGGTCAGAAAACCAAAATTATA
1571	CGGTCAGAAAACCAAAATTATAA
1572	GGTCAGAAAACCAAAATTATAAG
1573	GTCAGAAAACCAAAATTATAAGC
1574	TCAGAAAACCAAAATTATAAGCA
1575	CAGAAAACCAAAATTATAAGCAA
1576	AGAAAACCAAAATTATAAGCAAC
1577	GAAAACCAAAATTATAAGCAACA
1578	AAAACCAAAATTATAAGCAACAG
1579	AAACCAAAATTATAAGCAACAGA
1580	AACCAAAATTATAAGCAACAGAG
1581	ACCAAAATTATAAGCAACAGAGG
1582	CCAAAATTATAAGCAACAGAGGT
1583	CAAAATTATAAGCAACAGAGGTG
1584	AAAATTATAAGCAACAGAGGTGA
1585	AAATTATAAGCAACAGAGGTGAA
1586	AATTATAAGCAACAGAGGTGAAA
1587	ATTATAAGCAACAGAGGTGAAAA
1588	TTATAAGCAACAGAGGTGAAAAC
1589	TATAAGCAACAGAGGTGAAAACA
1590	ATAAGCAACAGAGGTGAAAACAG
1591	TAAGCAACAGAGGTGAAAACAGC
1592	AAGCAACAGAGGTGAAAACAGCT
1593	AGCAACAGAGGTGAAAACAGCTG
1594	GCAACAGAGGTGAAAACAGCTGC
1595	CAACAGAGGTGAAAACAGCTGCA
1596	AACAGAGGTGAAAACAGCTGCAA
1597	ACAGAGGTGAAAACAGCTGCAAG
1598	CAGAGGTGAAAACAGCTGCAAGG
1599	AGAGGTGAAAACAGCTGCAAGGC
1600	GAGGTGAAAACAGCTGCAAGGCC
1601	AGGTGAAAACAGCTGCAAGGCCA
1602	GGTGAAAACAGCTGCAAGGCCAC
1603	GTGAAAACAGCTGCAAGGCCACA
1604	TGAAAACAGCTGCAAGGCCACAG
1605	GAAAACAGCTGCAAGGCCACAGG
1606	AAAACAGCTGCAAGGCCACAGGC
1607	AAACAGCTGCAAGGCCACAGGCC
1608	AACAGCTGCAAGGCCACAGGCCA
1609	ACAGCTGCAAGGCCACAGGCCAG
1610	CAGCTGCAAGGCCACAGGCCAGG
1611	AGCTGCAAGGCCACAGGCCAGGT
1612	GCTGCAAGGCCACAGGCCAGGTC
1613	CTGCAAGGCCACAGGCCAGGTCT
1614	TGCAAGGCCACAGGCCAGGTCTG
1615	GCAAGGCCACAGGCCAGGTCTGC
1616	CAAGGCCACAGGCCAGGTCTGCC
1617	AAGGCCACAGGCCAGGTCTGCCA
1618	AGGCCACAGGCCAGGTCTGCCAT
1619	GGCCACAGGCCAGGTCTGCCATG
1620	GCCACAGGCCAGGTCTGCCATGC
1621	CCACAGGCCAGGTCTGCCATGCC
1622	CACAGGCCAGGTCTGCCATGCCT
1623	ACAGGCCAGGTCTGCCATGCCTT
1624	CAGGCCAGGTCTGCCATGCCTTG

Fig. 28 cont'd (Sheet 28 of 93)

ID	SEQUENCE
1625	AGGCCAGGTCTGCCATGCCTTGT
1626	GGCCAGGTCTGCCATGCCTTGTG
1627	GCCAGGTCTGCCATGCCTTGTGC
1628	CCAGGTCTGCCATGCCTTGTGCT
1629	CAGGTCTGCCATGCCTTGTGCTC
1630	AGGTCTGCCATGCCTTGTGCTCC
1631	GGTCTGCCATGCCTTGTGCTCCC
1632	GTCTGCCATGCCTTGTGCTCCCC
1633	TCTGCCATGCCTTGTGCTCCCCC
1634	CTGCCATGCCTTGTGCTCCCCCG
1635	TGCCATGCCTTGTGCTCCCCCGA
1636	GCCATGCCTTGTGCTCCCCCGAG
1637	CCATGCCTTGTGCTCCCCCGAGG
1638	CATGCCTTGTGCTCCCCCGAGGG
1639	ATGCCTTGTGCTCCCCCGAGGGC
1640	TGCCTTGTGCTCCCCCGAGGGCT
1641	GCCTTGTGCTCCCCCGAGGGCTG
1642	CCTTGTGCTCCCCCGAGGGCTGC
1643	CTTGTGCTCCCCCGAGGGCTGCT
1644	TTGTGCTCCCCCGAGGGCTGCTG
1645	TGTGCTCCCCCGAGGGCTGCTGG
1646	GTGCTCCCCCGAGGGCTGCTGGG
1647	TGCTCCCCCGAGGGCTGCTGGGG
1648	GCTCCCCCGAGGGCTGCTGGGGC
1649	CTCCCCCGAGGGCTGCTGGGGCC
1650	TCCCCCGAGGGCTGCTGGGGCCC
1651	CCCCCGAGGGCTGCTGGGGCCCG
1652	GGGCCCGGAGCCCAGGGACTGCG
1653	GGCCCGGAGCCCAGGGACTGCGT
1654	GCCCGGAGCCCAGGGACTGCGTC
1655	CCCGGAGCCCAGGGACTGCGTCT
1656	CCGGAGCCCAGGGACTGCGTCTC
1657	CGGAGCCCAGGGACTGCGTCTCT
1658	GGAGCCCAGGGACTGCGTCTCTT
1659	GAGCCCAGGGACTGCGTCTCTTG
1660	AGCCCAGGGACTGCGTCTCTTGC
1661	GCCCAGGGACTGCGTCTCTTGCC
1662	CCCAGGGACTGCGTCTCTTGCCG
1663	CCAGGGACTGCGTCTCTTGCCGG
1664	CAGGGACTGCGTCTCTTGCCGGA
1665	AGGGACTGCGTCTCTTGCCGGAA
1666	GGGACTGCGTCTCTTGCCGGAAT
1667	GGACTGCGTCTCTTGCCGGAATG
1668	GACTGCGTCTCTTGCCGGAATGT
1669	ACTGCGTCTCTTGCCGGAATGTC
1670	CTGCGTCTCTTGCCGGAATGTCA
1671	TGCGTCTCTTGCCGGAATGTCAG
1672	GCGTCTCTTGCCGGAATGTCAGC
1673	CGTCTCTTGCCGGAATGTCAGCC
1674	GTCTCTTGCCGGAATGTCAGCCG
1675	TCTCTTGCCGGAATGTCAGCCGA
1676	CTCTTGCCGGAATGTCAGCCGAG
1677	TCTTGCCGGAATGTCAGCCGAGG
1678	CTTGCCGGAATGTCAGCCGAGGC
1679	TTGCCGGAATGTCAGCCGAGGCA
1680	TGCCGGAATGTCAGCCGAGGCAG
1681	GCCGGAATGTCAGCCGAGGCAGG
1682	CCGGAATGTCAGCCGAGGCAGGG

Fig. 28 cont'd (Sheet 29 of 93)

ID	SEQUENCE
1683	CGGAATGTCAGCCGAGGCAGGGA
1684	GGAATGTCAGCCGAGGCAGGGAA
1685	GAATGTCAGCCGAGGCAGGGAAT
1686	AATGTCAGCCGAGGCAGGGAATG
1687	ATGTCAGCCGAGGCAGGGAATGC
1688	TGTCAGCCGAGGCAGGGAATGCG
1689	GTCAGCCGAGGCAGGGAATGCGT
1690	TCAGCCGAGGCAGGGAATGCGTG
1691	CAGCCGAGGCAGGGAATGCGTGG
1692	AGCCGAGGCAGGGAATGCGTGGA
1693	GCCGAGGCAGGGAATGCGTGGAC
1694	CCGAGGCAGGGAATGCGTGGACA
1695	CGAGGCAGGGAATGCGTGGACAA
1696	GAGGCAGGGAATGCGTGGACAAG
1697	AGGCAGGGAATGCGTGGACAAGT
1698	GGCAGGGAATGCGTGGACAAGTG
1699	GCAGGGAATGCGTGGACAAGTGC
1700	CAGGGAATGCGTGGACAAGTGCA
1701	AGGGAATGCGTGGACAAGTGCAA
1702	GGGAATGCGTGGACAAGTGCAAC
1703	GGAATGCGTGGACAAGTGCAACC
1704	GAATGCGTGGACAAGTGCAACCT
1705	AATGCGTGGACAAGTGCAACCTT
1706	ATGCGTGGACAAGTGCAACCTTC
1707	TGCGTGGACAAGTGCAACCTTCT
1708	GCGTGGACAAGTGCAACCTTCTG
1709	CGTGGACAAGTGCAACCTTCTGG
1710	GTGGACAAGTGCAACCTTCTGGA
1711	TGGACAAGTGCAACCTTCTGGAG
1712	GGACAAGTGCAACCTTCTGGAGG
1713	GACAAGTGCAACCTTCTGGAGGG
1714	ACAAGTGCAACCTTCTGGAGGGT
1715	CAAGTGCAACCTTCTGGAGGGTG
1716	AAGTGCAACCTTCTGGAGGGTGA
1717	AGTGCAACCTTCTGGAGGGTGAG
1718	GTGCAACCTTCTGGAGGGTGAGC
1719	TGCAACCTTCTGGAGGGTGAGCC
1720	GCAACCTTCTGGAGGGTGAGCCA
1721	CAACCTTCTGGAGGGTGAGCCAA
1722	AACCTTCTGGAGGGTGAGCCAAG
1723	ACCTTCTGGAGGGTGAGCCAAGG
1724	CCTTCTGGAGGGTGAGCCAAGGG
1725	CTTCTGGAGGGTGAGCCAAGGGA
1726	TTCTGGAGGGTGAGCCAAGGGAG
1727	TCTGGAGGGTGAGCCAAGGGAGT
1728	CTGGAGGGTGAGCCAAGGGAGTT
1729	TGGAGGGTGAGCCAAGGGAGTTT
1730	GGAGGGTGAGCCAAGGGAGTTTG
1731	GAGGGTGAGCCAAGGGAGTTTGT
1732	AGGGTGAGCCAAGGGAGTTTGTG
1733	GGGTGAGCCAAGGGAGTTTGTGG
1734	GGTGAGCCAAGGGAGTTTGTGGA
1735	GTGAGCCAAGGGAGTTTGTGGAG
1736	TGAGCCAAGGGAGTTTGTGGAGA
1737	GAGCCAAGGGAGTTTGTGGAGAA
1738	AGCCAAGGGAGTTTGTGGAGAAC
1739	GCCAAGGGAGTTTGTGGAGAACT
1740	CCAAGGGAGTTTGTGGAGAACTC

Fig. 28 cont'd (Sheet 30 of 93)

ID	SEQUENCE
1741	CAAGGGAGTTTGTGGAGAACTCT
1742	AAGGGAGTTTGTGGAGAACTCTG
1743	AGGGAGTTTGTGGAGAACTCTGA
1744	GGGAGTTTGTGGAGAACTCTGAG
1745	GGAGTTTGTGGAGAACTCTGAGT
1746	GAGTTTGTGGAGAACTCTGAGTG
1747	AGTTTGTGGAGAACTCTGAGTGC
1748	GTTTGTGGAGAACTCTGAGTGCA
1749	TTTGTGGAGAACTCTGAGTGCAT
1750	TTGTGGAGAACTCTGAGTGCATA
1751	TGTGGAGAACTCTGAGTGCATAC
1752	GTGGAGAACTCTGAGTGCATACA
1753	TGGAGAACTCTGAGTGCATACAG
1754	GGAGAACTCTGAGTGCATACAGT
1755	GAGAACTCTGAGTGCATACAGTG
1756	AGAACTCTGAGTGCATACAGTGC
1757	GAACTCTGAGTGCATACAGTGCC
1758	AACTCTGAGTGCATACAGTGCCA
1759	ACTCTGAGTGCATACAGTGCCAC
1760	CTCTGAGTGCATACAGTGCCACC
1761	TCTGAGTGCATACAGTGCCACCC
1762	CTGAGTGCATACAGTGCCACCCA
1763	TGAGTGCATACAGTGCCACCCAG
1764	GAGTGCATACAGTGCCACCCAGA
1765	AGTGCATACAGTGCCACCCAGAG
1766	GTGCATACAGTGCCACCCAGAGT
1767	TGCATACAGTGCCACCCAGAGTG
1768	GCATACAGTGCCACCCAGAGTGC
1769	CATACAGTGCCACCCAGAGTGCC
1770	ATACAGTGCCACCCAGAGTGCCT
1771	TACAGTGCCACCCAGAGTGCCTG
1772	ACAGTGCCACCCAGAGTGCCTGC
1773	CAGTGCCACCCAGAGTGCCTGCC
1774	AGTGCCACCCAGAGTGCCTGCCT
1775	GTGCCACCCAGAGTGCCTGCCTC
1776	TGCCACCCAGAGTGCCTGCCTCA
1777	GCCACCCAGAGTGCCTGCCTCAG
1778	CCACCCAGAGTGCCTGCCTCAGG
1779	CACCCAGAGTGCCTGCCTCAGGC
1780	ACCCAGAGTGCCTGCCTCAGGCC
1781	CCCAGAGTGCCTGCCTCAGGCCA
1782	CCAGAGTGCCTGCCTCAGGCCAT
1783	CAGAGTGCCTGCCTCAGGCCATG
1784	AGAGTGCCTGCCTCAGGCCATGA
1785	GAGTGCCTGCCTCAGGCCATGAA
1786	AGTGCCTGCCTCAGGCCATGAAC
1787	GTGCCTGCCTCAGGCCATGAACA
1788	TGCCTGCCTCAGGCCATGAACAT
1789	GCCTGCCTCAGGCCATGAACATC
1790	CCTGCCTCAGGCCATGAACATCA
1791	CTGCCTCAGGCCATGAACATCAC
1792	TGCCTCAGGCCATGAACATCACC
1793	GCCTCAGGCCATGAACATCACCT
1794	CCTCAGGCCATGAACATCACCTG
1795	CTCAGGCCATGAACATCACCTGC
1796	TCAGGCCATGAACATCACCTGCA
1797	CAGGCCATGAACATCACCTGCAC
1798	AGGCCATGAACATCACCTGCACA

Fig. 28 cont'd (Sheet 31 of 93)

ID	SEQUENCE
1799	GGCCATGAACATCACCTGCACAG
1800	GCCATGAACATCACCTGCACAGG
1801	CCATGAACATCACCTGCACAGGA
1802	CATGAACATCACCTGCACAGGAC
1803	ATGAACATCACCTGCACAGGACG
1804	TGAACATCACCTGCACAGGACGG
1805	GAACATCACCTGCACAGGACGGG
1806	AACATCACCTGCACAGGACGGGG
1807	ACATCACCTGCACAGGACGGGGA
1808	CATCACCTGCACAGGACGGGGAC
1809	ATCACCTGCACAGGACGGGGACC
1810	TCACCTGCACAGGACGGGGACCA
1811	CACCTGCACAGGACGGGGACCAG
1812	ACCTGCACAGGACGGGGACCAGA
1813	CCTGCACAGGACGGGGACCAGAC
1814	CTGCACAGGACGGGGACCAGACA
1815	TGCACAGGACGGGGACCAGACAA
1816	GCACAGGACGGGGACCAGACAAC
1817	CACAGGACGGGGACCAGACAACT
1818	ACAGGACGGGGACCAGACAACTG
1819	CAGGACGGGGACCAGACAACTGT
1820	AGGACGGGGACCAGACAACTGTA
1821	GGACGGGGACCAGACAACTGTAT
1822	GACGGGGACCAGACAACTGTATC
1823	ACGGGGACCAGACAACTGTATCC
1824	CGGGGACCAGACAACTGTATCCA
1825	GGGGACCAGACAACTGTATCCAG
1826	GGGACCAGACAACTGTATCCAGT
1827	GGACCAGACAACTGTATCCAGTG
1828	GACCAGACAACTGTATCCAGTGT
1829	ACCAGACAACTGTATCCAGTGTG
1830	CCAGACAACTGTATCCAGTGTGC
1831	CAGACAACTGTATCCAGTGTGCC
1832	AGACAACTGTATCCAGTGTGCCC
1833	GACAACTGTATCCAGTGTGCCCA
1834	ACAACTGTATCCAGTGTGCCCAC
1835	CAACTGTATCCAGTGTGCCCACT
1836	AACTGTATCCAGTGTGCCCACTA
1837	ACTGTATCCAGTGTGCCCACTAC
1838	CTGTATCCAGTGTGCCCACTACA
1839	TGTATCCAGTGTGCCCACTACAT
1840	GTATCCAGTGTGCCCACTACATT
1841	TATCCAGTGTGCCCACTACATTG
1842	ATCCAGTGTGCCCACTACATTGA
1843	TCCAGTGTGCCCACTACATTGAC
1844	CCAGTGTGCCCACTACATTGACG
1845	CAGTGTGCCCACTACATTGACGG
1846	AGTGTGCCCACTACATTGACGGC
1847	GTGTGCCCACTACATTGACGGCC
1848	TGTGCCCACTACATTGACGGCCC
1849	GTGCCCACTACATTGACGGCCCC
1850	TGCCCACTACATTGACGGCCCCC
1851	GCCCACTACATTGACGGCCCCCA
1852	CCCACTACATTGACGGCCCCCAC
1853	CCACTACATTGACGGCCCCCACT
1854	CACTACATTGACGGCCCCCACTG
1855	ACTACATTGACGGCCCCCACTGC
1856	CTACATTGACGGCCCCCACTGCG

Fig. 28 cont'd (Sheet 32 of 93)

ID	SEQUENCE
1857	TACATTGACGGCCCCCACTGCGT
1858	ACATTGACGGCCCCCACTGCGTC
1859	CATTGACGGCCCCCACTGCGTCA
1860	ATTGACGGCCCCCACTGCGTCAA
1861	TTGACGGCCCCCACTGCGTCAAG
1862	TGACGGCCCCCACTGCGTCAAGA
1863	GACGGCCCCCACTGCGTCAAGAC
1864	ACGGCCCCCACTGCGTCAAGACC
1865	CGGCCCCCACTGCGTCAAGACCT
1866	GGCCCCCACTGCGTCAAGACCTG
1867	GCCCCCACTGCGTCAAGACCTGC
1868	CCCCCACTGCGTCAAGACCTGCC
1869	CCCCACTGCGTCAAGACCTGCCC
1870	CCCACTGCGTCAAGACCTGCCCG
1871	CCACTGCGTCAAGACCTGCCCGG
1872	CACTGCGTCAAGACCTGCCCGGC
1873	ACTGCGTCAAGACCTGCCCGGCA
1874	CTGCGTCAAGACCTGCCCGGCAG
1875	TGCGTCAAGACCTGCCCGGCAGG
1876	GCGTCAAGACCTGCCCGGCAGGA
1877	CGTCAAGACCTGCCCGGCAGGAG
1878	GTCAAGACCTGCCCGGCAGGAGT
1879	TCAAGACCTGCCCGGCAGGAGTC
1880	CAAGACCTGCCCGGCAGGAGTCA
1881	AAGACCTGCCCGGCAGGAGTCAT
1882	AGACCTGCCCGGCAGGAGTCATG
1883	GACCTGCCCGGCAGGAGTCATGG
1884	ACCTGCCCGGCAGGAGTCATGGG
1885	CCTGCCCGGCAGGAGTCATGGGA
1886	CTGCCCGGCAGGAGTCATGGGAG
1887	TGCCCGGCAGGAGTCATGGGAGA
1888	GCCCGGCAGGAGTCATGGGAGAA
1889	CCCGGCAGGAGTCATGGGAGAAA
1890	CCGGCAGGAGTCATGGGAGAAAA
1891	CGGCAGGAGTCATGGGAGAAAAC
1892	GGCAGGAGTCATGGGAGAAAACA
1893	GCAGGAGTCATGGGAGAAAACAA
1894	CAGGAGTCATGGGAGAAAACAAC
1895	AGGAGTCATGGGAGAAAACAACA
1896	GGAGTCATGGGAGAAAACAACAC
1897	GAGTCATGGGAGAAAACAACACC
1898	AGTCATGGGAGAAAACAACACCC
1899	GTCATGGGAGAAAACAACACCCT
1900	TCATGGGAGAAAACAACACCCTG
1901	CATGGGAGAAAACAACACCCTGG
1902	ATGGGAGAAAACAACACCCTGGT
1903	TGGGAGAAAACAACACCCTGGTC
1904	GGGAGAAAACAACACCCTGGTCT
1905	GGAGAAAACAACACCCTGGTCTG
1906	GAGAAAACAACACCCTGGTCTGG
1907	AGAAAACAACACCCTGGTCTGGA
1908	GAAAACAACACCCTGGTCTGGAA
1909	AAAACAACACCCTGGTCTGGAAG
1910	AAACAACACCCTGGTCTGGAAGT
1911	AACAACACCCTGGTCTGGAAGTA
1912	ACAACACCCTGGTCTGGAAGTAC
1913	CAACACCCTGGTCTGGAAGTACG
1914	AACACCCTGGTCTGGAAGTACGC

Fig. 28 cont'd (Sheet 33 of 93)

ID	SEQUENCE
1915	ACACCCTGGTCTGGAAGTACGCA
1916	CACCCTGGTCTGGAAGTACGCAG
1917	ACCCTGGTCTGGAAGTACGCAGA
1918	CCCTGGTCTGGAAGTACGCAGAC
1919	CCTGGTCTGGAAGTACGCAGACG
1920	CTGGTCTGGAAGTACGCAGACGC
1921	TGGTCTGGAAGTACGCAGACGCC
1922	GGTCTGGAAGTACGCAGACGCCG
1923	GTCTGGAAGTACGCAGACGCCGG
1924	TCTGGAAGTACGCAGACGCCGGC
1925	CTGGAAGTACGCAGACGCCGGCC
1926	TGGAAGTACGCAGACGCCGGCCA
1927	GGAAGTACGCAGACGCCGGCCAT
1928	GAAGTACGCAGACGCCGGCCATG
1929	AAGTACGCAGACGCCGGCCATGT
1930	AGTACGCAGACGCCGGCCATGTG
1931	GTACGCAGACGCCGGCCATGTGT
1932	TACGCAGACGCCGGCCATGTGTG
1933	ACGCAGACGCCGGCCATGTGTGC
1934	CGCAGACGCCGGCCATGTGTGCC
1935	GCAGACGCCGGCCATGTGTGCCA
1936	CAGACGCCGGCCATGTGTGCCAC
1937	AGACGCCGGCCATGTGTGCCACC
1938	GACGCCGGCCATGTGTGCCACCT
1939	ACGCCGGCCATGTGTGCCACCTG
1940	CGCCGGCCATGTGTGCCACCTGT
1941	GCCGGCCATGTGTGCCACCTGTG
1942	CCGGCCATGTGTGCCACCTGTGC
1943	CGGCCATGTGTGCCACCTGTGCC
1944	GGCCATGTGTGCCACCTGTGCCA
1945	GCCATGTGTGCCACCTGTGCCAT
1946	CCATGTGTGCCACCTGTGCCATC
1947	CATGTGTGCCACCTGTGCCATCC
1948	ATGTGTGCCACCTGTGCCATCCA
1949	TGTGTGCCACCTGTGCCATCCAA
1950	GTGTGCCACCTGTGCCATCCAAA
1951	TGTGCCACCTGTGCCATCCAAAC
1952	GTGCCACCTGTGCCATCCAAACT
1953	TGCCACCTGTGCCATCCAAACTG
1954	GCCACCTGTGCCATCCAAACTGC
1955	CCACCTGTGCCATCCAAACTGCA
1956	CACCTGTGCCATCCAAACTGCAC
1957	ACCTGTGCCATCCAAACTGCACC
1958	CCTGTGCCATCCAAACTGCACCT
1959	CTGTGCCATCCAAACTGCACCTA
1960	TGTGCCATCCAAACTGCACCTAC
1961	GTGCCATCCAAACTGCACCTACG
1962	TGCCATCCAAACTGCACCTACGG
1963	GCCATCCAAACTGCACCTACGGA
1964	CCATCCAAACTGCACCTACGGAT
1965	CATCCAAACTGCACCTACGGATG
1966	ATCCAAACTGCACCTACGGATGC
1967	TCCAAACTGCACCTACGGATGCA
1968	CCAAACTGCACCTACGGATGCAC
1969	CAAACTGCACCTACGGATGCACT
1970	AAACTGCACCTACGGATGCACTG
1971	AACTGCACCTACGGATGCACTGG
1972	ACTGCACCTACGGATGCACTGGG

Fig. 28 cont'd (Sheet 34 of 93)

ID	SEQUENCE
1973	CTGCACCTACGGATGCACTGGGC
1974	TGCACCTACGGATGCACTGGGCC
1975	GCACCTACGGATGCACTGGGCCA
1976	CACCTACGGATGCACTGGGCCAG
1977	ACCTACGGATGCACTGGGCCAGG
1978	CCTACGGATGCACTGGGCCAGGT
1979	CTACGGATGCACTGGGCCAGGTC
1980	TACGGATGCACTGGGCCAGGTCT
1981	ACGGATGCACTGGGCCAGGTCTT
1982	CGGATGCACTGGGCCAGGTCTTG
1983	GGATGCACTGGGCCAGGTCTTGA
1984	GATGCACTGGGCCAGGTCTTGAA
1985	ATGCACTGGGCCAGGTCTTGAAG
1986	TGCACTGGGCCAGGTCTTGAAGG
1987	GCACTGGGCCAGGTCTTGAAGGC
1988	CACTGGGCCAGGTCTTGAAGGCT
1989	ACTGGGCCAGGTCTTGAAGGCTG
1990	CTGGGCCAGGTCTTGAAGGCTGT
1991	TGGGCCAGGTCTTGAAGGCTGTC
1992	GGGCCAGGTCTTGAAGGCTGTCC
1993	GGCCAGGTCTTGAAGGCTGTCCA
1994	GCCAGGTCTTGAAGGCTGTCCAA
1995	CCAGGTCTTGAAGGCTGTCCAAC
1996	CAGGTCTTGAAGGCTGTCCAACG
1997	AGGTCTTGAAGGCTGTCCAACGA
1998	GGTCTTGAAGGCTGTCCAACGAA
1999	GTCTTGAAGGCTGTCCAACGAAT
2000	TCTTGAAGGCTGTCCAACGAATG
2001	CTTGAAGGCTGTCCAACGAATGG
2002	TTGAAGGCTGTCCAACGAATGGG
2003	TGAAGGCTGTCCAACGAATGGGC
2004	GAAGGCTGTCCAACGAATGGGCC
2005	AAGGCTGTCCAACGAATGGGCCT
2006	AGGCTGTCCAACGAATGGGCCTA
2007	GGCTGTCCAACGAATGGGCCTAA
2008	GCTGTCCAACGAATGGGCCTAAG
2009	CTGTCCAACGAATGGGCCTAAGA
2010	TGTCCAACGAATGGGCCTAAGAT
2011	GTCCAACGAATGGGCCTAAGATC
2012	TCCAACGAATGGGCCTAAGATCC
2013	CCAACGAATGGGCCTAAGATCCC
2014	CAACGAATGGGCCTAAGATCCCG
2015	AACGAATGGGCCTAAGATCCCGT
2016	ACGAATGGGCCTAAGATCCCGTC
2017	CGAATGGGCCTAAGATCCCGTCC
2018	GAATGGGCCTAAGATCCCGTCCA
2019	AATGGGCCTAAGATCCCGTCCAT
2020	ATGGGCCTAAGATCCCGTCCATC
2021	TGGGCCTAAGATCCCGTCCATCG
2022	GGGCCTAAGATCCCGTCCATCGC
2023	GGCCTAAGATCCCGTCCATCGCC
2024	GCCTAAGATCCCGTCCATCGCCA
2025	CCTAAGATCCCGTCCATCGCCAC
2026	CTAAGATCCCGTCCATCGCCACT
2027	TAAGATCCCGTCCATCGCCACTG
2028	AAGATCCCGTCCATCGCCACTGG
2029	AGATCCCGTCCATCGCCACTGGG
2030	GATCCCGTCCATCGCCACTGGGA

Fig. 28 cont'd (Sheet 35 of 93)

ID	SEQUENCE
2031	ATCCCGTCCATCGCCACTGGGAT
2032	TCCCGTCCATCGCCACTGGGATG
2033	CCCGTCCATCGCCACTGGGATGG
2034	CCGTCCATCGCCACTGGGATGGT
2035	CGTCCATCGCCACTGGGATGGTG
2036	GTCCATCGCCACTGGGATGGTGG
2037	TCCATCGCCACTGGGATGGTGGG
2038	CCATCGCCACTGGGATGGTGGGG
2039	CATCGCCACTGGGATGGTGGGGG
2040	ATCGCCACTGGGATGGTGGGGGC
2041	TCGCCACTGGGATGGTGGGGGCC
2042	CGCCACTGGGATGGTGGGGGCCC
2043	GCCACTGGGATGGTGGGGGCCCT
2044	CCACTGGGATGGTGGGGGCCCTC
2045	CACTGGGATGGTGGGGGCCCTCC
2046	ACTGGGATGGTGGGGGCCCTCCT
2047	CTGGGATGGTGGGGGCCCTCCTC
2048	TGGGATGGTGGGGGCCCTCCTCT
2049	GGGATGGTGGGGGCCCTCCTCTT
2050	GGATGGTGGGGGCCCTCCTCTTG
2051	GATGGTGGGGGCCCTCCTCTTGC
2052	ATGGTGGGGGCCCTCCTCTTGCT
2053	TGGTGGGGGCCCTCCTCTTGCTG
2054	GGTGGGGGCCCTCCTCTTGCTGC
2055	GTGGGGGCCCTCCTCTTGCTGCT
2056	TGGGGGCCCTCCTCTTGCTGCTG
2057	GGGGGCCCTCCTCTTGCTGCTGG
2058	GGGGCCCTCCTCTTGCTGCTGGT
2059	GGGCCCTCCTCTTGCTGCTGGTG
2060	GGCCCTCCTCTTGCTGCTGGTGG
2061	GCCCTCCTCTTGCTGCTGGTGGT
2062	CCCTCCTCTTGCTGCTGGTGGTG
2063	CCTCCTCTTGCTGCTGGTGGTGG
2064	CTCCTCTTGCTGCTGGTGGTGGC
2065	TCCTCTTGCTGCTGGTGGTGGCC
2066	CCTCTTGCTGCTGGTGGTGGCCC
2067	CTCTTGCTGCTGGTGGTGGCCCT
2068	TCTTGCTGCTGGTGGTGGCCCTG
2069	CTTGCTGCTGGTGGTGGCCCTGG
2070	TTGCTGCTGGTGGTGGCCCTGGG
2071	TGCTGCTGGTGGTGGCCCTGGGG
2072	GCTGCTGGTGGTGGCCCTGGGGA
2073	CTGCTGGTGGTGGCCCTGGGGAT
2074	TGCTGGTGGTGGCCCTGGGGATC
2075	GCTGGTGGTGGCCCTGGGGATCG
2076	CTGGTGGTGGCCCTGGGGATCGG
2077	TGGTGGTGGCCCTGGGGATCGGC
2078	GGTGGTGGCCCTGGGGATCGGCC
2079	GTGGTGGCCCTGGGGATCGGCCT
2080	TGGTGGCCCTGGGGATCGGCCTC
2081	GGTGGCCCTGGGGATCGGCCTCT
2082	GTGGCCCTGGGGATCGGCCTCTT
2083	TGGCCCTGGGGATCGGCCTCTTC
2084	GGCCCTGGGGATCGGCCTCTTCA
2085	GCCCTGGGGATCGGCCTCTTCAT
2086	CCCTGGGGATCGGCCTCTTCATG
2087	CCTGGGGATCGGCCTCTTCATGC
2088	CTGGGGATCGGCCTCTTCATGCG

Fig. 28 cont'd (Sheet 36 of 93)

ID	SEQUENCE
2089	TGGGGATCGGCCTCTTCATGCGA
2090	GGGGATCGGCCTCTTCATGCGAA
2091	GGGATCGGCCTCTTCATGCGAAG
2092	GGATCGGCCTCTTCATGCGAAGG
2093	GATCGGCCTCTTCATGCGAAGGC
2094	ATCGGCCTCTTCATGCGAAGGCG
2095	TCGGCCTCTTCATGCGAAGGCGC
2096	CGGCCTCTTCATGCGAAGGCGCC
2097	GGCCTCTTCATGCGAAGGCGCCA
2098	GCCTCTTCATGCGAAGGCGCCAC
2099	CCTCTTCATGCGAAGGCGCCACA
2100	CTCTTCATGCGAAGGCGCCACAT
2101	TCTTCATGCGAAGGCGCCACATC
2102	CTTCATGCGAAGGCGCCACATCG
2103	TTCATGCGAAGGCGCCACATCGT
2104	TCATGCGAAGGCGCCACATCGTT
2105	CATGCGAAGGCGCCACATCGTTC
2106	ATGCGAAGGCGCCACATCGTTCG
2107	TGCGAAGGCGCCACATCGTTCGG
2108	GCGAAGGCGCCACATCGTTCGGA
2109	CGAAGGCGCCACATCGTTCGGAA
2110	GAAGGCGCCACATCGTTCGGAAG
2111	AAGGCGCCACATCGTTCGGAAGC
2112	AGGCGCCACATCGTTCGGAAGCG
2113	GGCGCCACATCGTTCGGAAGCGC
2114	GCGCCACATCGTTCGGAAGCGCA
2115	CGCCACATCGTTCGGAAGCGCAC
2116	GCCACATCGTTCGGAAGCGCACG
2117	CCACATCGTTCGGAAGCGCACGC
2118	CACATCGTTCGGAAGCGCACGCT
2119	ACATCGTTCGGAAGCGCACGCTG
2120	CATCGTTCGGAAGCGCACGCTGC
2121	ATCGTTCGGAAGCGCACGCTGCG
2122	TCGTTCGGAAGCGCACGCTGCGG
2123	CGTTCGGAAGCGCACGCTGCGGA
2124	GTTCGGAAGCGCACGCTGCGGAG
2125	TTCGGAAGCGCACGCTGCGGAGG
2126	TCGGAAGCGCACGCTGCGGAGGC
2127	CGGAAGCGCACGCTGCGGAGGCT
2128	GGAAGCGCACGCTGCGGAGGCTG
2129	GAAGCGCACGCTGCGGAGGCTGC
2130	AAGCGCACGCTGCGGAGGCTGCT
2131	AGCGCACGCTGCGGAGGCTGCTG
2132	GCGCACGCTGCGGAGGCTGCTGC
2133	CGCACGCTGCGGAGGCTGCTGCA
2134	GCACGCTGCGGAGGCTGCTGCAG
2135	CACGCTGCGGAGGCTGCTGCAGG
2136	ACGCTGCGGAGGCTGCTGCAGGA
2137	CGCTGCGGAGGCTGCTGCAGGAG
2138	GCTGCGGAGGCTGCTGCAGGAGA
2139	CTGCGGAGGCTGCTGCAGGAGAG
2140	TGCGGAGGCTGCTGCAGGAGAGG
2141	GCGGAGGCTGCTGCAGGAGAGGG
2142	CGGAGGCTGCTGCAGGAGAGGGA
2143	GGAGGCTGCTGCAGGAGAGGGAG
2144	GAGGCTGCTGCAGGAGAGGGAGC
2145	AGGCTGCTGCAGGAGAGGGAGCT
2146	GGCTGCTGCAGGAGAGGGAGCTT

Fig. 28 cont'd (Sheet 37 of 93)

ID	SEQUENCE
2147	GCTGCTGCAGGAGAGGGAGCTTG
2148	CTGCTGCAGGAGAGGGAGCTTGT
2149	TGCTGCAGGAGAGGGAGCTTGTG
2150	GCTGCAGGAGAGGGAGCTTGTGG
2151	CTGCAGGAGAGGGAGCTTGTGGA
2152	TGCAGGAGAGGGAGCTTGTGGAG
2153	GCAGGAGAGGGAGCTTGTGGAGC
2154	CAGGAGAGGGAGCTTGTGGAGCC
2155	AGGAGAGGGAGCTTGTGGAGCCT
2156	GGAGAGGGAGCTTGTGGAGCCTC
2157	GAGAGGGAGCTTGTGGAGCCTCT
2158	AGAGGGAGCTTGTGGAGCCTCTT
2159	GAGGGAGCTTGTGGAGCCTCTTA
2160	AGGGAGCTTGTGGAGCCTCTTAC
2161	GGGAGCTTGTGGAGCCTCTTACA
2162	GGAGCTTGTGGAGCCTCTTACAC
2163	GAGCTTGTGGAGCCTCTTACACC
2164	AGCTTGTGGAGCCTCTTACACCC
2165	GCTTGTGGAGCCTCTTACACCCA
2166	CTTGTGGAGCCTCTTACACCCAG
2167	TTGTGGAGCCTCTTACACCCAGT
2168	TGTGGAGCCTCTTACACCCAGTG
2169	GTGGAGCCTCTTACACCCAGTGG
2170	TGGAGCCTCTTACACCCAGTGGA
2171	GGAGCCTCTTACACCCAGTGGAG
2172	GAGCCTCTTACACCCAGTGGAGA
2173	AGCCTCTTACACCCAGTGGAGAA
2174	GCCTCTTACACCCAGTGGAGAAG
2175	CCTCTTACACCCAGTGGAGAAGC
2176	CTCTTACACCCAGTGGAGAAGCT
2177	TCTTACACCCAGTGGAGAAGCTC
2178	CTTACACCCAGTGGAGAAGCTCC
2179	TTACACCCAGTGGAGAAGCTCCC
2180	TACACCCAGTGGAGAAGCTCCCA
2181	ACACCCAGTGGAGAAGCTCCCAA
2182	CACCCAGTGGAGAAGCTCCCAAC
2183	ACCCAGTGGAGAAGCTCCCAACC
2184	CCCAGTGGAGAAGCTCCCAACCA
2185	CCAGTGGAGAAGCTCCCAACCAA
2186	CAGTGGAGAAGCTCCCAACCAAG
2187	AGTGGAGAAGCTCCCAACCAAGC
2188	GTGGAGAAGCTCCCAACCAAGCT
2189	TGGAGAAGCTCCCAACCAAGCTC
2190	GGAGAAGCTCCCAACCAAGCTCT
2191	GAGAAGCTCCCAACCAAGCTCTC
2192	AGAAGCTCCCAACCAAGCTCTCT
2193	GAAGCTCCCAACCAAGCTCTCTT
2194	AAGCTCCCAACCAAGCTCTCTTG
2195	AGCTCCCAACCAAGCTCTCTTGA
2196	GCTCCCAACCAAGCTCTCTTGAG
2197	CTCCCAACCAAGCTCTCTTGAGG
2198	TCCCAACCAAGCTCTCTTGAGGA
2199	CCCAACCAAGCTCTCTTGAGGAT
2200	CCAACCAAGCTCTCTTGAGGATC
2201	CAACCAAGCTCTCTTGAGGATCT
2202	AACCAAGCTCTCTTGAGGATCTT
2203	ACCAAGCTCTCTTGAGGATCTTG
2204	CCAAGCTCTCTTGAGGATCTTGA

Fig. 28 cont'd (Sheet 38 of 93)

ID	SEQUENCE
2205	CAAGCTCTCTTGAGGATCTTGAA
2206	AAGCTCTCTTGAGGATCTTGAAG
2207	AGCTCTCTTGAGGATCTTGAAGG
2208	GCTCTCTTGAGGATCTTGAAGGA
2209	CTCTCTTGAGGATCTTGAAGGAA
2210	TCTCTTGAGGATCTTGAAGGAAA
2211	CTCTTGAGGATCTTGAAGGAAAC
2212	TCTTGAGGATCTTGAAGGAAACT
2213	CTTGAGGATCTTGAAGGAAACTG
2214	TTGAGGATCTTGAAGGAAACTGA
2215	TGAGGATCTTGAAGGAAACTGAA
2216	GAGGATCTTGAAGGAAACTGAAT
2217	AGGATCTTGAAGGAAACTGAATT
2218	GGATCTTGAAGGAAACTGAATTC
2219	GATCTTGAAGGAAACTGAATTCA
2220	ATCTTGAAGGAAACTGAATTCAA
2221	TCTTGAAGGAAACTGAATTCAAA
2222	CTTGAAGGAAACTGAATTCAAAA
2223	TTGAAGGAAACTGAATTCAAAAA
2224	TGAAGGAAACTGAATTCAAAAAG
2225	GAAGGAAACTGAATTCAAAAAGA
2226	AAGGAAACTGAATTCAAAAAGAT
2227	AGGAAACTGAATTCAAAAAGATC
2228	GGAAACTGAATTCAAAAAGATCA
2229	GAAACTGAATTCAAAAAGATCAA
2230	AAACTGAATTCAAAAAGATCAAA
2231	AACTGAATTCAAAAAGATCAAAG
2232	ACTGAATTCAAAAAGATCAAAGT
2233	CTGAATTCAAAAAGATCAAAGTG
2234	TGAATTCAAAAAGATCAAAGTGC
2235	GAATTCAAAAAGATCAAAGTGCT
2236	AATTCAAAAAGATCAAAGTGCTG
2237	ATTCAAAAAGATCAAAGTGCTGG
2238	TTCAAAAAGATCAAAGTGCTGGG
2239	TCAAAAAGATCAAAGTGCTGGGC
2240	CAAAAAGATCAAAGTGCTGGGCT
2241	AAAAAGATCAAAGTGCTGGGCTC
2242	AAAAGATCAAAGTGCTGGGCTCC
2243	AAAGATCAAAGTGCTGGGCTCCG
2244	AAGATCAAAGTGCTGGGCTCCGG
2245	AGATCAAAGTGCTGGGCTCCGGT
2246	GATCAAAGTGCTGGGCTCCGGTG
2247	ATCAAAGTGCTGGGCTCCGGTGC
2248	TCAAAGTGCTGGGCTCCGGTGCG
2249	CAAAGTGCTGGGCTCCGGTGCGT
2250	AAAGTGCTGGGCTCCGGTGCGTT
2251	AAGTGCTGGGCTCCGGTGCGTTC
2252	AGTGCTGGGCTCCGGTGCGTTCG
2253	GTGCTGGGCTCCGGTGCGTTCGG
2254	TGCTGGGCTCCGGTGCGTTCGGC
2255	GCTGGGCTCCGGTGCGTTCGGCA
2256	CTGGGCTCCGGTGCGTTCGGCAC
2257	TGGGCTCCGGTGCGTTCGGCACG
2258	GGGCTCCGGTGCGTTCGGCACGG
2259	GGCTCCGGTGCGTTCGGCACGGT
2260	GCTCCGGTGCGTTCGGCACGGTG
2261	CTCCGGTGCGTTCGGCACGGTGT
2262	TCCGGTGCGTTCGGCACGGTGTA

Fig. 28 cont'd (Sheet 39 of 93)

ID	SEQUENCE
2263	CCGGTGCGTTCGGCACGGTGTAT
2264	CGGTGCGTTCGGCACGGTGTATA
2265	GGTGCGTTCGGCACGGTGTATAA
2266	GTGCGTTCGGCACGGTGTATAAG
2267	TGCGTTCGGCACGGTGTATAAGG
2268	GCGTTCGGCACGGTGTATAAGGG
2269	CGTTCGGCACGGTGTATAAGGGA
2270	GTTCGGCACGGTGTATAAGGGAC
2271	TTCGGCACGGTGTATAAGGGACT
2272	TCGGCACGGTGTATAAGGGACTC
2273	CGGCACGGTGTATAAGGGACTCT
2274	GGCACGGTGTATAAGGGACTCTG
2275	GCACGGTGTATAAGGGACTCTGG
2276	CACGGTGTATAAGGGACTCTGGA
2277	ACGGTGTATAAGGGACTCTGGAT
2278	CGGTGTATAAGGGACTCTGGATC
2279	GGTGTATAAGGGACTCTGGATCC
2280	GTGTATAAGGGACTCTGGATCCC
2281	TGTATAAGGGACTCTGGATCCCA
2282	GTATAAGGGACTCTGGATCCCAG
2283	TATAAGGGACTCTGGATCCCAGA
2284	ATAAGGGACTCTGGATCCCAGAA
2285	TAAGGGACTCTGGATCCCAGAAG
2286	AAGGGACTCTGGATCCCAGAAGG
2287	AGGGACTCTGGATCCCAGAAGGT
2288	GGGACTCTGGATCCCAGAAGGTG
2289	GGACTCTGGATCCCAGAAGGTGA
2290	GACTCTGGATCCCAGAAGGTGAG
2291	ACTCTGGATCCCAGAAGGTGAGA
2292	CTCTGGATCCCAGAAGGTGAGAA
2293	TCTGGATCCCAGAAGGTGAGAAA
2294	CTGGATCCCAGAAGGTGAGAAAG
2295	TGGATCCCAGAAGGTGAGAAAGT
2296	GGATCCCAGAAGGTGAGAAAGTT
2297	GATCCCAGAAGGTGAGAAAGTTA
2298	ATCCCAGAAGGTGAGAAAGTTAA
2299	TCCCAGAAGGTGAGAAAGTTAAA
2300	CCCAGAAGGTGAGAAAGTTAAAA
2301	CCAGAAGGTGAGAAAGTTAAAAT
2302	CAGAAGGTGAGAAAGTTAAAATT
2303	AGAAGGTGAGAAAGTTAAAATTC
2304	GAAGGTGAGAAAGTTAAAATTCC
2305	AAGGTGAGAAAGTTAAAATTCCC
2306	AGGTGAGAAAGTTAAAATTCCCG
2307	GGTGAGAAAGTTAAAATTCCCGT
2308	GTGAGAAAGTTAAAATTCCCGTC
2309	TGAGAAAGTTAAAATTCCCGTCG
2310	GAGAAAGTTAAAATTCCCGTCGC
2311	AGAAAGTTAAAATTCCCGTCGCT
2312	GAAAGTTAAAATTCCCGTCGCTA
2313	AAAGTTAAAATTCCCGTCGCTAT
2314	AAGTTAAAATTCCCGTCGCTATC
2315	AGTTAAAATTCCCGTCGCTATCA
2316	GTTAAAATTCCCGTCGCTATCAA
2317	TTAAAATTCCCGTCGCTATCAAG
2318	TAAAATTCCCGTCGCTATCAAGG
2319	AAAATTCCCGTCGCTATCAAGGA
2320	AAATTCCCGTCGCTATCAAGGAA

Fig. 28 cont'd (Sheet 40 of 93)

ID	SEQUENCE
2321	AATTCCCGTCGCTATCAAGGAAT
2322	ATTCCCGTCGCTATCAAGGAATT
2323	TTCCCGTCGCTATCAAGGAATTA
2324	TCCCGTCGCTATCAAGGAATTAA
2325	CCCGTCGCTATCAAGGAATTAAG
2326	CCGTCGCTATCAAGGAATTAAGA
2327	CGTCGCTATCAAGGAATTAAGAG
2328	GTCGCTATCAAGGAATTAAGAGA
2329	TCGCTATCAAGGAATTAAGAGAA
2330	CGCTATCAAGGAATTAAGAGAAG
2331	GCTATCAAGGAATTAAGAGAAGC
2332	CTATCAAGGAATTAAGAGAAGCA
2333	TATCAAGGAATTAAGAGAAGCAA
2334	ATCAAGGAATTAAGAGAAGCAAC
2335	TCAAGGAATTAAGAGAAGCAACA
2336	CAAGGAATTAAGAGAAGCAACAT
2337	AAGGAATTAAGAGAAGCAACATC
2338	AGGAATTAAGAGAAGCAACATCT
2339	GGAATTAAGAGAAGCAACATCTC
2340	GAATTAAGAGAAGCAACATCTCC
2341	AATTAAGAGAAGCAACATCTCCG
2342	ATTAAGAGAAGCAACATCTCCGA
2343	TTAAGAGAAGCAACATCTCCGAA
2344	TAAGAGAAGCAACATCTCCGAAA
2345	AAGAGAAGCAACATCTCCGAAAG
2346	AGAGAAGCAACATCTCCGAAAGC
2347	GAGAAGCAACATCTCCGAAAGCC
2348	AGAAGCAACATCTCCGAAAGCCA
2349	GAAGCAACATCTCCGAAAGCCAA
2350	AAGCAACATCTCCGAAAGCCAAC
2351	AGCAACATCTCCGAAAGCCAACA
2352	GCAACATCTCCGAAAGCCAACAA
2353	CAACATCTCCGAAAGCCAACAAG
2354	AACATCTCCGAAAGCCAACAAGG
2355	ACATCTCCGAAAGCCAACAAGGA
2356	CATCTCCGAAAGCCAACAAGGAA
2357	ATCTCCGAAAGCCAACAAGGAAA
2358	TCTCCGAAAGCCAACAAGGAAAT
2359	CTCCGAAAGCCAACAAGGAAATC
2360	TCCGAAAGCCAACAAGGAAATCC
2361	CCGAAAGCCAACAAGGAAATCCT
2362	CGAAAGCCAACAAGGAAATCCTC
2363	GAAAGCCAACAAGGAAATCCTCG
2364	AAAGCCAACAAGGAAATCCTCGA
2365	AAGCCAACAAGGAAATCCTCGAT
2366	AGCCAACAAGGAAATCCTCGATG
2367	GCCAACAAGGAAATCCTCGATGA
2368	CCAACAAGGAAATCCTCGATGAA
2369	CAACAAGGAAATCCTCGATGAAG
2370	AACAAGGAAATCCTCGATGAAGC
2371	ACAAGGAAATCCTCGATGAAGCC
2372	CAAGGAAATCCTCGATGAAGCCT
2373	AAGGAAATCCTCGATGAAGCCTA
2374	AGGAAATCCTCGATGAAGCCTAC
2375	GGAAATCCTCGATGAAGCCTACG
2376	GAAATCCTCGATGAAGCCTACGT
2377	AAATCCTCGATGAAGCCTACGTG
2378	AATCCTCGATGAAGCCTACGTGA

Fig. 28 cont'd (Sheet 41 of 93)

ID	SEQUENCE
2379	ATCCTCGATGAAGCCTACGTGAT
2380	TCCTCGATGAAGCCTACGTGATG
2381	CCTCGATGAAGCCTACGTGATGG
2382	CTCGATGAAGCCTACGTGATGGC
2383	TCGATGAAGCCTACGTGATGGCC
2384	CGATGAAGCCTACGTGATGGCCA
2385	GATGAAGCCTACGTGATGGCCAG
2386	ATGAAGCCTACGTGATGGCCAGC
2387	TGAAGCCTACGTGATGGCCAGCG
2388	GAAGCCTACGTGATGGCCAGCGT
2389	AAGCCTACGTGATGGCCAGCGTG
2390	AGCCTACGTGATGGCCAGCGTGG
2391	GCCTACGTGATGGCCAGCGTGGA
2392	CCTACGTGATGGCCAGCGTGGAC
2393	CTACGTGATGGCCAGCGTGGACA
2394	TACGTGATGGCCAGCGTGGACAA
2395	ACGTGATGGCCAGCGTGGACAAC
2396	CGTGATGGCCAGCGTGGACAACC
2397	GTGATGGCCAGCGTGGACAACCC
2398	TGATGGCCAGCGTGGACAACCCC
2399	GATGGCCAGCGTGGACAACCCCC
2400	ATGGCCAGCGTGGACAACCCCCA
2401	TGGCCAGCGTGGACAACCCCCAC
2402	GGCCAGCGTGGACAACCCCCACG
2403	GCCAGCGTGGACAACCCCCACGT
2404	CCAGCGTGGACAACCCCCACGTG
2405	CAGCGTGGACAACCCCCACGTGT
2406	AGCGTGGACAACCCCCACGTGTG
2407	GCGTGGACAACCCCCACGTGTGC
2408	CGTGGACAACCCCCACGTGTGCC
2409	GTGGACAACCCCCACGTGTGCCG
2410	TGGACAACCCCCACGTGTGCCGC
2411	GGACAACCCCCACGTGTGCCGCC
2412	GACAACCCCCACGTGTGCCGCCT
2413	ACAACCCCCACGTGTGCCGCCTG
2414	CAACCCCCACGTGTGCCGCCTGC
2415	AACCCCCACGTGTGCCGCCTGCT
2416	ACCCCCACGTGTGCCGCCTGCTG
2417	CCCCCACGTGTGCCGCCTGCTGG
2418	CCCCACGTGTGCCGCCTGCTGGG
2419	CCCACGTGTGCCGCCTGCTGGGC
2420	CCACGTGTGCCGCCTGCTGGGCA
2421	CACGTGTGCCGCCTGCTGGGCAT
2422	ACGTGTGCCGCCTGCTGGGCATC
2423	CGTGTGCCGCCTGCTGGGCATCT
2424	GTGTGCCGCCTGCTGGGCATCTG
2425	TGTGCCGCCTGCTGGGCATCTGC
2426	GTGCCGCCTGCTGGGCATCTGCC
2427	TGCCGCCTGCTGGGCATCTGCCT
2428	GCCGCCTGCTGGGCATCTGCCTC
2429	CCGCCTGCTGGGCATCTGCCTCA
2430	CGCCTGCTGGGCATCTGCCTCAC
2431	GCCTGCTGGGCATCTGCCTCACC
2432	CCTGCTGGGCATCTGCCTCACCT
2433	CTGCTGGGCATCTGCCTCACCTC
2434	TGCTGGGCATCTGCCTCACCTCC
2435	GCTGGGCATCTGCCTCACCTCCA
2436	CTGGGCATCTGCCTCACCTCCAC

Fig. 28 cont'd (Sheet 42 of 93)

ID	SEQUENCE
2437	TGGGCATCTGCCTCACCTCCACC
2438	GGGCATCTGCCTCACCTCCACCG
2439	GGCATCTGCCTCACCTCCACCGT
2440	GCATCTGCCTCACCTCCACCGTG
2441	CATCTGCCTCACCTCCACCGTGC
2442	ATCTGCCTCACCTCCACCGTGCA
2443	TCTGCCTCACCTCCACCGTGCAG
2444	CTGCCTCACCTCCACCGTGCAGC
2445	TGCCTCACCTCCACCGTGCAGCT
2446	GCCTCACCTCCACCGTGCAGCTC
2447	CCTCACCTCCACCGTGCAGCTCA
2448	CTCACCTCCACCGTGCAGCTCAT
2449	TCACCTCCACCGTGCAGCTCATC
2450	CACCTCCACCGTGCAGCTCATCA
2451	ACCTCCACCGTGCAGCTCATCAC
2452	CCTCCACCGTGCAGCTCATCACG
2453	CTCCACCGTGCAGCTCATCACGC
2454	TCCACCGTGCAGCTCATCACGCA
2455	CCACCGTGCAGCTCATCACGCAG
2456	CACCGTGCAGCTCATCACGCAGC
2457	ACCGTGCAGCTCATCACGCAGCT
2458	CCGTGCAGCTCATCACGCAGCTC
2459	CGTGCAGCTCATCACGCAGCTCA
2460	GTGCAGCTCATCACGCAGCTCAT
2461	TGCAGCTCATCACGCAGCTCATG
2462	GCAGCTCATCACGCAGCTCATGC
2463	CAGCTCATCACGCAGCTCATGCC
2464	AGCTCATCACGCAGCTCATGCCC
2465	GCTCATCACGCAGCTCATGCCCT
2466	CTCATCACGCAGCTCATGCCCTT
2467	TCATCACGCAGCTCATGCCCTTC
2468	CATCACGCAGCTCATGCCCTTCG
2469	ATCACGCAGCTCATGCCCTTCGG
2470	TCACGCAGCTCATGCCCTTCGGC
2471	CACGCAGCTCATGCCCTTCGGCT
2472	ACGCAGCTCATGCCCTTCGGCTG
2473	CGCAGCTCATGCCCTTCGGCTGC
2474	GCAGCTCATGCCCTTCGGCTGCC
2475	CAGCTCATGCCCTTCGGCTGCCT
2476	AGCTCATGCCCTTCGGCTGCCTC
2477	GCTCATGCCCTTCGGCTGCCTCC
2478	CTCATGCCCTTCGGCTGCCTCCT
2479	TCATGCCCTTCGGCTGCCTCCTG
2480	CATGCCCTTCGGCTGCCTCCTGG
2481	ATGCCCTTCGGCTGCCTCCTGGA
2482	TGCCCTTCGGCTGCCTCCTGGAC
2483	GCCCTTCGGCTGCCTCCTGGACT
2484	CCCTTCGGCTGCCTCCTGGACTA
2485	CCTTCGGCTGCCTCCTGGACTAT
2486	CTTCGGCTGCCTCCTGGACTATG
2487	TTCGGCTGCCTCCTGGACTATGT
2488	TCGGCTGCCTCCTGGACTATGTC
2489	CGGCTGCCTCCTGGACTATGTCC
2490	GGCTGCCTCCTGGACTATGTCCG
2491	GCTGCCTCCTGGACTATGTCCGG
2492	CTGCCTCCTGGACTATGTCCGGG
2493	TGCCTCCTGGACTATGTCCGGGA
2494	GCCTCCTGGACTATGTCCGGGAA

Fig. 28 cont'd (Sheet 43 of 93)

ID	SEQUENCE
2495	CCTCCTGGACTATGTCCGGGAAC
2496	CTCCTGGACTATGTCCGGGAACA
2497	TCCTGGACTATGTCCGGGAACAC
2498	CCTGGACTATGTCCGGGAACACA
2499	CTGGACTATGTCCGGGAACACAA
2500	TGGACTATGTCCGGGAACACAAA
2501	GGACTATGTCCGGGAACACAAAG
2502	GACTATGTCCGGGAACACAAAGA
2503	ACTATGTCCGGGAACACAAAGAC
2504	CTATGTCCGGGAACACAAAGACA
2505	TATGTCCGGGAACACAAAGACAA
2506	ATGTCCGGGAACACAAAGACAAT
2507	TGTCCGGGAACACAAAGACAATA
2508	GTCCGGGAACACAAAGACAATAT
2509	TCCGGGAACACAAAGACAATATT
2510	CCGGGAACACAAAGACAATATTG
2511	CGGGAACACAAAGACAATATTGG
2512	GGGAACACAAAGACAATATTGGC
2513	GGAACACAAAGACAATATTGGCT
2514	GAACACAAAGACAATATTGGCTC
2515	AACACAAAGACAATATTGGCTCC
2516	ACACAAAGACAATATTGGCTCCC
2517	CACAAAGACAATATTGGCTCCCA
2518	ACAAAGACAATATTGGCTCCCAG
2519	CAAAGACAATATTGGCTCCCAGT
2520	AAAGACAATATTGGCTCCCAGTA
2521	AAGACAATATTGGCTCCCAGTAC
2522	AGACAATATTGGCTCCCAGTACC
2523	GACAATATTGGCTCCCAGTACCT
2524	ACAATATTGGCTCCCAGTACCTG
2525	CAATATTGGCTCCCAGTACCTGC
2526	AATATTGGCTCCCAGTACCTGCT
2527	ATATTGGCTCCCAGTACCTGCTC
2528	TATTGGCTCCCAGTACCTGCTCA
2529	ATTGGCTCCCAGTACCTGCTCAA
2530	TTGGCTCCCAGTACCTGCTCAAC
2531	TGGCTCCCAGTACCTGCTCAACT
2532	GGCTCCCAGTACCTGCTCAACTG
2533	GCTCCCAGTACCTGCTCAACTGG
2534	CTCCCAGTACCTGCTCAACTGGT
2535	TCCCAGTACCTGCTCAACTGGTG
2536	CCCAGTACCTGCTCAACTGGTGT
2537	CCAGTACCTGCTCAACTGGTGTG
2538	CAGTACCTGCTCAACTGGTGTGT
2539	AGTACCTGCTCAACTGGTGTGTG
2540	GTACCTGCTCAACTGGTGTGTGC
2541	TACCTGCTCAACTGGTGTGTGCA
2542	ACCTGCTCAACTGGTGTGTGCAG
2543	CCTGCTCAACTGGTGTGTGCAGA
2544	CTGCTCAACTGGTGTGTGCAGAT
2545	TGCTCAACTGGTGTGTGCAGATC
2546	GCTCAACTGGTGTGTGCAGATCG
2547	CTCAACTGGTGTGTGCAGATCGC
2548	TCAACTGGTGTGTGCAGATCGCA
2549	CAACTGGTGTGTGCAGATCGCAA
2550	AACTGGTGTGTGCAGATCGCAAA
2551	ACTGGTGTGTGCAGATCGCAAAG
2552	CTGGTGTGTGCAGATCGCAAAGG

Fig. 28 cont'd (Sheet 44 of 93)

ID	SEQUENCE
2553	TGGTGTGTGCAGATCGCAAAGGG
2554	GGTGTGTGCAGATCGCAAAGGGC
2555	GTGTGTGCAGATCGCAAAGGGCA
2556	TGTGTGCAGATCGCAAAGGGCAT
2557	GTGTGCAGATCGCAAAGGGCATG
2558	TGTGCAGATCGCAAAGGGCATGA
2559	GTGCAGATCGCAAAGGGCATGAA
2560	TGCAGATCGCAAAGGGCATGAAC
2561	GCAGATCGCAAAGGGCATGAACT
2562	CAGATCGCAAAGGGCATGAACTA
2563	AGATCGCAAAGGGCATGAACTAC
2564	GATCGCAAAGGGCATGAACTACT
2565	ATCGCAAAGGGCATGAACTACTT
2566	TCGCAAAGGGCATGAACTACTTG
2567	CGCAAAGGGCATGAACTACTTGG
2568	GCAAAGGGCATGAACTACTTGGA
2569	CAAAGGGCATGAACTACTTGGAG
2570	AAAGGGCATGAACTACTTGGAGG
2571	AAGGGCATGAACTACTTGGAGGA
2572	AGGGCATGAACTACTTGGAGGAC
2573	GGGCATGAACTACTTGGAGGACC
2574	GGCATGAACTACTTGGAGGACCG
2575	GCATGAACTACTTGGAGGACCGT
2576	CATGAACTACTTGGAGGACCGTC
2577	ATGAACTACTTGGAGGACCGTCG
2578	TGAACTACTTGGAGGACCGTCGC
2579	GAACTACTTGGAGGACCGTCGCT
2580	AACTACTTGGAGGACCGTCGCTT
2581	ACTACTTGGAGGACCGTCGCTTG
2582	CTACTTGGAGGACCGTCGCTTGG
2583	TACTTGGAGGACCGTCGCTTGGT
2584	ACTTGGAGGACCGTCGCTTGGTG
2585	CTTGGAGGACCGTCGCTTGGTGC
2586	TTGGAGGACCGTCGCTTGGTGCA
2587	TGGAGGACCGTCGCTTGGTGCAC
2588	GGAGGACCGTCGCTTGGTGCACC
2589	GAGGACCGTCGCTTGGTGCACCG
2590	AGGACCGTCGCTTGGTGCACCGC
2591	GGACCGTCGCTTGGTGCACCGCG
2592	GACCGTCGCTTGGTGCACCGCGA
2593	ACCGTCGCTTGGTGCACCGCGAC
2594	CCGTCGCTTGGTGCACCGCGACC
2595	CGTCGCTTGGTGCACCGCGACCT
2596	GTCGCTTGGTGCACCGCGACCTG
2597	TCGCTTGGTGCACCGCGACCTGG
2598	CGCTTGGTGCACCGCGACCTGGC
2599	GCTTGGTGCACCGCGACCTGGCA
2600	CTTGGTGCACCGCGACCTGGCAG
2601	TTGGTGCACCGCGACCTGGCAGC
2602	TGGTGCACCGCGACCTGGCAGCC
2603	GGTGCACCGCGACCTGGCAGCCA
2604	GTGCACCGCGACCTGGCAGCCAG
2605	TGCACCGCGACCTGGCAGCCAGG
2606	GCACCGCGACCTGGCAGCCAGGA
2607	CACCGCGACCTGGCAGCCAGGAA
2608	ACCGCGACCTGGCAGCCAGGAAC
2609	CCGCGACCTGGCAGCCAGGAACG
2610	CGCGACCTGGCAGCCAGGAACGT

Fig. 28 cont'd (Sheet 45 of 93)

ID	SEQUENCE
2611	GCGACCTGGCAGCCAGGAACGTA
2612	CGACCTGGCAGCCAGGAACGTAC
2613	GACCTGGCAGCCAGGAACGTACT
2614	ACCTGGCAGCCAGGAACGTACTG
2615	CCTGGCAGCCAGGAACGTACTGG
2616	CTGGCAGCCAGGAACGTACTGGT
2617	TGGCAGCCAGGAACGTACTGGTG
2618	GGCAGCCAGGAACGTACTGGTGA
2619	GCAGCCAGGAACGTACTGGTGAA
2620	CAGCCAGGAACGTACTGGTGAAA
2621	AGCCAGGAACGTACTGGTGAAAA
2622	GCCAGGAACGTACTGGTGAAAAC
2623	CCAGGAACGTACTGGTGAAAACA
2624	CAGGAACGTACTGGTGAAAACAC
2625	AGGAACGTACTGGTGAAAACACC
2626	GGAACGTACTGGTGAAAACACCG
2627	GAACGTACTGGTGAAAACACCGC
2628	AACGTACTGGTGAAAACACCGCA
2629	ACGTACTGGTGAAAACACCGCAG
2630	CGTACTGGTGAAAACACCGCAGC
2631	GTACTGGTGAAAACACCGCAGCA
2632	TACTGGTGAAAACACCGCAGCAT
2633	ACTGGTGAAAACACCGCAGCATG
2634	CTGGTGAAAACACCGCAGCATGT
2635	TGGTGAAAACACCGCAGCATGTC
2636	GGTGAAAACACCGCAGCATGTCA
2637	GTGAAAACACCGCAGCATGTCAA
2638	TGAAAACACCGCAGCATGTCAAG
2639	GAAAACACCGCAGCATGTCAAGA
2640	AAAACACCGCAGCATGTCAAGAT
2641	AAACACCGCAGCATGTCAAGATC
2642	AACACCGCAGCATGTCAAGATCA
2643	ACACCGCAGCATGTCAAGATCAC
2644	CACCGCAGCATGTCAAGATCACA
2645	ACCGCAGCATGTCAAGATCACAG
2646	CCGCAGCATGTCAAGATCACAGA
2647	CGCAGCATGTCAAGATCACAGAT
2648	GCAGCATGTCAAGATCACAGATT
2649	CAGCATGTCAAGATCACAGATTT
2650	AGCATGTCAAGATCACAGATTTT
2651	GCATGTCAAGATCACAGATTTTG
2652	CATGTCAAGATCACAGATTTTGG
2653	ATGTCAAGATCACAGATTTTGGG
2654	TGTCAAGATCACAGATTTTGGGC
2655	GTCAAGATCACAGATTTTGGGCT
2656	TCAAGATCACAGATTTTGGGCTG
2657	CAAGATCACAGATTTTGGGCTGG
2658	AAGATCACAGATTTTGGGCTGGC
2659	AGATCACAGATTTTGGGCTGGCC
2660	GATCACAGATTTTGGGCTGGCCA
2661	ATCACAGATTTTGGGCTGGCCAA
2662	TCACAGATTTTGGGCTGGCCAAA
2663	CACAGATTTTGGGCTGGCCAAAC
2664	ACAGATTTTGGGCTGGCCAAACT
2665	CAGATTTTGGGCTGGCCAAACTG
2666	AGATTTTGGGCTGGCCAAACTGC
2667	GATTTTGGGCTGGCCAAACTGCT
2668	ATTTTGGGCTGGCCAAACTGCTG

Fig. 28 cont'd (Sheet 46 of 93)

ID	SEQUENCE
2669	TTTTGGGCTGGCCAAACTGCTGG
2670	TTTGGGCTGGCCAAACTGCTGGG
2671	TTGGGCTGGCCAAACTGCTGGGT
2672	TGGGCTGGCCAAACTGCTGGGTG
2673	GGGCTGGCCAAACTGCTGGGTGC
2674	GGCTGGCCAAACTGCTGGGTGCG
2675	GCTGGCCAAACTGCTGGGTGCGG
2676	CTGGCCAAACTGCTGGGTGCGGA
2677	TGGCCAAACTGCTGGGTGCGGAA
2678	GGCCAAACTGCTGGGTGCGGAAG
2679	GCCAAACTGCTGGGTGCGGAAGA
2680	CCAAACTGCTGGGTGCGGAAGAG
2681	CAAACTGCTGGGTGCGGAAGAGA
2682	AAACTGCTGGGTGCGGAAGAGAA
2683	AACTGCTGGGTGCGGAAGAGAAA
2684	ACTGCTGGGTGCGGAAGAGAAAG
2685	CTGCTGGGTGCGGAAGAGAAAGA
2686	TGCTGGGTGCGGAAGAGAAAGAA
2687	GCTGGGTGCGGAAGAGAAAGAAT
2688	CTGGGTGCGGAAGAGAAAGAATA
2689	TGGGTGCGGAAGAGAAAGAATAC
2690	GGGTGCGGAAGAGAAAGAATACC
2691	GGTGCGGAAGAGAAAGAATACCA
2692	GTGCGGAAGAGAAAGAATACCAT
2693	TGCGGAAGAGAAAGAATACCATG
2694	GCGGAAGAGAAAGAATACCATGC
2695	CGGAAGAGAAAGAATACCATGCA
2696	GGAAGAGAAAGAATACCATGCAG
2697	GAAGAGAAAGAATACCATGCAGA
2698	AAGAGAAAGAATACCATGCAGAA
2699	AGAGAAAGAATACCATGCAGAAG
2700	GAGAAAGAATACCATGCAGAAGG
2701	AGAAAGAATACCATGCAGAAGGA
2702	GAAAGAATACCATGCAGAAGGAG
2703	AAAGAATACCATGCAGAAGGAGG
2704	AAGAATACCATGCAGAAGGAGGC
2705	AGAATACCATGCAGAAGGAGGCA
2706	GAATACCATGCAGAAGGAGGCAA
2707	AATACCATGCAGAAGGAGGCAAA
2708	ATACCATGCAGAAGGAGGCAAAG
2709	TACCATGCAGAAGGAGGCAAAGT
2710	ACCATGCAGAAGGAGGCAAAGTG
2711	CCATGCAGAAGGAGGCAAAGTGC
2712	CATGCAGAAGGAGGCAAAGTGCC
2713	ATGCAGAAGGAGGCAAAGTGCCT
2714	TGCAGAAGGAGGCAAAGTGCCTA
2715	GCAGAAGGAGGCAAAGTGCCTAT
2716	CAGAAGGAGGCAAAGTGCCTATC
2717	AGAAGGAGGCAAAGTGCCTATCA
2718	GAAGGAGGCAAAGTGCCTATCAA
2719	AAGGAGGCAAAGTGCCTATCAAG
2720	AGGAGGCAAAGTGCCTATCAAGT
2721	GGAGGCAAAGTGCCTATCAAGTG
2722	GAGGCAAAGTGCCTATCAAGTGG
2723	AGGCAAAGTGCCTATCAAGTGGA
2724	GGCAAAGTGCCTATCAAGTGGAT
2725	GCAAAGTGCCTATCAAGTGGATG
2726	CAAAGTGCCTATCAAGTGGATGG

Fig. 28 cont'd (Sheet 47 of 93)

ID	SEQUENCE
2727	AAAGTGCCTATCAAGTGGATGGC
2728	AAGTGCCTATCAAGTGGATGGCA
2729	AGTGCCTATCAAGTGGATGGCAT
2730	GTGCCTATCAAGTGGATGGCATT
2731	TGCCTATCAAGTGGATGGCATTG
2732	GCCTATCAAGTGGATGGCATTGG
2733	CCTATCAAGTGGATGGCATTGGA
2734	CTATCAAGTGGATGGCATTGGAA
2735	TATCAAGTGGATGGCATTGGAAT
2736	ATCAAGTGGATGGCATTGGAATC
2737	TCAAGTGGATGGCATTGGAATCA
2738	CAAGTGGATGGCATTGGAATCAA
2739	AAGTGGATGGCATTGGAATCAAT
2740	AGTGGATGGCATTGGAATCAATT
2741	GTGGATGGCATTGGAATCAATTT
2742	TGGATGGCATTGGAATCAATTTT
2743	GGATGGCATTGGAATCAATTTTA
2744	GATGGCATTGGAATCAATTTTAC
2745	ATGGCATTGGAATCAATTTTACA
2746	TGGCATTGGAATCAATTTTACAC
2747	GGCATTGGAATCAATTTTACACA
2748	GCATTGGAATCAATTTTACACAG
2749	CATTGGAATCAATTTTACACAGA
2750	ATTGGAATCAATTTTACACAGAA
2751	TTGGAATCAATTTTACACAGAAT
2752	TGGAATCAATTTTACACAGAATC
2753	GGAATCAATTTTACACAGAATCT
2754	GAATCAATTTTACACAGAATCTA
2755	AATCAATTTTACACAGAATCTAT
2756	ATCAATTTTACACAGAATCTATA
2757	TCAATTTTACACAGAATCTATAC
2758	CAATTTTACACAGAATCTATACC
2759	AATTTTACACAGAATCTATACCC
2760	ATTTTACACAGAATCTATACCCA
2761	TTTTACACAGAATCTATACCCAC
2762	TTTACACAGAATCTATACCCACC
2763	TTACACAGAATCTATACCCACCA
2764	TACACAGAATCTATACCCACCAG
2765	ACACAGAATCTATACCCACCAGA
2766	CACAGAATCTATACCCACCAGAG
2767	ACAGAATCTATACCCACCAGAGT
2768	CAGAATCTATACCCACCAGAGTG
2769	AGAATCTATACCCACCAGAGTGA
2770	GAATCTATACCCACCAGAGTGAT
2771	AATCTATACCCACCAGAGTGATG
2772	ATCTATACCCACCAGAGTGATGT
2773	TCTATACCCACCAGAGTGATGTC
2774	CTATACCCACCAGAGTGATGTCT
2775	TATACCCACCAGAGTGATGTCTG
2776	ATACCCACCAGAGTGATGTCTGG
2777	TACCCACCAGAGTGATGTCTGGA
2778	ACCCACCAGAGTGATGTCTGGAG
2779	CCCACCAGAGTGATGTCTGGAGC
2780	CCACCAGAGTGATGTCTGGAGCT
2781	CACCAGAGTGATGTCTGGAGCTA
2782	ACCAGAGTGATGTCTGGAGCTAC
2783	CCAGAGTGATGTCTGGAGCTACG
2784	CAGAGTGATGTCTGGAGCTACGG

Fig. 28 cont'd (Sheet 48 of 93)

ID	SEQUENCE
2785	AGAGTGATGTCTGGAGCTACGGG
2786	GAGTGATGTCTGGAGCTACGGGG
2787	AGTGATGTCTGGAGCTACGGGGT
2788	GTGATGTCTGGAGCTACGGGGTG
2789	TGATGTCTGGAGCTACGGGGTGA
2790	GATGTCTGGAGCTACGGGGTGAC
2791	ATGTCTGGAGCTACGGGGTGACC
2792	TGTCTGGAGCTACGGGGTGACCG
2793	GTCTGGAGCTACGGGGTGACCGT
2794	TCTGGAGCTACGGGGTGACCGTT
2795	CTGGAGCTACGGGGTGACCGTTT
2796	TGGAGCTACGGGGTGACCGTTTG
2797	GGAGCTACGGGGTGACCGTTTGG
2798	GAGCTACGGGGTGACCGTTTGGG
2799	AGCTACGGGGTGACCGTTTGGGA
2800	GCTACGGGGTGACCGTTTGGGAG
2801	CTACGGGGTGACCGTTTGGGAGT
2802	TACGGGGTGACCGTTTGGGAGTT
2803	ACGGGGTGACCGTTTGGGAGTTG
2804	CGGGGTGACCGTTTGGGAGTTGA
2805	GGGGTGACCGTTTGGGAGTTGAT
2806	GGGTGACCGTTTGGGAGTTGATG
2807	GGTGACCGTTTGGGAGTTGATGA
2808	GTGACCGTTTGGGAGTTGATGAC
2809	TGACCGTTTGGGAGTTGATGACC
2810	GACCGTTTGGGAGTTGATGACCT
2811	ACCGTTTGGGAGTTGATGACCTT
2812	CCGTTTGGGAGTTGATGACCTTT
2813	CGTTTGGGAGTTGATGACCTTTG
2814	GTTTGGGAGTTGATGACCTTTGG
2815	TTTGGGAGTTGATGACCTTTGGA
2816	TTGGGAGTTGATGACCTTTGGAT
2817	TGGGAGTTGATGACCTTTGGATC
2818	GGGAGTTGATGACCTTTGGATCC
2819	GGAGTTGATGACCTTTGGATCCA
2820	GAGTTGATGACCTTTGGATCCAA
2821	AGTTGATGACCTTTGGATCCAAG
2822	GTTGATGACCTTTGGATCCAAGC
2823	TTGATGACCTTTGGATCCAAGCC
2824	TGATGACCTTTGGATCCAAGCCA
2825	GATGACCTTTGGATCCAAGCCAT
2826	ATGACCTTTGGATCCAAGCCATA
2827	TGACCTTTGGATCCAAGCCATAT
2828	GACCTTTGGATCCAAGCCATATG
2829	ACCTTTGGATCCAAGCCATATGA
2830	CCTTTGGATCCAAGCCATATGAC
2831	CTTTGGATCCAAGCCATATGACG
2832	TTTGGATCCAAGCCATATGACGG
2833	TTGGATCCAAGCCATATGACGGA
2834	TGGATCCAAGCCATATGACGGAA
2835	GGATCCAAGCCATATGACGGAAT
2836	GATCCAAGCCATATGACGGAATC
2837	ATCCAAGCCATATGACGGAATCC
2838	TCCAAGCCATATGACGGAATCCC
2839	CCAAGCCATATGACGGAATCCCT
2840	CAAGCCATATGACGGAATCCCTG
2841	AAGCCATATGACGGAATCCCTGC
2842	AGCCATATGACGGAATCCCTGCC

Fig. 28 cont'd (Sheet 49 of 93)

ID	SEQUENCE
2843	GCCATATGACGGAATCCCTGCCA
2844	CCATATGACGGAATCCCTGCCAG
2845	CATATGACGGAATCCCTGCCAGC
2846	ATATGACGGAATCCCTGCCAGCG
2847	TATGACGGAATCCCTGCCAGCGA
2848	ATGACGGAATCCCTGCCAGCGAG
2849	TGACGGAATCCCTGCCAGCGAGA
2850	GACGGAATCCCTGCCAGCGAGAT
2851	ACGGAATCCCTGCCAGCGAGATC
2852	CGGAATCCCTGCCAGCGAGATCT
2853	GGAATCCCTGCCAGCGAGATCTC
2854	GAATCCCTGCCAGCGAGATCTCC
2855	AATCCCTGCCAGCGAGATCTCCT
2856	ATCCCTGCCAGCGAGATCTCCTC
2857	TCCCTGCCAGCGAGATCTCCTCC
2858	CCCTGCCAGCGAGATCTCCTCCA
2859	CCTGCCAGCGAGATCTCCTCCAT
2860	CTGCCAGCGAGATCTCCTCCATC
2861	TGCCAGCGAGATCTCCTCCATCC
2862	GCCAGCGAGATCTCCTCCATCCT
2863	CCAGCGAGATCTCCTCCATCCTG
2864	CAGCGAGATCTCCTCCATCCTGG
2865	AGCGAGATCTCCTCCATCCTGGA
2866	GCGAGATCTCCTCCATCCTGGAG
2867	CGAGATCTCCTCCATCCTGGAGA
2868	GAGATCTCCTCCATCCTGGAGAA
2869	AGATCTCCTCCATCCTGGAGAAA
2870	GATCTCCTCCATCCTGGAGAAAG
2871	ATCTCCTCCATCCTGGAGAAAGG
2872	TCTCCTCCATCCTGGAGAAAGGA
2873	CTCCTCCATCCTGGAGAAAGGAG
2874	TCCTCCATCCTGGAGAAAGGAGA
2875	CCTCCATCCTGGAGAAAGGAGAA
2876	CTCCATCCTGGAGAAAGGAGAAC
2877	TCCATCCTGGAGAAAGGAGAACG
2878	CCATCCTGGAGAAAGGAGAACGC
2879	CATCCTGGAGAAAGGAGAACGCC
2880	ATCCTGGAGAAAGGAGAACGCCT
2881	TCCTGGAGAAAGGAGAACGCCTC
2882	CCTGGAGAAAGGAGAACGCCTCC
2883	CTGGAGAAAGGAGAACGCCTCCC
2884	TGGAGAAAGGAGAACGCCTCCCT
2885	GGAGAAAGGAGAACGCCTCCCTC
2886	GAGAAAGGAGAACGCCTCCCTCA
2887	AGAAAGGAGAACGCCTCCCTCAG
2888	GAAAGGAGAACGCCTCCCTCAGC
2889	AAAGGAGAACGCCTCCCTCAGCC
2890	AAGGAGAACGCCTCCCTCAGCCA
2891	AGGAGAACGCCTCCCTCAGCCAC
2892	GGAGAACGCCTCCCTCAGCCACC
2893	GAGAACGCCTCCCTCAGCCACCC
2894	AGAACGCCTCCCTCAGCCACCCA
2895	GAACGCCTCCCTCAGCCACCCAT
2896	AACGCCTCCCTCAGCCACCCATA
2897	ACGCCTCCCTCAGCCACCCATAT
2898	CGCCTCCCTCAGCCACCCATATG
2899	GCCTCCCTCAGCCACCCATATGT
2900	CCTCCCTCAGCCACCCATATGTA

Fig. 28 cont'd (Sheet 50 of 93)

ID	SEQUENCE
2901	CTCCCTCAGCCACCCATATGTAC
2902	TCCCTCAGCCACCCATATGTACC
2903	CCCTCAGCCACCCATATGTACCA
2904	CCTCAGCCACCCATATGTACCAT
2905	CTCAGCCACCCATATGTACCATC
2906	TCAGCCACCCATATGTACCATCG
2907	CAGCCACCCATATGTACCATCGA
2908	AGCCACCCATATGTACCATCGAT
2909	GCCACCCATATGTACCATCGATG
2910	CCACCCATATGTACCATCGATGT
2911	CACCCATATGTACCATCGATGTC
2912	ACCCATATGTACCATCGATGTCT
2913	CCCATATGTACCATCGATGTCTA
2914	CCATATGTACCATCGATGTCTAC
2915	CATATGTACCATCGATGTCTACA
2916	ATATGTACCATCGATGTCTACAT
2917	TATGTACCATCGATGTCTACATG
2918	ATGTACCATCGATGTCTACATGA
2919	TGTACCATCGATGTCTACATGAT
2920	GTACCATCGATGTCTACATGATC
2921	TACCATCGATGTCTACATGATCA
2922	ACCATCGATGTCTACATGATCAT
2923	CCATCGATGTCTACATGATCATG
2924	CATCGATGTCTACATGATCATGG
2925	ATCGATGTCTACATGATCATGGT
2926	TCGATGTCTACATGATCATGGTC
2927	CGATGTCTACATGATCATGGTCA
2928	GATGTCTACATGATCATGGTCAA
2929	ATGTCTACATGATCATGGTCAAG
2930	TGTCTACATGATCATGGTCAAGT
2931	GTCTACATGATCATGGTCAAGTG
2932	TCTACATGATCATGGTCAAGTGC
2933	CTACATGATCATGGTCAAGTGCT
2934	TACATGATCATGGTCAAGTGCTG
2935	ACATGATCATGGTCAAGTGCTGG
2936	CATGATCATGGTCAAGTGCTGGA
2937	ATGATCATGGTCAAGTGCTGGAT
2938	TGATCATGGTCAAGTGCTGGATG
2939	GATCATGGTCAAGTGCTGGATGA
2940	ATCATGGTCAAGTGCTGGATGAT
2941	TCATGGTCAAGTGCTGGATGATA
2942	CATGGTCAAGTGCTGGATGATAG
2943	ATGGTCAAGTGCTGGATGATAGA
2944	TGGTCAAGTGCTGGATGATAGAC
2945	GGTCAAGTGCTGGATGATAGACG
2946	GTCAAGTGCTGGATGATAGACGC
2947	TCAAGTGCTGGATGATAGACGCA
2948	CAAGTGCTGGATGATAGACGCAG
2949	AAGTGCTGGATGATAGACGCAGA
2950	AGTGCTGGATGATAGACGCAGAT
2951	GTGCTGGATGATAGACGCAGATA
2952	TGCTGGATGATAGACGCAGATAG
2953	GCTGGATGATAGACGCAGATAGT
2954	CTGGATGATAGACGCAGATAGTC
2955	TGGATGATAGACGCAGATAGTCG
2956	GGATGATAGACGCAGATAGTCGC
2957	GATGATAGACGCAGATAGTCGCC
2958	ATGATAGACGCAGATAGTCGCCC

Fig. 28 cont'd (Sheet 51 of 93)

ID	SEQUENCE
2959	TGATAGACGCAGATAGTCGCCCA
2960	GATAGACGCAGATAGTCGCCCAA
2961	ATAGACGCAGATAGTCGCCCAAA
2962	TAGACGCAGATAGTCGCCCAAAG
2963	AGACGCAGATAGTCGCCCAAAGT
2964	GACGCAGATAGTCGCCCAAAGTT
2965	ACGCAGATAGTCGCCCAAAGTTC
2966	CGCAGATAGTCGCCCAAAGTTCC
2967	GCAGATAGTCGCCCAAAGTTCCG
2968	CAGATAGTCGCCCAAAGTTCCGT
2969	AGATAGTCGCCCAAAGTTCCGTG
2970	GATAGTCGCCCAAAGTTCCGTGA
2971	ATAGTCGCCCAAAGTTCCGTGAG
2972	TAGTCGCCCAAAGTTCCGTGAGT
2973	AGTCGCCCAAAGTTCCGTGAGTT
2974	GTCGCCCAAAGTTCCGTGAGTTG
2975	TCGCCCAAAGTTCCGTGAGTTGA
2976	CGCCCAAAGTTCCGTGAGTTGAT
2977	GCCCAAAGTTCCGTGAGTTGATC
2978	CCCAAAGTTCCGTGAGTTGATCA
2979	CCAAAGTTCCGTGAGTTGATCAT
2980	CAAAGTTCCGTGAGTTGATCATC
2981	AAAGTTCCGTGAGTTGATCATCG
2982	AAGTTCCGTGAGTTGATCATCGA
2983	AGTTCCGTGAGTTGATCATCGAA
2984	GTTCCGTGAGTTGATCATCGAAT
2985	TTCCGTGAGTTGATCATCGAATT
2986	TCCGTGAGTTGATCATCGAATTC
2987	CCGTGAGTTGATCATCGAATTCT
2988	CGTGAGTTGATCATCGAATTCTC
2989	GTGAGTTGATCATCGAATTCTCC
2990	TGAGTTGATCATCGAATTCTCCA
2991	GAGTTGATCATCGAATTCTCCAA
2992	AGTTGATCATCGAATTCTCCAAA
2993	GTTGATCATCGAATTCTCCAAAA
2994	TTGATCATCGAATTCTCCAAAAT
2995	TGATCATCGAATTCTCCAAAATG
2996	GATCATCGAATTCTCCAAAATGG
2997	ATCATCGAATTCTCCAAAATGGC
2998	TCATCGAATTCTCCAAAATGGCC
2999	CATCGAATTCTCCAAAATGGCCC
3000	ATCGAATTCTCCAAAATGGCCCG
3001	TCGAATTCTCCAAAATGGCCCGA
3002	CGAATTCTCCAAAATGGCCCGAG
3003	GAATTCTCCAAAATGGCCCGAGA
3004	AATTCTCCAAAATGGCCCGAGAC
3005	ATTCTCCAAAATGGCCCGAGACC
3006	TTCTCCAAAATGGCCCGAGACCC
3007	TCTCCAAAATGGCCCGAGACCCC
3008	CTCCAAAATGGCCCGAGACCCCC
3009	TCCAAAATGGCCCGAGACCCCCA
3010	CCAAAATGGCCCGAGACCCCCAG
3011	CAAAATGGCCCGAGACCCCCAGC
3012	AAAATGGCCCGAGACCCCCAGCG
3013	AAATGGCCCGAGACCCCCAGCGC
3014	AATGGCCCGAGACCCCCAGCGCT
3015	ATGGCCCGAGACCCCCAGCGCTA
3016	TGGCCCGAGACCCCCAGCGCTAC

Fig. 28 cont'd (Sheet 52 of 93)

ID	SEQUENCE
3017	GGCCCGAGACCCCCAGCGCTACC
3018	GCCCGAGACCCCCAGCGCTACCT
3019	CCCGAGACCCCCAGCGCTACCTT
3020	CCGAGACCCCCAGCGCTACCTTG
3021	CGAGACCCCCAGCGCTACCTTGT
3022	GAGACCCCCAGCGCTACCTTGTC
3023	AGACCCCCAGCGCTACCTTGTCA
3024	GACCCCCAGCGCTACCTTGTCAT
3025	ACCCCCAGCGCTACCTTGTCATT
3026	CCCCCAGCGCTACCTTGTCATTC
3027	CCCCAGCGCTACCTTGTCATTCA
3028	CCCAGCGCTACCTTGTCATTCAG
3029	CCAGCGCTACCTTGTCATTCAGG
3030	CAGCGCTACCTTGTCATTCAGGG
3031	AGCGCTACCTTGTCATTCAGGGG
3032	GCGCTACCTTGTCATTCAGGGGG
3033	CGCTACCTTGTCATTCAGGGGGA
3034	GCTACCTTGTCATTCAGGGGGAT
3035	CTACCTTGTCATTCAGGGGGATG
3036	TACCTTGTCATTCAGGGGGATGA
3037	ACCTTGTCATTCAGGGGGATGAA
3038	CCTTGTCATTCAGGGGGATGAAA
3039	CTTGTCATTCAGGGGGATGAAAG
3040	TTGTCATTCAGGGGGATGAAAGA
3041	TGTCATTCAGGGGGATGAAAGAA
3042	GTCATTCAGGGGGATGAAAGAAT
3043	TCATTCAGGGGGATGAAAGAATG
3044	CATTCAGGGGGATGAAAGAATGC
3045	ATTCAGGGGGATGAAAGAATGCA
3046	TTCAGGGGGATGAAAGAATGCAT
3047	TCAGGGGGATGAAAGAATGCATT
3048	CAGGGGGATGAAAGAATGCATTT
3049	AGGGGGATGAAAGAATGCATTTG
3050	GGGGGATGAAAGAATGCATTTGC
3051	GGGGATGAAAGAATGCATTTGCC
3052	GGGATGAAAGAATGCATTTGCCA
3053	GGATGAAAGAATGCATTTGCCAA
3054	GATGAAAGAATGCATTTGCCAAG
3055	ATGAAAGAATGCATTTGCCAAGT
3056	TGAAAGAATGCATTTGCCAAGTC
3057	GAAAGAATGCATTTGCCAAGTCC
3058	AAAGAATGCATTTGCCAAGTCCT
3059	AAGAATGCATTTGCCAAGTCCTA
3060	AGAATGCATTTGCCAAGTCCTAC
3061	GAATGCATTTGCCAAGTCCTACA
3062	AATGCATTTGCCAAGTCCTACAG
3063	ATGCATTTGCCAAGTCCTACAGA
3064	TGCATTTGCCAAGTCCTACAGAC
3065	GCATTTGCCAAGTCCTACAGACT
3066	CATTTGCCAAGTCCTACAGACTC
3067	ATTTGCCAAGTCCTACAGACTCC
3068	TTTGCCAAGTCCTACAGACTCCA
3069	TTGCCAAGTCCTACAGACTCCAA
3070	TGCCAAGTCCTACAGACTCCAAC
3071	GCCAAGTCCTACAGACTCCAACT
3072	CCAAGTCCTACAGACTCCAACTT
3073	CAAGTCCTACAGACTCCAACTTC
3074	AAGTCCTACAGACTCCAACTTCT

Fig. 28 cont'd (Sheet 53 of 93)

ID	SEQUENCE
3075	AGTCCTACAGACTCCAACTTCTA
3076	GTCCTACAGACTCCAACTTCTAC
3077	TCCTACAGACTCCAACTTCTACC
3078	CCTACAGACTCCAACTTCTACCG
3079	CTACAGACTCCAACTTCTACCGT
3080	TACAGACTCCAACTTCTACCGTG
3081	ACAGACTCCAACTTCTACCGTGC
3082	CAGACTCCAACTTCTACCGTGCC
3083	AGACTCCAACTTCTACCGTGCCC
3084	GACTCCAACTTCTACCGTGCCCT
3085	ACTCCAACTTCTACCGTGCCCTG
3086	CTCCAACTTCTACCGTGCCCTGA
3087	TCCAACTTCTACCGTGCCCTGAT
3088	CCAACTTCTACCGTGCCCTGATG
3089	CAACTTCTACCGTGCCCTGATGG
3090	AACTTCTACCGTGCCCTGATGGA
3091	ACTTCTACCGTGCCCTGATGGAT
3092	CTTCTACCGTGCCCTGATGGATG
3093	TTCTACCGTGCCCTGATGGATGA
3094	TCTACCGTGCCCTGATGGATGAA
3095	CTACCGTGCCCTGATGGATGAAG
3096	TACCGTGCCCTGATGGATGAAGA
3097	ACCGTGCCCTGATGGATGAAGAA
3098	CCGTGCCCTGATGGATGAAGAAG
3099	CGTGCCCTGATGGATGAAGAAGA
3100	GTGCCCTGATGGATGAAGAAGAC
3101	TGCCCTGATGGATGAAGAAGACA
3102	GCCCTGATGGATGAAGAAGACAT
3103	CCCTGATGGATGAAGAAGACATG
3104	CCTGATGGATGAAGAAGACATGG
3105	CTGATGGATGAAGAAGACATGGA
3106	TGATGGATGAAGAAGACATGGAC
3107	GATGGATGAAGAAGACATGGACG
3108	ATGGATGAAGAAGACATGGACGA
3109	TGGATGAAGAAGACATGGACGAC
3110	GGATGAAGAAGACATGGACGACG
3111	GATGAAGAAGACATGGACGACGT
3112	ATGAAGAAGACATGGACGACGTG
3113	TGAAGAAGACATGGACGACGTGG
3114	GAAGAAGACATGGACGACGTGGT
3115	AAGAAGACATGGACGACGTGGTG
3116	AGAAGACATGGACGACGTGGTGG
3117	GAAGACATGGACGACGTGGTGGA
3118	AAGACATGGACGACGTGGTGGAT
3119	AGACATGGACGACGTGGTGGATG
3120	GACATGGACGACGTGGTGGATGC
3121	ACATGGACGACGTGGTGGATGCC
3122	CATGGACGACGTGGTGGATGCCG
3123	ATGGACGACGTGGTGGATGCCGA
3124	TGGACGACGTGGTGGATGCCGAC
3125	GGACGACGTGGTGGATGCCGACG
3126	GACGACGTGGTGGATGCCGACGA
3127	ACGACGTGGTGGATGCCGACGAG
3128	CGACGTGGTGGATGCCGACGAGT
3129	GACGTGGTGGATGCCGACGAGTA
3130	ACGTGGTGGATGCCGACGAGTAC
3131	CGTGGTGGATGCCGACGAGTACC
3132	GTGGTGGATGCCGACGAGTACCT

Fig. 28 cont'd (Sheet 54 of 93)

ID	SEQUENCE
3133	TGGTGGATGCCGACGAGTACCTC
3134	GGTGGATGCCGACGAGTACCTCA
3135	GTGGATGCCGACGAGTACCTCAT
3136	TGGATGCCGACGAGTACCTCATC
3137	GGATGCCGACGAGTACCTCATCC
3138	GATGCCGACGAGTACCTCATCCC
3139	ATGCCGACGAGTACCTCATCCCA
3140	TGCCGACGAGTACCTCATCCCAC
3141	GCCGACGAGTACCTCATCCCACA
3142	CCGACGAGTACCTCATCCCACAG
3143	CGACGAGTACCTCATCCCACAGC
3144	GACGAGTACCTCATCCCACAGCA
3145	ACGAGTACCTCATCCCACAGCAG
3146	CGAGTACCTCATCCCACAGCAGG
3147	GAGTACCTCATCCCACAGCAGGG
3148	AGTACCTCATCCCACAGCAGGGC
3149	GTACCTCATCCCACAGCAGGGCT
3150	TACCTCATCCCACAGCAGGGCTT
3151	ACCTCATCCCACAGCAGGGCTTC
3152	CCTCATCCCACAGCAGGGCTTCT
3153	CTCATCCCACAGCAGGGCTTCTT
3154	TCATCCCACAGCAGGGCTTCTTC
3155	CATCCCACAGCAGGGCTTCTTCA
3156	ATCCCACAGCAGGGCTTCTTCAG
3157	TCCCACAGCAGGGCTTCTTCAGC
3158	CCCACAGCAGGGCTTCTTCAGCA
3159	CCACAGCAGGGCTTCTTCAGCAG
3160	CACAGCAGGGCTTCTTCAGCAGC
3161	ACAGCAGGGCTTCTTCAGCAGCC
3162	CAGCAGGGCTTCTTCAGCAGCCC
3163	AGCAGGGCTTCTTCAGCAGCCCC
3164	GCAGGGCTTCTTCAGCAGCCCCT
3165	CAGGGCTTCTTCAGCAGCCCCTC
3166	AGGGCTTCTTCAGCAGCCCCTCC
3167	GGGCTTCTTCAGCAGCCCCTCCA
3168	GGCTTCTTCAGCAGCCCCTCCAC
3169	GCTTCTTCAGCAGCCCCTCCACG
3170	CTTCTTCAGCAGCCCCTCCACGT
3171	TTCTTCAGCAGCCCCTCCACGTC
3172	TCTTCAGCAGCCCCTCCACGTCA
3173	CTTCAGCAGCCCCTCCACGTCAC
3174	TTCAGCAGCCCCTCCACGTCACG
3175	TCAGCAGCCCCTCCACGTCACGG
3176	CAGCAGCCCCTCCACGTCACGGA
3177	AGCAGCCCCTCCACGTCACGGAC
3178	GCAGCCCCTCCACGTCACGGACT
3179	CAGCCCCTCCACGTCACGGACTC
3180	AGCCCCTCCACGTCACGGACTCC
3181	GCCCCTCCACGTCACGGACTCCC
3182	CCCCTCCACGTCACGGACTCCCC
3183	CCCTCCACGTCACGGACTCCCCT
3184	CCTCCACGTCACGGACTCCCCTC
3185	CTCCACGTCACGGACTCCCCTCC
3186	TCCACGTCACGGACTCCCCTCCT
3187	CCACGTCACGGACTCCCCTCCTG
3188	CACGTCACGGACTCCCCTCCTGA
3189	ACGTCACGGACTCCCCTCCTGAG
3190	CGTCACGGACTCCCCTCCTGAGC

Fig. 28 cont'd (Sheet 55 of 93)

ID	SEQUENCE
3191	GTCACGGACTCCCCTCCTGAGCT
3192	TCACGGACTCCCCTCCTGAGCTC
3193	CACGGACTCCCCTCCTGAGCTCT
3194	ACGGACTCCCCTCCTGAGCTCTC
3195	CGGACTCCCCTCCTGAGCTCTCT
3196	GGACTCCCCTCCTGAGCTCTCTG
3197	GACTCCCCTCCTGAGCTCTCTGA
3198	ACTCCCCTCCTGAGCTCTCTGAG
3199	CTCCCCTCCTGAGCTCTCTGAGT
3200	TCCCCTCCTGAGCTCTCTGAGTG
3201	CCCCTCCTGAGCTCTCTGAGTGC
3202	CCCTCCTGAGCTCTCTGAGTGCA
3203	CCTCCTGAGCTCTCTGAGTGCAA
3204	CTCCTGAGCTCTCTGAGTGCAAC
3205	TCCTGAGCTCTCTGAGTGCAACC
3206	CCTGAGCTCTCTGAGTGCAACCA
3207	CTGAGCTCTCTGAGTGCAACCAG
3208	TGAGCTCTCTGAGTGCAACCAGC
3209	GAGCTCTCTGAGTGCAACCAGCA
3210	AGCTCTCTGAGTGCAACCAGCAA
3211	GCTCTCTGAGTGCAACCAGCAAC
3212	CTCTCTGAGTGCAACCAGCAACA
3213	TCTCTGAGTGCAACCAGCAACAA
3214	CTCTGAGTGCAACCAGCAACAAT
3215	TCTGAGTGCAACCAGCAACAATT
3216	CTGAGTGCAACCAGCAACAATTC
3217	TGAGTGCAACCAGCAACAATTCC
3218	GAGTGCAACCAGCAACAATTCCA
3219	AGTGCAACCAGCAACAATTCCAC
3220	GTGCAACCAGCAACAATTCCACC
3221	TGCAACCAGCAACAATTCCACCG
3222	GCAACCAGCAACAATTCCACCGT
3223	CAACCAGCAACAATTCCACCGTG
3224	AACCAGCAACAATTCCACCGTGG
3225	ACCAGCAACAATTCCACCGTGGC
3226	CCAGCAACAATTCCACCGTGGCT
3227	CAGCAACAATTCCACCGTGGCTT
3228	AGCAACAATTCCACCGTGGCTTG
3229	GCAACAATTCCACCGTGGCTTGC
3230	CAACAATTCCACCGTGGCTTGCA
3231	AACAATTCCACCGTGGCTTGCAT
3232	ACAATTCCACCGTGGCTTGCATT
3233	CAATTCCACCGTGGCTTGCATTG
3234	AATTCCACCGTGGCTTGCATTGA
3235	ATTCCACCGTGGCTTGCATTGAT
3236	TTCCACCGTGGCTTGCATTGATA
3237	TCCACCGTGGCTTGCATTGATAG
3238	CCACCGTGGCTTGCATTGATAGA
3239	CACCGTGGCTTGCATTGATAGAA
3240	ACCGTGGCTTGCATTGATAGAAA
3241	CCGTGGCTTGCATTGATAGAAAT
3242	CGTGGCTTGCATTGATAGAAATG
3243	GTGGCTTGCATTGATAGAAATGG
3244	TGGCTTGCATTGATAGAAATGGG
3245	GGCTTGCATTGATAGAAATGGGC
3246	GCTTGCATTGATAGAAATGGGCT
3247	CTTGCATTGATAGAAATGGGCTG
3248	TTGCATTGATAGAAATGGGCTGC

Fig. 28 cont'd (Sheet 56 of 93)

ID	SEQUENCE
3249	TGCATTGATAGAAATGGGCTGCA
3250	GCATTGATAGAAATGGGCTGCAA
3251	CATTGATAGAAATGGGCTGCAAA
3252	ATTGATAGAAATGGGCTGCAAAG
3253	TTGATAGAAATGGGCTGCAAAGC
3254	TGATAGAAATGGGCTGCAAAGCT
3255	GATAGAAATGGGCTGCAAAGCTG
3256	ATAGAAATGGGCTGCAAAGCTGT
3257	TAGAAATGGGCTGCAAAGCTGTC
3258	AGAAATGGGCTGCAAAGCTGTCC
3259	GAAATGGGCTGCAAAGCTGTCCC
3260	AAATGGGCTGCAAAGCTGTCCCA
3261	AATGGGCTGCAAAGCTGTCCCAT
3262	ATGGGCTGCAAAGCTGTCCCATC
3263	TGGGCTGCAAAGCTGTCCCATCA
3264	GGGCTGCAAAGCTGTCCCATCAA
3265	GGCTGCAAAGCTGTCCCATCAAG
3266	GCTGCAAAGCTGTCCCATCAAGG
3267	CTGCAAAGCTGTCCCATCAAGGA
3268	TGCAAAGCTGTCCCATCAAGGAA
3269	GCAAAGCTGTCCCATCAAGGAAG
3270	CAAAGCTGTCCCATCAAGGAAGA
3271	AAAGCTGTCCCATCAAGGAAGAC
3272	AAGCTGTCCCATCAAGGAAGACA
3273	AGCTGTCCCATCAAGGAAGACAG
3274	GCTGTCCCATCAAGGAAGACAGC
3275	CTGTCCCATCAAGGAAGACAGCT
3276	TGTCCCATCAAGGAAGACAGCTT
3277	GTCCCATCAAGGAAGACAGCTTC
3278	TCCCATCAAGGAAGACAGCTTCT
3279	CCCATCAAGGAAGACAGCTTCTT
3280	CCATCAAGGAAGACAGCTTCTTG
3281	CATCAAGGAAGACAGCTTCTTGC
3282	ATCAAGGAAGACAGCTTCTTGCA
3283	TCAAGGAAGACAGCTTCTTGCAG
3284	CAAGGAAGACAGCTTCTTGCAGC
3285	AAGGAAGACAGCTTCTTGCAGCG
3286	AGGAAGACAGCTTCTTGCAGCGA
3287	GGAAGACAGCTTCTTGCAGCGAT
3288	GAAGACAGCTTCTTGCAGCGATA
3289	AAGACAGCTTCTTGCAGCGATAC
3290	AGACAGCTTCTTGCAGCGATACA
3291	GACAGCTTCTTGCAGCGATACAG
3292	ACAGCTTCTTGCAGCGATACAGC
3293	CAGCTTCTTGCAGCGATACAGCT
3294	AGCTTCTTGCAGCGATACAGCTC
3295	GCTTCTTGCAGCGATACAGCTCA
3296	CTTCTTGCAGCGATACAGCTCAG
3297	TTCTTGCAGCGATACAGCTCAGA
3298	TCTTGCAGCGATACAGCTCAGAC
3299	CTTGCAGCGATACAGCTCAGACC
3300	TTGCAGCGATACAGCTCAGACCC
3301	TGCAGCGATACAGCTCAGACCCC
3302	GCAGCGATACAGCTCAGACCCCA
3303	CAGCGATACAGCTCAGACCCCAC
3304	AGCGATACAGCTCAGACCCCACA
3305	GCGATACAGCTCAGACCCCACAG
3306	CGATACAGCTCAGACCCCACAGG

Fig. 28 cont'd (Sheet 57 of 93)

ID	SEQUENCE
3307	GATACAGCTCAGACCCCACAGGC
3308	ATACAGCTCAGACCCCACAGGCG
3309	TACAGCTCAGACCCCACAGGCGC
3310	ACAGCTCAGACCCCACAGGCGCC
3311	CAGCTCAGACCCCACAGGCGCCT
3312	AGCTCAGACCCCACAGGCGCCTT
3313	GCTCAGACCCCACAGGCGCCTTG
3314	CTCAGACCCCACAGGCGCCTTGA
3315	TCAGACCCCACAGGCGCCTTGAC
3316	CAGACCCCACAGGCGCCTTGACT
3317	AGACCCCACAGGCGCCTTGACTG
3318	GACCCCACAGGCGCCTTGACTGA
3319	ACCCCACAGGCGCCTTGACTGAG
3320	CCCCACAGGCGCCTTGACTGAGG
3321	CCCACAGGCGCCTTGACTGAGGA
3322	CCACAGGCGCCTTGACTGAGGAC
3323	CACAGGCGCCTTGACTGAGGACA
3324	ACAGGCGCCTTGACTGAGGACAG
3325	CAGGCGCCTTGACTGAGGACAGC
3326	AGGCGCCTTGACTGAGGACAGCA
3327	GGCGCCTTGACTGAGGACAGCAT
3328	GCGCCTTGACTGAGGACAGCATA
3329	CGCCTTGACTGAGGACAGCATAG
3330	GCCTTGACTGAGGACAGCATAGA
3331	CCTTGACTGAGGACAGCATAGAC
3332	CTTGACTGAGGACAGCATAGACG
3333	TTGACTGAGGACAGCATAGACGA
3334	TGACTGAGGACAGCATAGACGAC
3335	GACTGAGGACAGCATAGACGACA
3336	ACTGAGGACAGCATAGACGACAC
3337	CTGAGGACAGCATAGACGACACC
3338	TGAGGACAGCATAGACGACACCT
3339	GAGGACAGCATAGACGACACCTT
3340	AGGACAGCATAGACGACACCTTC
3341	GGACAGCATAGACGACACCTTCC
3342	GACAGCATAGACGACACCTTCCT
3343	ACAGCATAGACGACACCTTCCTC
3344	CAGCATAGACGACACCTTCCTCC
3345	AGCATAGACGACACCTTCCTCCC
3346	GCATAGACGACACCTTCCTCCCA
3347	CATAGACGACACCTTCCTCCCAG
3348	ATAGACGACACCTTCCTCCCAGT
3349	TAGACGACACCTTCCTCCCAGTG
3350	AGACGACACCTTCCTCCCAGTGC
3351	GACGACACCTTCCTCCCAGTGCC
3352	ACGACACCTTCCTCCCAGTGCCT
3353	CGACACCTTCCTCCCAGTGCCTG
3354	GACACCTTCCTCCCAGTGCCTGA
3355	ACACCTTCCTCCCAGTGCCTGAA
3356	CACCTTCCTCCCAGTGCCTGAAT
3357	ACCTTCCTCCCAGTGCCTGAATA
3358	CCTTCCTCCCAGTGCCTGAATAC
3359	CTTCCTCCCAGTGCCTGAATACA
3360	TTCCTCCCAGTGCCTGAATACAT
3361	TCCTCCCAGTGCCTGAATACATA
3362	CCTCCCAGTGCCTGAATACATAA
3363	CTCCCAGTGCCTGAATACATAAA
3364	TCCCAGTGCCTGAATACATAAAC

Fig. 28 cont'd (Sheet 58 of 93)

ID	SEQUENCE
3365	CCCAGTGCCTGAATACATAAACC
3366	CCAGTGCCTGAATACATAAACCA
3367	CAGTGCCTGAATACATAAACCAG
3368	AGTGCCTGAATACATAAACCAGT
3369	GTGCCTGAATACATAAACCAGTC
3370	TGCCTGAATACATAAACCAGTCC
3371	GCCTGAATACATAAACCAGTCCG
3372	CCTGAATACATAAACCAGTCCGT
3373	CTGAATACATAAACCAGTCCGTT
3374	TGAATACATAAACCAGTCCGTTC
3375	GAATACATAAACCAGTCCGTTCC
3376	AATACATAAACCAGTCCGTTCCC
3377	ATACATAAACCAGTCCGTTCCCA
3378	TACATAAACCAGTCCGTTCCCAA
3379	ACATAAACCAGTCCGTTCCCAAA
3380	CATAAACCAGTCCGTTCCCAAAA
3381	ATAAACCAGTCCGTTCCCAAAAG
3382	TAAACCAGTCCGTTCCCAAAAGG
3383	AAACCAGTCCGTTCCCAAAAGGC
3384	AACCAGTCCGTTCCCAAAAGGCC
3385	ACCAGTCCGTTCCCAAAAGGCCC
3386	CCAGTCCGTTCCCAAAAGGCCCG
3387	CAGTCCGTTCCCAAAAGGCCCGC
3388	AGTCCGTTCCCAAAAGGCCCGCT
3389	GTCCGTTCCCAAAAGGCCCGCTG
3390	TCCGTTCCCAAAAGGCCCGCTGG
3391	CCGTTCCCAAAAGGCCCGCTGGC
3392	CGTTCCCAAAAGGCCCGCTGGCT
3393	GTTCCCAAAAGGCCCGCTGGCTC
3394	TTCCCAAAAGGCCCGCTGGCTCT
3395	TCCCAAAAGGCCCGCTGGCTCTG
3396	CCCAAAAGGCCCGCTGGCTCTGT
3397	CCAAAAGGCCCGCTGGCTCTGTG
3398	CAAAAGGCCCGCTGGCTCTGTGC
3399	AAAAGGCCCGCTGGCTCTGTGCA
3400	AAAGGCCCGCTGGCTCTGTGCAG
3401	AAGGCCCGCTGGCTCTGTGCAGA
3402	AGGCCCGCTGGCTCTGTGCAGAA
3403	GGCCCGCTGGCTCTGTGCAGAAT
3404	GCCCGCTGGCTCTGTGCAGAATC
3405	CCCGCTGGCTCTGTGCAGAATCC
3406	CCGCTGGCTCTGTGCAGAATCCT
3407	CGCTGGCTCTGTGCAGAATCCTG
3408	GCTGGCTCTGTGCAGAATCCTGT
3409	CTGGCTCTGTGCAGAATCCTGTC
3410	TGGCTCTGTGCAGAATCCTGTCT
3411	GGCTCTGTGCAGAATCCTGTCTA
3412	GCTCTGTGCAGAATCCTGTCTAT
3413	CTCTGTGCAGAATCCTGTCTATC
3414	TCTGTGCAGAATCCTGTCTATCA
3415	CTGTGCAGAATCCTGTCTATCAC
3416	TGTGCAGAATCCTGTCTATCACA
3417	GTGCAGAATCCTGTCTATCACAA
3418	TGCAGAATCCTGTCTATCACAAT
3419	GCAGAATCCTGTCTATCACAATC
3420	CAGAATCCTGTCTATCACAATCA
3421	AGAATCCTGTCTATCACAATCAG
3422	GAATCCTGTCTATCACAATCAGC

Fig. 28 cont'd (Sheet 59 of 93)

ID	SEQUENCE
3423	AATCCTGTCTATCACAATCAGCC
3424	ATCCTGTCTATCACAATCAGCCT
3425	TCCTGTCTATCACAATCAGCCTC
3426	CCTGTCTATCACAATCAGCCTCT
3427	CTGTCTATCACAATCAGCCTCTG
3428	TGTCTATCACAATCAGCCTCTGA
3429	GTCTATCACAATCAGCCTCTGAA
3430	TCTATCACAATCAGCCTCTGAAC
3431	CTATCACAATCAGCCTCTGAACC
3432	TATCACAATCAGCCTCTGAACCC
3433	ATCACAATCAGCCTCTGAACCCC
3434	TCACAATCAGCCTCTGAACCCCG
3435	CACAATCAGCCTCTGAACCCCGC
3436	ACAATCAGCCTCTGAACCCCGCG
3437	CAATCAGCCTCTGAACCCCGCGC
3438	CCGCGCCCAGCAGAGACCCACAC
3439	CGCGCCCAGCAGAGACCCACACT
3440	GCGCCCAGCAGAGACCCACACTA
3441	CGCCCAGCAGAGACCCACACTAC
3442	GCCCAGCAGAGACCCACACTACC
3443	CCCAGCAGAGACCCACACTACCA
3444	CCAGCAGAGACCCACACTACCAG
3445	CAGCAGAGACCCACACTACCAGG
3446	AGCAGAGACCCACACTACCAGGA
3447	GCAGAGACCCACACTACCAGGAC
3448	CAGAGACCCACACTACCAGGACC
3449	AGAGACCCACACTACCAGGACCC
3450	GAGACCCACACTACCAGGACCCC
3451	AGACCCACACTACCAGGACCCCC
3452	GACCCACACTACCAGGACCCCCA
3453	ACCCACACTACCAGGACCCCCAC
3454	CCCACACTACCAGGACCCCCACA
3455	CCACACTACCAGGACCCCCACAG
3456	CACACTACCAGGACCCCCACAGC
3457	ACACTACCAGGACCCCCACAGCA
3458	CACTACCAGGACCCCCACAGCAC
3459	ACTACCAGGACCCCCACAGCACT
3460	CTACCAGGACCCCCACAGCACTG
3461	TACCAGGACCCCCACAGCACTGC
3462	ACCAGGACCCCCACAGCACTGCA
3463	CCAGGACCCCCACAGCACTGCAG
3464	CAGGACCCCCACAGCACTGCAGT
3465	AGGACCCCCACAGCACTGCAGTG
3466	GGACCCCCACAGCACTGCAGTGG
3467	GACCCCCACAGCACTGCAGTGGG
3468	ACCCCCACAGCACTGCAGTGGGC
3469	CCCCCACAGCACTGCAGTGGGCA
3470	CCCCACAGCACTGCAGTGGGCAA
3471	CCCACAGCACTGCAGTGGGCAAC
3472	CCACAGCACTGCAGTGGGCAACC
3473	CACAGCACTGCAGTGGGCAACCC
3474	ACAGCACTGCAGTGGGCAACCCC
3475	CAGCACTGCAGTGGGCAACCCCG
3476	AGCACTGCAGTGGGCAACCCCGA
3477	GCACTGCAGTGGGCAACCCCGAG
3478	CACTGCAGTGGGCAACCCCGAGT
3479	ACTGCAGTGGGCAACCCCGAGTA
3480	CTGCAGTGGGCAACCCCGAGTAT

Fig. 28 cont'd (Sheet 60 of 93)

ID	SEQUENCE
3481	TGCAGTGGGCAACCCCGAGTATC
3482	GCAGTGGGCAACCCCGAGTATCT
3483	CAGTGGGCAACCCCGAGTATCTC
3484	AGTGGGCAACCCCGAGTATCTCA
3485	GTGGGCAACCCCGAGTATCTCAA
3486	TGGGCAACCCCGAGTATCTCAAC
3487	GGGCAACCCCGAGTATCTCAACA
3488	GGCAACCCCGAGTATCTCAACAC
3489	GCAACCCCGAGTATCTCAACACT
3490	CAACCCCGAGTATCTCAACACTG
3491	AACCCCGAGTATCTCAACACTGT
3492	ACCCCGAGTATCTCAACACTGTC
3493	CCCCGAGTATCTCAACACTGTCC
3494	CCCGAGTATCTCAACACTGTCCA
3495	CCGAGTATCTCAACACTGTCCAG
3496	CGAGTATCTCAACACTGTCCAGC
3497	GAGTATCTCAACACTGTCCAGCC
3498	AGTATCTCAACACTGTCCAGCCC
3499	GTATCTCAACACTGTCCAGCCCA
3500	TATCTCAACACTGTCCAGCCCAC
3501	ATCTCAACACTGTCCAGCCCACC
3502	TCTCAACACTGTCCAGCCCACCT
3503	CTCAACACTGTCCAGCCCACCTG
3504	TCAACACTGTCCAGCCCACCTGT
3505	CAACACTGTCCAGCCCACCTGTG
3506	AACACTGTCCAGCCCACCTGTGT
3507	ACACTGTCCAGCCCACCTGTGTC
3508	CACTGTCCAGCCCACCTGTGTCA
3509	ACTGTCCAGCCCACCTGTGTCAA
3510	CTGTCCAGCCCACCTGTGTCAAC
3511	TGTCCAGCCCACCTGTGTCAACA
3512	GTCCAGCCCACCTGTGTCAACAG
3513	TCCAGCCCACCTGTGTCAACAGC
3514	CCAGCCCACCTGTGTCAACAGCA
3515	CAGCCCACCTGTGTCAACAGCAC
3516	AGCCCACCTGTGTCAACAGCACA
3517	GCCCACCTGTGTCAACAGCACAT
3518	CCCACCTGTGTCAACAGCACATT
3519	CCACCTGTGTCAACAGCACATTC
3520	CACCTGTGTCAACAGCACATTCG
3521	ACCTGTGTCAACAGCACATTCGA
3522	CCTGTGTCAACAGCACATTCGAC
3523	CTGTGTCAACAGCACATTCGACA
3524	TGTGTCAACAGCACATTCGACAG
3525	GTGTCAACAGCACATTCGACAGC
3526	TGTCAACAGCACATTCGACAGCC
3527	GTCAACAGCACATTCGACAGCCC
3528	TCAACAGCACATTCGACAGCCCT
3529	CAACAGCACATTCGACAGCCCTG
3530	AACAGCACATTCGACAGCCCTGC
3531	ACAGCACATTCGACAGCCCTGCC
3532	CAGCACATTCGACAGCCCTGCCC
3533	AGCACATTCGACAGCCCTGCCCA
3534	GCACATTCGACAGCCCTGCCCAC
3535	CACATTCGACAGCCCTGCCCACT
3536	ACATTCGACAGCCCTGCCCACTG
3537	CATTCGACAGCCCTGCCCACTGG
3538	ATTCGACAGCCCTGCCCACTGGG

Fig. 28 cont'd (Sheet 61 of 93)

ID	SEQUENCE
3539	TTCGACAGCCCTGCCCACTGGGC
3540	TCGACAGCCCTGCCCACTGGGCC
3541	CGACAGCCCTGCCCACTGGGCCC
3542	GACAGCCCTGCCCACTGGGCCCA
3543	ACAGCCCTGCCCACTGGGCCCAG
3544	CAGCCCTGCCCACTGGGCCCAGA
3545	AGCCCTGCCCACTGGGCCCAGAA
3546	GCCCTGCCCACTGGGCCCAGAAA
3547	CCCTGCCCACTGGGCCCAGAAAG
3548	CCTGCCCACTGGGCCCAGAAAGG
3549	CTGCCCACTGGGCCCAGAAAGGC
3550	TGCCCACTGGGCCCAGAAAGGCA
3551	GCCCACTGGGCCCAGAAAGGCAG
3552	CCCACTGGGCCCAGAAAGGCAGC
3553	CCACTGGGCCCAGAAAGGCAGCC
3554	CACTGGGCCCAGAAAGGCAGCCA
3555	ACTGGGCCCAGAAAGGCAGCCAC
3556	CTGGGCCCAGAAAGGCAGCCACC
3557	TGGGCCCAGAAAGGCAGCCACCA
3558	GGGCCCAGAAAGGCAGCCACCAA
3559	GGCCCAGAAAGGCAGCCACCAAA
3560	GCCCAGAAAGGCAGCCACCAAAT
3561	CCCAGAAAGGCAGCCACCAAATT
3562	CCAGAAAGGCAGCCACCAAATTA
3563	CAGAAAGGCAGCCACCAAATTAG
3564	AGAAAGGCAGCCACCAAATTAGC
3565	GAAAGGCAGCCACCAAATTAGCC
3566	AAAGGCAGCCACCAAATTAGCCT
3567	AAGGCAGCCACCAAATTAGCCTG
3568	AGGCAGCCACCAAATTAGCCTGG
3569	GGCAGCCACCAAATTAGCCTGGA
3570	GCAGCCACCAAATTAGCCTGGAC
3571	CAGCCACCAAATTAGCCTGGACA
3572	AGCCACCAAATTAGCCTGGACAA
3573	GCCACCAAATTAGCCTGGACAAC
3574	CCACCAAATTAGCCTGGACAACC
3575	CACCAAATTAGCCTGGACAACCC
3576	ACCAAATTAGCCTGGACAACCCT
3577	CCAAATTAGCCTGGACAACCCTG
3578	CAAATTAGCCTGGACAACCCTGA
3579	AAATTAGCCTGGACAACCCTGAC
3580	AATTAGCCTGGACAACCCTGACT
3581	ATTAGCCTGGACAACCCTGACTA
3582	TTAGCCTGGACAACCCTGACTAC
3583	TAGCCTGGACAACCCTGACTACC
3584	AGCCTGGACAACCCTGACTACCA
3585	GCCTGGACAACCCTGACTACCAG
3586	CCTGGACAACCCTGACTACCAGC
3587	CTGGACAACCCTGACTACCAGCA
3588	TGGACAACCCTGACTACCAGCAG
3589	GGACAACCCTGACTACCAGCAGG
3590	GACAACCCTGACTACCAGCAGGA
3591	ACAACCCTGACTACCAGCAGGAC
3592	CAACCCTGACTACCAGCAGGACT
3593	AACCCTGACTACCAGCAGGACTT
3594	ACCCTGACTACCAGCAGGACTTC
3595	CCCTGACTACCAGCAGGACTTCT
3596	CCTGACTACCAGCAGGACTTCTT

Fig. 28 cont'd (Sheet 62 of 93)

ID	SEQUENCE
3597	CTGACTACCAGCAGGACTTCTTT
3598	TGACTACCAGCAGGACTTCTTTC
3599	GACTACCAGCAGGACTTCTTTCC
3600	ACTACCAGCAGGACTTCTTTCCC
3601	CTACCAGCAGGACTTCTTTCCCA
3602	TACCAGCAGGACTTCTTTCCCAA
3603	ACCAGCAGGACTTCTTTCCCAAG
3604	CCAGCAGGACTTCTTTCCCAAGG
3605	CAGCAGGACTTCTTTCCCAAGGA
3606	AGCAGGACTTCTTTCCCAAGGAA
3607	GCAGGACTTCTTTCCCAAGGAAG
3608	CAGGACTTCTTTCCCAAGGAAGC
3609	AGGACTTCTTTCCCAAGGAAGCC
3610	GGACTTCTTTCCCAAGGAAGCCA
3611	GACTTCTTTCCCAAGGAAGCCAA
3612	ACTTCTTTCCCAAGGAAGCCAAG
3613	CTTCTTTCCCAAGGAAGCCAAGC
3614	TTCTTTCCCAAGGAAGCCAAGCC
3615	TCTTTCCCAAGGAAGCCAAGCCA
3616	CTTTCCCAAGGAAGCCAAGCCAA
3617	TTTCCCAAGGAAGCCAAGCCAAA
3618	TTCCCAAGGAAGCCAAGCCAAAT
3619	TCCCAAGGAAGCCAAGCCAAATG
3620	CCCAAGGAAGCCAAGCCAAATGG
3621	CCAAGGAAGCCAAGCCAAATGGC
3622	CAAGGAAGCCAAGCCAAATGGCA
3623	AAGGAAGCCAAGCCAAATGGCAT
3624	AGGAAGCCAAGCCAAATGGCATC
3625	GGAAGCCAAGCCAAATGGCATCT
3626	GAAGCCAAGCCAAATGGCATCTT
3627	AAGCCAAGCCAAATGGCATCTTT
3628	AGCCAAGCCAAATGGCATCTTTA
3629	GCCAAGCCAAATGGCATCTTTAA
3630	CCAAGCCAAATGGCATCTTTAAG
3631	CAAGCCAAATGGCATCTTTAAGG
3632	AAGCCAAATGGCATCTTTAAGGG
3633	AGCCAAATGGCATCTTTAAGGGC
3634	GCCAAATGGCATCTTTAAGGGCT
3635	CCAAATGGCATCTTTAAGGGCTC
3636	CAAATGGCATCTTTAAGGGCTCC
3637	AAATGGCATCTTTAAGGGCTCCA
3638	AATGGCATCTTTAAGGGCTCCAC
3639	ATGGCATCTTTAAGGGCTCCACA
3640	TGGCATCTTTAAGGGCTCCACAG
3641	GGCATCTTTAAGGGCTCCACAGC
3642	GCATCTTTAAGGGCTCCACAGCT
3643	CATCTTTAAGGGCTCCACAGCTG
3644	ATCTTTAAGGGCTCCACAGCTGA
3645	TCTTTAAGGGCTCCACAGCTGAA
3646	CTTTAAGGGCTCCACAGCTGAAA
3647	TTTAAGGGCTCCACAGCTGAAAA
3648	TTAAGGGCTCCACAGCTGAAAAT
3649	TAAGGGCTCCACAGCTGAAAATG
3650	AAGGGCTCCACAGCTGAAAATGC
3651	AGGGCTCCACAGCTGAAAATGCA
3652	GGGCTCCACAGCTGAAAATGCAG
3653	GGCTCCACAGCTGAAAATGCAGA
3654	GCTCCACAGCTGAAAATGCAGAA

Fig. 28 cont'd (Sheet 63 of 93)

ID	SEQUENCE
3655	CTCCACAGCTGAAAATGCAGAAT
3656	TCCACAGCTGAAAATGCAGAATA
3657	CCACAGCTGAAAATGCAGAATAC
3658	CACAGCTGAAAATGCAGAATACC
3659	ACAGCTGAAAATGCAGAATACCT
3660	CAGCTGAAAATGCAGAATACCTA
3661	AGCTGAAAATGCAGAATACCTAA
3662	GCTGAAAATGCAGAATACCTAAG
3663	CTGAAAATGCAGAATACCTAAGG
3664	TGAAAATGCAGAATACCTAAGGG
3665	GAAAATGCAGAATACCTAAGGGT
3666	AAAATGCAGAATACCTAAGGGTC
3667	AAATGCAGAATACCTAAGGGTCG
3668	AATGCAGAATACCTAAGGGTCGC
3669	ATGCAGAATACCTAAGGGTCGCG
3670	TGCAGAATACCTAAGGGTCGCGC
3671	GCAGAATACCTAAGGGTCGCGCC
3672	CAGAATACCTAAGGGTCGCGCCA
3673	AGAATACCTAAGGGTCGCGCCAC
3674	GAATACCTAAGGGTCGCGCCACA
3675	AATACCTAAGGGTCGCGCCACAA
3676	ATACCTAAGGGTCGCGCCACAAA
3677	TACCTAAGGGTCGCGCCACAAAG
3678	ACCTAAGGGTCGCGCCACAAAGC
3679	CCTAAGGGTCGCGCCACAAAGCA
3680	CTAAGGGTCGCGCCACAAAGCAG
3681	TAAGGGTCGCGCCACAAAGCAGT
3682	AAGGGTCGCGCCACAAAGCAGTG
3683	AGGGTCGCGCCACAAAGCAGTGA
3684	GGGTCGCGCCACAAAGCAGTGAA
3685	GGTCGCGCCACAAAGCAGTGAAT
3686	GTCGCGCCACAAAGCAGTGAATT
3687	TCGCGCCACAAAGCAGTGAATTT
3688	CGCGCCACAAAGCAGTGAATTTA
3689	GCGCCACAAAGCAGTGAATTTAT
3690	CGCCACAAAGCAGTGAATTTATT
3691	GCCACAAAGCAGTGAATTTATTG
3692	CCACAAAGCAGTGAATTTATTGG
3693	CACAAAGCAGTGAATTTATTGGA
3694	ACAAAGCAGTGAATTTATTGGAG
3695	CAAAGCAGTGAATTTATTGGAGC
3696	AAAGCAGTGAATTTATTGGAGCA
3697	AAGCAGTGAATTTATTGGAGCAT
3698	AGCAGTGAATTTATTGGAGCATG
3699	CCACGGAGGATAGTATGAGCCCT
3700	CACGGAGGATAGTATGAGCCCTA
3701	ACGGAGGATAGTATGAGCCCTAA
3702	CGGAGGATAGTATGAGCCCTAAA
3703	GGAGGATAGTATGAGCCCTAAAA
3704	GAGGATAGTATGAGCCCTAAAAA
3705	AGGATAGTATGAGCCCTAAAAAT
3706	GGATAGTATGAGCCCTAAAAATC
3707	GATAGTATGAGCCCTAAAAATCC
3708	ATAGTATGAGCCCTAAAAATCCA
3709	TAGTATGAGCCCTAAAAATCCAG
3710	AGTATGAGCCCTAAAAATCCAGA
3711	GTATGAGCCCTAAAAATCCAGAC
3712	TATGAGCCCTAAAAATCCAGACT

Fig. 28 cont'd (Sheet 64 of 93)

ID	SEQUENCE
3713	ATGAGCCCTAAAAATCCAGACTC
3714	TGAGCCCTAAAAATCCAGACTCT
3715	GAGCCCTAAAAATCCAGACTCTT
3716	AGCCCTAAAAATCCAGACTCTTT
3717	GCCCTAAAAATCCAGACTCTTTC
3718	CCCTAAAAATCCAGACTCTTTCG
3719	CCTAAAAATCCAGACTCTTTCGA
3720	CTAAAAATCCAGACTCTTTCGAT
3721	TAAAAATCCAGACTCTTTCGATA
3722	AAAAATCCAGACTCTTTCGATAC
3723	AAAATCCAGACTCTTTCGATACC
3724	AAATCCAGACTCTTTCGATACCC
3725	AATCCAGACTCTTTCGATACCCA
3726	ATCCAGACTCTTTCGATACCCAG
3727	TCCAGACTCTTTCGATACCCAGG
3728	CCAGACTCTTTCGATACCCAGGA
3729	CAGACTCTTTCGATACCCAGGAC
3730	AGACTCTTTCGATACCCAGGACC
3731	GACTCTTTCGATACCCAGGACCA
3732	ACTCTTTCGATACCCAGGACCAA
3733	CTCTTTCGATACCCAGGACCAAG
3734	TCTTTCGATACCCAGGACCAAGC
3735	CTTTCGATACCCAGGACCAAGCC
3736	TTTCGATACCCAGGACCAAGCCA
3737	TTCGATACCCAGGACCAAGCCAC
3738	TCGATACCCAGGACCAAGCCACA
3739	CGATACCCAGGACCAAGCCACAG
3740	GATACCCAGGACCAAGCCACAGC
3741	ATACCCAGGACCAAGCCACAGCA
3742	TACCCAGGACCAAGCCACAGCAG
3743	ACCCAGGACCAAGCCACAGCAGG
3744	CCCAGGACCAAGCCACAGCAGGT
3745	CCAGGACCAAGCCACAGCAGGTC
3746	CAGGACCAAGCCACAGCAGGTCC
3747	AGGACCAAGCCACAGCAGGTCCT
3748	GGACCAAGCCACAGCAGGTCCTC
3749	GACCAAGCCACAGCAGGTCCTCC
3750	ACCAAGCCACAGCAGGTCCTCCA
3751	CCAAGCCACAGCAGGTCCTCCAT
3752	CAAGCCACAGCAGGTCCTCCATC
3753	AAGCCACAGCAGGTCCTCCATCC
3754	AGCCACAGCAGGTCCTCCATCCC
3755	GCCACAGCAGGTCCTCCATCCCA
3756	CCACAGCAGGTCCTCCATCCCAA
3757	CACAGCAGGTCCTCCATCCCAAC
3758	ACAGCAGGTCCTCCATCCCAACA
3759	CAGCAGGTCCTCCATCCCAACAG
3760	AGCAGGTCCTCCATCCCAACAGC
3761	GCAGGTCCTCCATCCCAACAGCC
3762	CAGGTCCTCCATCCCAACAGCCA
3763	AGGTCCTCCATCCCAACAGCCAT
3764	GGTCCTCCATCCCAACAGCCATG
3765	GTCCTCCATCCCAACAGCCATGC
3766	TCCTCCATCCCAACAGCCATGCC
3767	CCTCCATCCCAACAGCCATGCCC
3768	CTCCATCCCAACAGCCATGCCCG
3769	TCCATCCCAACAGCCATGCCCGC
3770	CCATCCCAACAGCCATGCCCGCA

Fig. 28 cont'd (Sheet 65 of 93)

ID	SEQUENCE
3771	CATCCCAACAGCCATGCCCGCAT
3772	ATCCCAACAGCCATGCCCGCATT
3773	TCCCAACAGCCATGCCCGCATTA
3774	CCCAACAGCCATGCCCGCATTAG
3775	CCAACAGCCATGCCCGCATTAGC
3776	CAACAGCCATGCCCGCATTAGCT
3777	AACAGCCATGCCCGCATTAGCTC
3778	ACAGCCATGCCCGCATTAGCTCT
3779	CAGCCATGCCCGCATTAGCTCTT
3780	AGCCATGCCCGCATTAGCTCTTA
3781	GCCATGCCCGCATTAGCTCTTAG
3782	CCATGCCCGCATTAGCTCTTAGA
3783	CATGCCCGCATTAGCTCTTAGAC
3784	ATGCCCGCATTAGCTCTTAGACC
3785	TGCCCGCATTAGCTCTTAGACCC
3786	GCCCGCATTAGCTCTTAGACCCA
3787	CCCGCATTAGCTCTTAGACCCAC
3788	CCGCATTAGCTCTTAGACCCACA
3789	CGCATTAGCTCTTAGACCCACAG
3790	GCATTAGCTCTTAGACCCACAGA
3791	CATTAGCTCTTAGACCCACAGAC
3792	ATTAGCTCTTAGACCCACAGACT
3793	TTAGCTCTTAGACCCACAGACTG
3794	TAGCTCTTAGACCCACAGACTGG
3795	AGCTCTTAGACCCACAGACTGGT
3796	GCTCTTAGACCCACAGACTGGTT
3797	CTCTTAGACCCACAGACTGGTTT
3798	TCTTAGACCCACAGACTGGTTTT
3799	CTTAGACCCACAGACTGGTTTTG
3800	TTAGACCCACAGACTGGTTTTGC
3801	TAGACCCACAGACTGGTTTTGCA
3802	AGACCCACAGACTGGTTTTGCAA
3803	GACCCACAGACTGGTTTTGCAAC
3804	ACCCACAGACTGGTTTTGCAACG
3805	CCCACAGACTGGTTTTGCAACGT
3806	CCACAGACTGGTTTTGCAACGTT
3807	CACAGACTGGTTTTGCAACGTTT
3808	ACAGACTGGTTTTGCAACGTTTA
3809	CAGACTGGTTTTGCAACGTTTAC
3810	AGACTGGTTTTGCAACGTTTACA
3811	GACTGGTTTTGCAACGTTTACAC
3812	ACTGGTTTTGCAACGTTTACACC
3813	CTGGTTTTGCAACGTTTACACCG
3814	TGGTTTTGCAACGTTTACACCGA
3815	GGTTTTGCAACGTTTACACCGAC
3816	GTTTTGCAACGTTTACACCGACT
3817	TTTTGCAACGTTTACACCGACTA
3818	TTTGCAACGTTTACACCGACTAG
3819	TTGCAACGTTTACACCGACTAGC
3820	TGCAACGTTTACACCGACTAGCC
3821	GCAACGTTTACACCGACTAGCCA
3822	CAACGTTTACACCGACTAGCCAG
3823	AACGTTTACACCGACTAGCCAGG
3824	ACGTTTACACCGACTAGCCAGGA
3825	CGTTTACACCGACTAGCCAGGAA
3826	GTTTACACCGACTAGCCAGGAAG
3827	TTTACACCGACTAGCCAGGAAGT
3828	TTACACCGACTAGCCAGGAAGTA

Fig. 28 cont'd (Sheet 66 of 93)

ID	SEQUENCE
3829	TACACCGACTAGCCAGGAAGTAC
3830	ACACCGACTAGCCAGGAAGTACT
3831	CACCGACTAGCCAGGAAGTACTT
3832	ACCGACTAGCCAGGAAGTACTTC
3833	CCGACTAGCCAGGAAGTACTTCC
3834	CGACTAGCCAGGAAGTACTTCCA
3835	GACTAGCCAGGAAGTACTTCCAC
3836	ACTAGCCAGGAAGTACTTCCACC
3837	CTAGCCAGGAAGTACTTCCACCT
3838	TAGCCAGGAAGTACTTCCACCTC
3839	AGCCAGGAAGTACTTCCACCTCG
3840	GCCAGGAAGTACTTCCACCTCGG
3841	CCAGGAAGTACTTCCACCTCGGG
3842	CAGGAAGTACTTCCACCTCGGGC
3843	AGGAAGTACTTCCACCTCGGGCA
3844	GGAAGTACTTCCACCTCGGGCAC
3845	GAAGTACTTCCACCTCGGGCACA
3846	AAGTACTTCCACCTCGGGCACAT
3847	AGTACTTCCACCTCGGGCACATT
3848	GTACTTCCACCTCGGGCACATTT
3849	TACTTCCACCTCGGGCACATTTT
3850	ACTTCCACCTCGGGCACATTTTG
3851	CTTCCACCTCGGGCACATTTTGG
3852	TTCCACCTCGGGCACATTTTGGG
3853	TCCACCTCGGGCACATTTTGGGA
3854	CCACCTCGGGCACATTTTGGGAA
3855	CACCTCGGGCACATTTTGGGAAG
3856	ACCTCGGGCACATTTTGGGAAGT
3857	CCTCGGGCACATTTTGGGAAGTT
3858	CTCGGGCACATTTTGGGAAGTTG
3859	TCGGGCACATTTTGGGAAGTTGC
3860	CGGGCACATTTTGGGAAGTTGCA
3861	GGGCACATTTTGGGAAGTTGCAT
3862	GGCACATTTTGGGAAGTTGCATT
3863	GCACATTTTGGGAAGTTGCATTC
3864	CACATTTTGGGAAGTTGCATTCC
3865	ACATTTTGGGAAGTTGCATTCCT
3866	CATTTTGGGAAGTTGCATTCCTT
3867	ATTTTGGGAAGTTGCATTCCTTT
3868	TTTTGGGAAGTTGCATTCCTTTG
3869	TTTGGGAAGTTGCATTCCTTTGT
3870	TTGGGAAGTTGCATTCCTTTGTC
3871	TGGGAAGTTGCATTCCTTTGTCT
3872	GGGAAGTTGCATTCCTTTGTCTT
3873	GGAAGTTGCATTCCTTTGTCTTC
3874	GAAGTTGCATTCCTTTGTCTTCA
3875	AAGTTGCATTCCTTTGTCTTCAA
3876	AGTTGCATTCCTTTGTCTTCAAA
3877	GTTGCATTCCTTTGTCTTCAAAC
3878	TTGCATTCCTTTGTCTTCAAACT
3879	TGCATTCCTTTGTCTTCAAACTG
3880	GCATTCCTTTGTCTTCAAACTGT
3881	CATTCCTTTGTCTTCAAACTGTG
3882	ATTCCTTTGTCTTCAAACTGTGA
3883	TTCCTTTGTCTTCAAACTGTGAA
3884	TCCTTTGTCTTCAAACTGTGAAG
3885	CCTTTGTCTTCAAACTGTGAAGC
3886	CTTTGTCTTCAAACTGTGAAGCA

Fig. 28 cont'd (Sheet 67 of 93)

ID	SEQUENCE
3887	TTTGTCTTCAAACTGTGAAGCAT
3888	TTGTCTTCAAACTGTGAAGCATT
3889	TGTCTTCAAACTGTGAAGCATTT
3890	GTCTTCAAACTGTGAAGCATTTA
3891	TCTTCAAACTGTGAAGCATTTAC
3892	CTTCAAACTGTGAAGCATTTACA
3893	TTCAAACTGTGAAGCATTTACAG
3894	TCAAACTGTGAAGCATTTACAGA
3895	CAAACTGTGAAGCATTTACAGAA
3896	AAACTGTGAAGCATTTACAGAAA
3897	AACTGTGAAGCATTTACAGAAAC
3898	ACTGTGAAGCATTTACAGAAACG
3899	CTGTGAAGCATTTACAGAAACGC
3900	TGTGAAGCATTTACAGAAACGCA
3901	GTGAAGCATTTACAGAAACGCAT
3902	TGAAGCATTTACAGAAACGCATC
3903	GAAGCATTTACAGAAACGCATCC
3904	AAGCATTTACAGAAACGCATCCA
3905	AGCATTTACAGAAACGCATCCAG
3906	GCATTTACAGAAACGCATCCAGC
3907	CATTTACAGAAACGCATCCAGCA
3908	ATTTACAGAAACGCATCCAGCAA
3909	TTTACAGAAACGCATCCAGCAAG
3910	TTACAGAAACGCATCCAGCAAGA
3911	TACAGAAACGCATCCAGCAAGAA
3912	ACAGAAACGCATCCAGCAAGAAT
3913	CAGAAACGCATCCAGCAAGAATA
3914	AGAAACGCATCCAGCAAGAATAT
3915	GAAACGCATCCAGCAAGAATATT
3916	AAACGCATCCAGCAAGAATATTG
3917	AACGCATCCAGCAAGAATATTGT
3918	ACGCATCCAGCAAGAATATTGTC
3919	CGCATCCAGCAAGAATATTGTCC
3920	GCATCCAGCAAGAATATTGTCCC
3921	CATCCAGCAAGAATATTGTCCCT
3922	ATCCAGCAAGAATATTGTCCCTT
3923	TCCAGCAAGAATATTGTCCCTTT
3924	CCAGCAAGAATATTGTCCCTTTG
3925	CAGCAAGAATATTGTCCCTTTGA
3926	AGCAAGAATATTGTCCCTTTGAG
3927	GCAAGAATATTGTCCCTTTGAGC
3928	CAAGAATATTGTCCCTTTGAGCA
3929	AAGAATATTGTCCCTTTGAGCAG
3930	AGAATATTGTCCCTTTGAGCAGA
3931	GAATATTGTCCCTTTGAGCAGAA
3932	AATATTGTCCCTTTGAGCAGAAA
3933	ATATTGTCCCTTTGAGCAGAAAT
3934	TATTGTCCCTTTGAGCAGAAATT
3935	ATTGTCCCTTTGAGCAGAAATTT
3936	TTGTCCCTTTGAGCAGAAATTTA
3937	TGTCCCTTTGAGCAGAAATTTAT
3938	GTCCCTTTGAGCAGAAATTTATC
3939	TCCCTTTGAGCAGAAATTTATCT
3940	CCCTTTGAGCAGAAATTTATCTT
3941	CCTTTGAGCAGAAATTTATCTTT
3942	CTTTGAGCAGAAATTTATCTTTC
3943	TTTGAGCAGAAATTTATCTTTCA
3944	TTGAGCAGAAATTTATCTTTCAA

Fig. 28 cont'd (Sheet 68 of 93)

ID	SEQUENCE
3945	TGAGCAGAAATTTATCTTTCAAA
3946	GAGCAGAAATTTATCTTTCAAAG
3947	AGCAGAAATTTATCTTTCAAAGA
3948	GCAGAAATTTATCTTTCAAAGAG
3949	CAGAAATTTATCTTTCAAAGAGG
3950	AGAAATTTATCTTTCAAAGAGGT
3951	GAAATTTATCTTTCAAAGAGGTA
3952	AAATTTATCTTTCAAAGAGGTAT
3953	AATTTATCTTTCAAAGAGGTATA
3954	ATTTATCTTTCAAAGAGGTATAT
3955	TTTATCTTTCAAAGAGGTATATT
3956	TTATCTTTCAAAGAGGTATATTT
3957	TATCTTTCAAAGAGGTATATTTG
3958	ATCTTTCAAAGAGGTATATTTGA
3959	TCTTTCAAAGAGGTATATTTGAA
3960	CTTTCAAAGAGGTATATTTGAAA
3961	TTTCAAAGAGGTATATTTGAAAA
3962	TTCAAAGAGGTATATTTGAAAAA
3963	TCAAAGAGGTATATTTGAAAAAA
3964	CAAAGAGGTATATTTGAAAAAAA
3965	AAAGAGGTATATTTGAAAAAAAA
3966	AAAAAAAAGTATATGTGAGGATT
3967	AAAAAAAGTATATGTGAGGATTT
3968	AAAAAAGTATATGTGAGGATTTT
3969	AAAAAGTATATGTGAGGATTTTT
3970	AAAAGTATATGTGAGGATTTTTA
3971	AAAGTATATGTGAGGATTTTTAT
3972	AAGTATATGTGAGGATTTTTATT
3973	AGTATATGTGAGGATTTTTATTG
3974	GTATATGTGAGGATTTTTATTGA
3975	TATATGTGAGGATTTTTATTGAT
3976	ATATGTGAGGATTTTTATTGATT
3977	TATGTGAGGATTTTTATTGATTG
3978	ATGTGAGGATTTTTATTGATTGG
3979	TGTGAGGATTTTTATTGATTGGG
3980	GTGAGGATTTTTATTGATTGGGG
3981	TGAGGATTTTTATTGATTGGGGA
3982	GAGGATTTTTATTGATTGGGGAT
3983	AGGATTTTTATTGATTGGGGATC
3984	GGATTTTTATTGATTGGGGATCT
3985	GATTTTTATTGATTGGGGATCTT
3986	ATTTTTATTGATTGGGGATCTTG
3987	TTTTTATTGATTGGGGATCTTGG
3988	TTTTATTGATTGGGGATCTTGGA
3989	TTTATTGATTGGGGATCTTGGAG
3990	TTATTGATTGGGGATCTTGGAGT
3991	TATTGATTGGGGATCTTGGAGTT
3992	ATTGATTGGGGATCTTGGAGTTT
3993	TTGATTGGGGATCTTGGAGTTTT
3994	TGATTGGGGATCTTGGAGTTTTT
3995	GATTGGGGATCTTGGAGTTTTTC
3996	ATTGGGGATCTTGGAGTTTTTCA
3997	TTGGGGATCTTGGAGTTTTTCAT
3998	TGGGGATCTTGGAGTTTTTCATT
3999	GGGGATCTTGGAGTTTTTCATTG
4000	GGGATCTTGGAGTTTTTCATTGT
4001	GGATCTTGGAGTTTTTCATTGTC
4002	GATCTTGGAGTTTTTCATTGTCG

Fig. 28 cont'd (Sheet 69 of 93)

ID	SEQUENCE
4003	ATCTTGGAGTTTTTCATTGTCGC
4004	TCTTGGAGTTTTTCATTGTCGCT
4005	CTTGGAGTTTTTCATTGTCGCTA
4006	TTGGAGTTTTTCATTGTCGCTAT
4007	TGGAGTTTTTCATTGTCGCTATT
4008	GGAGTTTTTCATTGTCGCTATTG
4009	GAGTTTTTCATTGTCGCTATTGA
4010	AGTTTTTCATTGTCGCTATTGAT
4011	GTTTTTCATTGTCGCTATTGATT
4012	TTTTTCATTGTCGCTATTGATTT
4013	TTTTCATTGTCGCTATTGATTTT
4014	TTTCATTGTCGCTATTGATTTTT
4015	TTCATTGTCGCTATTGATTTTTA
4016	TCATTGTCGCTATTGATTTTTAC
4017	CATTGTCGCTATTGATTTTTACT
4018	ATTGTCGCTATTGATTTTTACTT
4019	TTGTCGCTATTGATTTTTACTTC
4020	TGTCGCTATTGATTTTTACTTCA
4021	GTCGCTATTGATTTTTACTTCAA
4022	TCGCTATTGATTTTTACTTCAAT
4023	CGCTATTGATTTTTACTTCAATG
4024	GCTATTGATTTTTACTTCAATGG
4025	CTATTGATTTTTACTTCAATGGG
4026	TATTGATTTTTACTTCAATGGGC
4027	ATTGATTTTTACTTCAATGGGCT
4028	TTGATTTTTACTTCAATGGGCTC
4029	TGATTTTTACTTCAATGGGCTCT
4030	GATTTTTACTTCAATGGGCTCTT
4031	ATTTTTACTTCAATGGGCTCTTC
4032	TTTTTACTTCAATGGGCTCTTCC
4033	TTTTACTTCAATGGGCTCTTCCA
4034	TTTACTTCAATGGGCTCTTCCAA
4035	TTACTTCAATGGGCTCTTCCAAC
4036	TACTTCAATGGGCTCTTCCAACA
4037	ACTTCAATGGGCTCTTCCAACAA
4038	CTTCAATGGGCTCTTCCAACAAG
4039	TTCAATGGGCTCTTCCAACAAGG
4040	TCAATGGGCTCTTCCAACAAGGA
4041	CAATGGGCTCTTCCAACAAGGAA
4042	AATGGGCTCTTCCAACAAGGAAG
4043	ATGGGCTCTTCCAACAAGGAAGA
4044	TGGGCTCTTCCAACAAGGAAGAA
4045	GGGCTCTTCCAACAAGGAAGAAG
4046	GGCTCTTCCAACAAGGAAGAAGC
4047	GCTCTTCCAACAAGGAAGAAGCT
4048	CTCTTCCAACAAGGAAGAAGCTT
4049	TCTTCCAACAAGGAAGAAGCTTG
4050	CTTCCAACAAGGAAGAAGCTTGC
4051	TTCCAACAAGGAAGAAGCTTGCT
4052	TCCAACAAGGAAGAAGCTTGCTG
4053	CCAACAAGGAAGAAGCTTGCTGG
4054	CAACAAGGAAGAAGCTTGCTGGT
4055	AACAAGGAAGAAGCTTGCTGGTA
4056	ACAAGGAAGAAGCTTGCTGGTAG
4057	CAAGGAAGAAGCTTGCTGGTAGC
4058	AAGGAAGAAGCTTGCTGGTAGCA
4059	AGGAAGAAGCTTGCTGGTAGCAC
4060	GGAAGAAGCTTGCTGGTAGCACT

Fig. 28 cont'd (Sheet 70 of 93)

ID	SEQUENCE
4061	GAAGAAGCTTGCTGGTAGCACTT
4062	AAGAAGCTTGCTGGTAGCACTTG
4063	AGAAGCTTGCTGGTAGCACTTGC
4064	GAAGCTTGCTGGTAGCACTTGCT
4065	AAGCTTGCTGGTAGCACTTGCTA
4066	AGCTTGCTGGTAGCACTTGCTAC
4067	GCTTGCTGGTAGCACTTGCTACC
4068	CTTGCTGGTAGCACTTGCTACCC
4069	TTGCTGGTAGCACTTGCTACCCT
4070	TGCTGGTAGCACTTGCTACCCTG
4071	GCTGGTAGCACTTGCTACCCTGA
4072	CTGGTAGCACTTGCTACCCTGAG
4073	TGGTAGCACTTGCTACCCTGAGT
4074	GGTAGCACTTGCTACCCTGAGTT
4075	GTAGCACTTGCTACCCTGAGTTC
4076	TAGCACTTGCTACCCTGAGTTCA
4077	AGCACTTGCTACCCTGAGTTCAT
4078	GCACTTGCTACCCTGAGTTCATC
4079	CACTTGCTACCCTGAGTTCATCC
4080	ACTTGCTACCCTGAGTTCATCCA
4081	CTTGCTACCCTGAGTTCATCCAG
4082	TTGCTACCCTGAGTTCATCCAGG
4083	TGCTACCCTGAGTTCATCCAGGC
4084	GCTACCCTGAGTTCATCCAGGCC
4085	CTACCCTGAGTTCATCCAGGCCC
4086	TACCCTGAGTTCATCCAGGCCCA
4087	ACCCTGAGTTCATCCAGGCCCAA
4088	CCCTGAGTTCATCCAGGCCCAAC
4089	CCTGAGTTCATCCAGGCCCAACT
4090	CTGAGTTCATCCAGGCCCAACTG
4091	TGAGTTCATCCAGGCCCAACTGT
4092	GAGTTCATCCAGGCCCAACTGTG
4093	AGTTCATCCAGGCCCAACTGTGA
4094	GTTCATCCAGGCCCAACTGTGAG
4095	TTCATCCAGGCCCAACTGTGAGC
4096	TCATCCAGGCCCAACTGTGAGCA
4097	CATCCAGGCCCAACTGTGAGCAA
4098	ATCCAGGCCCAACTGTGAGCAAG
4099	TCCAGGCCCAACTGTGAGCAAGG
4100	CCAGGCCCAACTGTGAGCAAGGA
4101	CAGGCCCAACTGTGAGCAAGGAG
4102	AGGCCCAACTGTGAGCAAGGAGC
4103	GGCCCAACTGTGAGCAAGGAGCA
4104	GCCCAACTGTGAGCAAGGAGCAC
4105	CCCAACTGTGAGCAAGGAGCACA
4106	CCAACTGTGAGCAAGGAGCACAA
4107	CAACTGTGAGCAAGGAGCACAAG
4108	AACTGTGAGCAAGGAGCACAAGC
4109	ACTGTGAGCAAGGAGCACAAGCC
4110	CTGTGAGCAAGGAGCACAAGCCA
4111	TGTGAGCAAGGAGCACAAGCCAC
4112	GTGAGCAAGGAGCACAAGCCACA
4113	TGAGCAAGGAGCACAAGCCACAA
4114	GAGCAAGGAGCACAAGCCACAAG
4115	AGCAAGGAGCACAAGCCACAAGT
4116	GCAAGGAGCACAAGCCACAAGTC
4117	CAAGGAGCACAAGCCACAAGTCT
4118	AAGGAGCACAAGCCACAAGTCTT

Fig. 28 cont'd (Sheet 71 of 93)

ID	SEQUENCE
4119	AGGAGCACAAGCCACAAGTCTTC
4120	GGAGCACAAGCCACAAGTCTTCC
4121	GAGCACAAGCCACAAGTCTTCCA
4122	AGCACAAGCCACAAGTCTTCCAG
4123	GCACAAGCCACAAGTCTTCCAGA
4124	CACAAGCCACAAGTCTTCCAGAG
4125	ACAAGCCACAAGTCTTCCAGAGG
4126	CAAGCCACAAGTCTTCCAGAGGA
4127	AAGCCACAAGTCTTCCAGAGGAT
4128	AGCCACAAGTCTTCCAGAGGATG
4129	GCCACAAGTCTTCCAGAGGATGC
4130	CCACAAGTCTTCCAGAGGATGCT
4131	CACAAGTCTTCCAGAGGATGCTT
4132	ACAAGTCTTCCAGAGGATGCTTG
4133	CAAGTCTTCCAGAGGATGCTTGA
4134	AAGTCTTCCAGAGGATGCTTGAT
4135	AGTCTTCCAGAGGATGCTTGATT
4136	GTCTTCCAGAGGATGCTTGATTC
4137	TCTTCCAGAGGATGCTTGATTCC
4138	CTTCCAGAGGATGCTTGATTCCA
4139	TTCCAGAGGATGCTTGATTCCAG
4140	TCCAGAGGATGCTTGATTCCAGT
4141	CCAGAGGATGCTTGATTCCAGTG
4142	CAGAGGATGCTTGATTCCAGTGG
4143	AGAGGATGCTTGATTCCAGTGGT
4144	GAGGATGCTTGATTCCAGTGGTT
4145	AGGATGCTTGATTCCAGTGGTTC
4146	GGATGCTTGATTCCAGTGGTTCT
4147	GATGCTTGATTCCAGTGGTTCTG
4148	ATGCTTGATTCCAGTGGTTCTGC
4149	TGCTTGATTCCAGTGGTTCTGCT
4150	GCTTGATTCCAGTGGTTCTGCTT
4151	CTTGATTCCAGTGGTTCTGCTTC
4152	TTGATTCCAGTGGTTCTGCTTCA
4153	TGATTCCAGTGGTTCTGCTTCAA
4154	GATTCCAGTGGTTCTGCTTCAAG
4155	ATTCCAGTGGTTCTGCTTCAAGG
4156	TTCCAGTGGTTCTGCTTCAAGGC
4157	TCCAGTGGTTCTGCTTCAAGGCT
4158	CCAGTGGTTCTGCTTCAAGGCTT
4159	CAGTGGTTCTGCTTCAAGGCTTC
4160	AGTGGTTCTGCTTCAAGGCTTCC
4161	GTGGTTCTGCTTCAAGGCTTCCA
4162	TGGTTCTGCTTCAAGGCTTCCAC
4163	GGTTCTGCTTCAAGGCTTCCACT
4164	GTTCTGCTTCAAGGCTTCCACTG
4165	TTCTGCTTCAAGGCTTCCACTGC
4166	TCTGCTTCAAGGCTTCCACTGCA
4167	CTGCTTCAAGGCTTCCACTGCAA
4168	TGCTTCAAGGCTTCCACTGCAAA
4169	GCTTCAAGGCTTCCACTGCAAAA
4170	CTTCAAGGCTTCCACTGCAAAAC
4171	TTCAAGGCTTCCACTGCAAAACA
4172	TCAAGGCTTCCACTGCAAAACAC
4173	CAAGGCTTCCACTGCAAAACACT
4174	AAGGCTTCCACTGCAAAACACTA
4175	AGGCTTCCACTGCAAAACACTAA
4176	GGCTTCCACTGCAAAACACTAAA

Fig. 28 cont'd (Sheet 72 of 93)

ID	SEQUENCE
4177	GCTTCCACTGCAAAACACTAAAG
4178	CTTCCACTGCAAAACACTAAAGA
4179	TTCCACTGCAAAACACTAAAGAT
4180	TCCACTGCAAAACACTAAAGATC
4181	CCACTGCAAAACACTAAAGATCC
4182	CACTGCAAAACACTAAAGATCCA
4183	ACTGCAAAACACTAAAGATCCAA
4184	CTGCAAAACACTAAAGATCCAAG
4185	TGCAAAACACTAAAGATCCAAGA
4186	GCAAAACACTAAAGATCCAAGAA
4187	CAAAACACTAAAGATCCAAGAAG
4188	AAAACACTAAAGATCCAAGAAGG
4189	AAACACTAAAGATCCAAGAAGGC
4190	AACACTAAAGATCCAAGAAGGCC
4191	ACACTAAAGATCCAAGAAGGCCT
4192	CACTAAAGATCCAAGAAGGCCTT
4193	ACTAAAGATCCAAGAAGGCCTTC
4194	CTAAAGATCCAAGAAGGCCTTCA
4195	TAAAGATCCAAGAAGGCCTTCAT
4196	AAAGATCCAAGAAGGCCTTCATG
4197	AAGATCCAAGAAGGCCTTCATGG
4198	AGATCCAAGAAGGCCTTCATGGC
4199	GATCCAAGAAGGCCTTCATGGCC
4200	ATCCAAGAAGGCCTTCATGGCCC
4201	TCCAAGAAGGCCTTCATGGCCCC
4202	CCAAGAAGGCCTTCATGGCCCCA
4203	CAAGAAGGCCTTCATGGCCCCAG
4204	AAGAAGGCCTTCATGGCCCCAGC
4205	AGAAGGCCTTCATGGCCCCAGCA
4206	GAAGGCCTTCATGGCCCCAGCAG
4207	AAGGCCTTCATGGCCCCAGCAGG
4208	AGGCCTTCATGGCCCCAGCAGGC
4209	GGCCTTCATGGCCCCAGCAGGCC
4210	GCCTTCATGGCCCCAGCAGGCCG
4211	CCTTCATGGCCCCAGCAGGCCGG
4212	CTTCATGGCCCCAGCAGGCCGGA
4213	TTCATGGCCCCAGCAGGCCGGAT
4214	TCATGGCCCCAGCAGGCCGGATC
4215	CATGGCCCCAGCAGGCCGGATCG
4216	ATGGCCCCAGCAGGCCGGATCGG
4217	TGGCCCCAGCAGGCCGGATCGGT
4218	GGCCCCAGCAGGCCGGATCGGTA
4219	GCCCCAGCAGGCCGGATCGGTAC
4220	CCCCAGCAGGCCGGATCGGTACT
4221	CCCAGCAGGCCGGATCGGTACTG
4222	CCAGCAGGCCGGATCGGTACTGT
4223	CAGCAGGCCGGATCGGTACTGTA
4224	AGCAGGCCGGATCGGTACTGTAT
4225	GCAGGCCGGATCGGTACTGTATC
4226	CAGGCCGGATCGGTACTGTATCA
4227	AGGCCGGATCGGTACTGTATCAA
4228	GGCCGGATCGGTACTGTATCAAG
4229	GCCGGATCGGTACTGTATCAAGT
4230	CCGGATCGGTACTGTATCAAGTC
4231	CGGATCGGTACTGTATCAAGTCA
4232	GGATCGGTACTGTATCAAGTCAT
4233	GATCGGTACTGTATCAAGTCATG
4234	ATCGGTACTGTATCAAGTCATGG

Fig. 28 cont'd (Sheet 73 of 93)

ID	SEQUENCE
4235	TCGGTACTGTATCAAGTCATGGC
4236	CGGTACTGTATCAAGTCATGGCA
4237	GGTACTGTATCAAGTCATGGCAG
4238	GTACTGTATCAAGTCATGGCAGG
4239	TACTGTATCAAGTCATGGCAGGT
4240	ACTGTATCAAGTCATGGCAGGTA
4241	CTGTATCAAGTCATGGCAGGTAC
4242	TGTATCAAGTCATGGCAGGTACA
4243	GTATCAAGTCATGGCAGGTACAG
4244	TATCAAGTCATGGCAGGTACAGT
4245	ATCAAGTCATGGCAGGTACAGTA
4246	TCAAGTCATGGCAGGTACAGTAG
4247	CAAGTCATGGCAGGTACAGTAGG
4248	AAGTCATGGCAGGTACAGTAGGA
4249	AGTCATGGCAGGTACAGTAGGAT
4250	GTCATGGCAGGTACAGTAGGATA
4251	TCATGGCAGGTACAGTAGGATAA
4252	CATGGCAGGTACAGTAGGATAAG
4253	ATGGCAGGTACAGTAGGATAAGC
4254	TGGCAGGTACAGTAGGATAAGCC
4255	GGCAGGTACAGTAGGATAAGCCA
4256	GCAGGTACAGTAGGATAAGCCAC
4257	CAGGTACAGTAGGATAAGCCACT
4258	AGGTACAGTAGGATAAGCCACTC
4259	GGTACAGTAGGATAAGCCACTCT
4260	GTACAGTAGGATAAGCCACTCTG
4261	TACAGTAGGATAAGCCACTCTGT
4262	ACAGTAGGATAAGCCACTCTGTC
4263	CAGTAGGATAAGCCACTCTGTCC
4264	AGTAGGATAAGCCACTCTGTCCC
4265	GTAGGATAAGCCACTCTGTCCCT
4266	TAGGATAAGCCACTCTGTCCCTT
4267	AGGATAAGCCACTCTGTCCCTTC
4268	GGATAAGCCACTCTGTCCCTTCC
4269	GATAAGCCACTCTGTCCCTTCCT
4270	ATAAGCCACTCTGTCCCTTCCTG
4271	TAAGCCACTCTGTCCCTTCCTGG
4272	AAGCCACTCTGTCCCTTCCTGGG
4273	AGCCACTCTGTCCCTTCCTGGGC
4274	GCCACTCTGTCCCTTCCTGGGCA
4275	CCACTCTGTCCCTTCCTGGGCAA
4276	CACTCTGTCCCTTCCTGGGCAAA
4277	ACTCTGTCCCTTCCTGGGCAAAG
4278	CTCTGTCCCTTCCTGGGCAAAGA
4279	TCTGTCCCTTCCTGGGCAAAGAA
4280	CTGTCCCTTCCTGGGCAAAGAAG
4281	TGTCCCTTCCTGGGCAAAGAAGA
4282	GTCCCTTCCTGGGCAAAGAAGAA
4283	TCCCTTCCTGGGCAAAGAAGAAA
4284	CCCTTCCTGGGCAAAGAAGAAAC
4285	CCTTCCTGGGCAAAGAAGAAACG
4286	CTTCCTGGGCAAAGAAGAAACGG
4287	TTCCTGGGCAAAGAAGAAACGGA
4288	TCCTGGGCAAAGAAGAAACGGAG
4289	CCTGGGCAAAGAAGAAACGGAGG
4290	CTGGGCAAAGAAGAAACGGAGGG
4291	TGGGCAAAGAAGAAACGGAGGGG
4292	GGGCAAAGAAGAAACGGAGGGGA

Fig. 28 cont'd (Sheet 74 of 93)

ID	SEQUENCE
4293	GGCAAAGAAGAAACGGAGGGGAT
4294	GCAAAGAAGAAACGGAGGGGATG
4295	CAAAGAAGAAACGGAGGGGATGG
4296	AAAGAAGAAACGGAGGGGATGGA
4297	AAGAAGAAACGGAGGGGATGGAA
4298	AGAAGAAACGGAGGGGATGGAAT
4299	GAAGAAACGGAGGGGATGGAATT
4300	AAGAAACGGAGGGGATGGAATTC
4301	AGAAACGGAGGGGATGGAATTCT
4302	GAAACGGAGGGGATGGAATTCTT
4303	AAACGGAGGGGATGGAATTCTTC
4304	AACGGAGGGGATGGAATTCTTCC
4305	ACGGAGGGGATGGAATTCTTCCT
4306	CGGAGGGGATGGAATTCTTCCTT
4307	GGAGGGGATGGAATTCTTCCTTA
4308	GAGGGGATGGAATTCTTCCTTAG
4309	AGGGGATGGAATTCTTCCTTAGA
4310	GGGGATGGAATTCTTCCTTAGAC
4311	GGGATGGAATTCTTCCTTAGACT
4312	GGATGGAATTCTTCCTTAGACTT
4313	GATGGAATTCTTCCTTAGACTTA
4314	ATGGAATTCTTCCTTAGACTTAC
4315	TGGAATTCTTCCTTAGACTTACT
4316	GGAATTCTTCCTTAGACTTACTT
4317	GAATTCTTCCTTAGACTTACTTT
4318	AATTCTTCCTTAGACTTACTTTT
4319	ATTCTTCCTTAGACTTACTTTTG
4320	TTCTTCCTTAGACTTACTTTTGT
4321	TCTTCCTTAGACTTACTTTTGTA
4322	CTTCCTTAGACTTACTTTTGTAA
4323	TTCCTTAGACTTACTTTTGTAAA
4324	TCCTTAGACTTACTTTTGTAAAA
4325	CCTTAGACTTACTTTTGTAAAAA
4326	CTTAGACTTACTTTTGTAAAAAT
4327	TTAGACTTACTTTTGTAAAAATG
4328	TAGACTTACTTTTGTAAAAATGT
4329	AGACTTACTTTTGTAAAAATGTC
4330	GACTTACTTTTGTAAAAATGTCC
4331	ACTTACTTTTGTAAAAATGTCCC
4332	CTTACTTTTGTAAAAATGTCCCC
4333	TTACTTTTGTAAAAATGTCCCCA
4334	TACTTTTGTAAAAATGTCCCCAC
4335	ACTTTTGTAAAAATGTCCCCACG
4336	CTTTTGTAAAAATGTCCCCACGG
4337	TTTTGTAAAAATGTCCCCACGGT
4338	TTTGTAAAAATGTCCCCACGGTA
4339	TTGTAAAAATGTCCCCACGGTAC
4340	TGTAAAAATGTCCCCACGGTACT
4341	GTAAAAATGTCCCCACGGTACTT
4342	TAAAAATGTCCCCACGGTACTTA
4343	AAAAATGTCCCCACGGTACTTAC
4344	AAAATGTCCCCACGGTACTTACT
4345	AAATGTCCCCACGGTACTTACTC
4346	AATGTCCCCACGGTACTTACTCC
4347	ATGTCCCCACGGTACTTACTCCC
4348	TGTCCCCACGGTACTTACTCCCC
4349	GTCCCCACGGTACTTACTCCCCA
4350	TCCCCACGGTACTTACTCCCCAC

Fig. 28 cont'd (Sheet 75 of 93)

ID	SEQUENCE
4351	CCCCACGGTACTTACTCCCCACT
4352	CCCACGGTACTTACTCCCCACTG
4353	CCACGGTACTTACTCCCCACTGA
4354	CACGGTACTTACTCCCCACTGAT
4355	ACGGTACTTACTCCCCACTGATG
4356	CGGTACTTACTCCCCACTGATGG
4357	GGTACTTACTCCCCACTGATGGA
4358	GTACTTACTCCCCACTGATGGAC
4359	TACTTACTCCCCACTGATGGACC
4360	ACTTACTCCCCACTGATGGACCA
4361	CTTACTCCCCACTGATGGACCAG
4362	TTACTCCCCACTGATGGACCAGT
4363	TACTCCCCACTGATGGACCAGTG
4364	ACTCCCCACTGATGGACCAGTGG
4365	CTCCCCACTGATGGACCAGTGGT
4366	TCCCCACTGATGGACCAGTGGTT
4367	CCCCACTGATGGACCAGTGGTTT
4368	CCCACTGATGGACCAGTGGTTTC
4369	CCACTGATGGACCAGTGGTTTCC
4370	CACTGATGGACCAGTGGTTTCCA
4371	ACTGATGGACCAGTGGTTTCCAG
4372	CTGATGGACCAGTGGTTTCCAGT
4373	TGATGGACCAGTGGTTTCCAGTC
4374	GATGGACCAGTGGTTTCCAGTCA
4375	ATGGACCAGTGGTTTCCAGTCAT
4376	TGGACCAGTGGTTTCCAGTCATG
4377	GGACCAGTGGTTTCCAGTCATGA
4378	GACCAGTGGTTTCCAGTCATGAG
4379	ACCAGTGGTTTCCAGTCATGAGC
4380	CCAGTGGTTTCCAGTCATGAGCG
4381	CAGTGGTTTCCAGTCATGAGCGT
4382	AGTGGTTTCCAGTCATGAGCGTT
4383	GTGGTTTCCAGTCATGAGCGTTA
4384	TGGTTTCCAGTCATGAGCGTTAG
4385	GGTTTCCAGTCATGAGCGTTAGA
4386	GTTTCCAGTCATGAGCGTTAGAC
4387	TTTCCAGTCATGAGCGTTAGACT
4388	TTCCAGTCATGAGCGTTAGACTG
4389	TCCAGTCATGAGCGTTAGACTGA
4390	CCAGTCATGAGCGTTAGACTGAC
4391	CAGTCATGAGCGTTAGACTGACT
4392	AGTCATGAGCGTTAGACTGACTT
4393	GTCATGAGCGTTAGACTGACTTG
4394	TCATGAGCGTTAGACTGACTTGT
4395	CATGAGCGTTAGACTGACTTGTT
4396	ATGAGCGTTAGACTGACTTGTTT
4397	TGAGCGTTAGACTGACTTGTTTG
4398	GAGCGTTAGACTGACTTGTTTGT
4399	AGCGTTAGACTGACTTGTTTGTC
4400	GCGTTAGACTGACTTGTTTGTCT
4401	CGTTAGACTGACTTGTTTGTCTT
4402	GTTAGACTGACTTGTTTGTCTTC
4403	TTAGACTGACTTGTTTGTCTTCC
4404	TAGACTGACTTGTTTGTCTTCCA
4405	AGACTGACTTGTTTGTCTTCCAT
4406	GACTGACTTGTTTGTCTTCCATT
4407	ACTGACTTGTTTGTCTTCCATTC
4408	CTGACTTGTTTGTCTTCCATTCC

Fig. 28 cont'd (Sheet 76 of 93)

ID	SEQUENCE
4409	TGACTTGTTTGTCTTCCATTCCA
4410	GACTTGTTTGTCTTCCATTCCAT
4411	ACTTGTTTGTCTTCCATTCCATT
4412	CTTGTTTGTCTTCCATTCCATTG
4413	TTGTTTGTCTTCCATTCCATTGT
4414	TGTTTGTCTTCCATTCCATTGTT
4415	GTTTGTCTTCCATTCCATTGTTT
4416	TTTGTCTTCCATTCCATTGTTTT
4417	TTGTCTTCCATTCCATTGTTTTG
4418	TGTCTTCCATTCCATTGTTTTGA
4419	GTCTTCCATTCCATTGTTTTGAA
4420	TCTTCCATTCCATTGTTTTGAAA
4421	CTTCCATTCCATTGTTTTGAAAC
4422	TTCCATTCCATTGTTTTGAAACT
4423	TCCATTCCATTGTTTTGAAACTC
4424	CCATTCCATTGTTTTGAAACTCA
4425	CATTCCATTGTTTTGAAACTCAG
4426	ATTCCATTGTTTTGAAACTCAGT
4427	TTCCATTGTTTTGAAACTCAGTA
4428	TCCATTGTTTTGAAACTCAGTAT
4429	CCATTGTTTTGAAACTCAGTATG
4430	CATTGTTTTGAAACTCAGTATGC
4431	ATTGTTTTGAAACTCAGTATGCT
4432	TTGTTTTGAAACTCAGTATGCTG
4433	TGTTTTGAAACTCAGTATGCTGC
4434	GTTTTGAAACTCAGTATGCTGCC
4435	TTTTGAAACTCAGTATGCTGCCC
4436	TTTGAAACTCAGTATGCTGCCCC
4437	TTGAAACTCAGTATGCTGCCCCT
4438	TGAAACTCAGTATGCTGCCCCTG
4439	GAAACTCAGTATGCTGCCCCTGT
4440	AAACTCAGTATGCTGCCCCTGTC
4441	AACTCAGTATGCTGCCCCTGTCT
4442	ACTCAGTATGCTGCCCCTGTCTT
4443	CTCAGTATGCTGCCCCTGTCTTG
4444	TCAGTATGCTGCCCCTGTCTTGC
4445	CAGTATGCTGCCCCTGTCTTGCT
4446	AGTATGCTGCCCCTGTCTTGCTG
4447	GTATGCTGCCCCTGTCTTGCTGT
4448	TATGCTGCCCCTGTCTTGCTGTC
4449	ATGCTGCCCCTGTCTTGCTGTCA
4450	TGCTGCCCCTGTCTTGCTGTCAT
4451	GCTGCCCCTGTCTTGCTGTCATG
4452	CTGCCCCTGTCTTGCTGTCATGA
4453	TGCCCCTGTCTTGCTGTCATGAA
4454	GCCCCTGTCTTGCTGTCATGAAA
4455	CCCCTGTCTTGCTGTCATGAAAT
4456	CCCTGTCTTGCTGTCATGAAATC
4457	CCTGTCTTGCTGTCATGAAATCA
4458	CTGTCTTGCTGTCATGAAATCAG
4459	TGTCTTGCTGTCATGAAATCAGC
4460	GTCTTGCTGTCATGAAATCAGCA
4461	TCTTGCTGTCATGAAATCAGCAA
4462	CTTGCTGTCATGAAATCAGCAAG
4463	TTGCTGTCATGAAATCAGCAAGA
4464	TGCTGTCATGAAATCAGCAAGAG
4465	GCTGTCATGAAATCAGCAAGAGA
4466	CTGTCATGAAATCAGCAAGAGAG

Fig. 28 cont'd (Sheet 77 of 93)

ID	SEQUENCE
4467	TGTCATGAAATCAGCAAGAGAGG
4468	GTCATGAAATCAGCAAGAGAGGA
4469	TCATGAAATCAGCAAGAGAGGAT
4470	CATGAAATCAGCAAGAGAGGATG
4471	ATGAAATCAGCAAGAGAGGATGA
4472	TGAAATCAGCAAGAGAGGATGAC
4473	GAAATCAGCAAGAGAGGATGACA
4474	AAATCAGCAAGAGAGGATGACAC
4475	AATCAGCAAGAGAGGATGACACA
4476	ATCAGCAAGAGAGGATGACACAT
4477	TCAGCAAGAGAGGATGACACATC
4478	CAGCAAGAGAGGATGACACATCA
4479	AGCAAGAGAGGATGACACATCAA
4480	GCAAGAGAGGATGACACATCAAA
4481	CAAGAGAGGATGACACATCAAAT
4482	AAGAGAGGATGACACATCAAATA
4483	AGAGAGGATGACACATCAAATAA
4484	GAGAGGATGACACATCAAATAAT
4485	AGAGGATGACACATCAAATAATA
4486	GAGGATGACACATCAAATAATAA
4487	AGGATGACACATCAAATAATAAC
4488	GGATGACACATCAAATAATAACT
4489	GATGACACATCAAATAATAACTC
4490	ATGACACATCAAATAATAACTCG
4491	TGACACATCAAATAATAACTCGG
4492	GACACATCAAATAATAACTCGGA
4493	ACACATCAAATAATAACTCGGAT
4494	CACATCAAATAATAACTCGGATT
4495	ACATCAAATAATAACTCGGATTC
4496	CATCAAATAATAACTCGGATTCC
4497	ATCAAATAATAACTCGGATTCCA
4498	TCAAATAATAACTCGGATTCCAG
4499	CAAATAATAACTCGGATTCCAGC
4500	AAATAATAACTCGGATTCCAGCC
4501	AATAATAACTCGGATTCCAGCCC
4502	ATAATAACTCGGATTCCAGCCCA
4503	TAATAACTCGGATTCCAGCCCAC
4504	AATAACTCGGATTCCAGCCCACA
4505	ATAACTCGGATTCCAGCCCACAT
4506	TAACTCGGATTCCAGCCCACATT
4507	AACTCGGATTCCAGCCCACATTG
4508	ACTCGGATTCCAGCCCACATTGG
4509	CTCGGATTCCAGCCCACATTGGA
4510	TCGGATTCCAGCCCACATTGGAT
4511	CGGATTCCAGCCCACATTGGATT
4512	GGATTCCAGCCCACATTGGATTC
4513	GATTCCAGCCCACATTGGATTCA
4514	ATTCCAGCCCACATTGGATTCAT
4515	TTCCAGCCCACATTGGATTCATC
4516	TCCAGCCCACATTGGATTCATCA
4517	CCAGCCCACATTGGATTCATCAG
4518	CAGCCCACATTGGATTCATCAGC
4519	AGCCCACATTGGATTCATCAGCA
4520	GCCCACATTGGATTCATCAGCAT
4521	CCCACATTGGATTCATCAGCATT
4522	CCACATTGGATTCATCAGCATTT
4523	CACATTGGATTCATCAGCATTTG
4524	ACATTGGATTCATCAGCATTTGG

Fig. 28 cont'd (Sheet 78 of 93)

ID	SEQUENCE
4525	CATTGGATTCATCAGCATTTGGA
4526	ATTGGATTCATCAGCATTTGGAC
4527	TTGGATTCATCAGCATTTGGACC
4528	TGGATTCATCAGCATTTGGACCA
4529	GGATTCATCAGCATTTGGACCAA
4530	GATTCATCAGCATTTGGACCAAT
4531	ATTCATCAGCATTTGGACCAATA
4532	TTCATCAGCATTTGGACCAATAG
4533	TCATCAGCATTTGGACCAATAGC
4534	CATCAGCATTTGGACCAATAGCC
4535	ATCAGCATTTGGACCAATAGCCC
4536	TCAGCATTTGGACCAATAGCCCA
4537	CAGCATTTGGACCAATAGCCCAC
4538	AGCATTTGGACCAATAGCCCACA
4539	GCATTTGGACCAATAGCCCACAG
4540	CATTTGGACCAATAGCCCACAGC
4541	ATTTGGACCAATAGCCCACAGCT
4542	TTTGGACCAATAGCCCACAGCTG
4543	TTGGACCAATAGCCCACAGCTGA
4544	TGGACCAATAGCCCACAGCTGAG
4545	GGACCAATAGCCCACAGCTGAGA
4546	GACCAATAGCCCACAGCTGAGAA
4547	ACCAATAGCCCACAGCTGAGAAT
4548	CCAATAGCCCACAGCTGAGAATG
4549	CAATAGCCCACAGCTGAGAATGT
4550	AATAGCCCACAGCTGAGAATGTG
4551	ATAGCCCACAGCTGAGAATGTGG
4552	TAGCCCACAGCTGAGAATGTGGA
4553	AGCCCACAGCTGAGAATGTGGAA
4554	GCCCACAGCTGAGAATGTGGAAT
4555	CCCACAGCTGAGAATGTGGAATA
4556	CCACAGCTGAGAATGTGGAATAC
4557	CACAGCTGAGAATGTGGAATACC
4558	ACAGCTGAGAATGTGGAATACCT
4559	CAGCTGAGAATGTGGAATACCTA
4560	AGCTGAGAATGTGGAATACCTAA
4561	GCTGAGAATGTGGAATACCTAAG
4562	CTGAGAATGTGGAATACCTAAGG
4563	TGAGAATGTGGAATACCTAAGGA
4564	GAGAATGTGGAATACCTAAGGAT
4565	AGAATGTGGAATACCTAAGGATA
4566	GAATGTGGAATACCTAAGGATAG
4567	AATGTGGAATACCTAAGGATAGC
4568	ATGTGGAATACCTAAGGATAGCA
4569	TGTGGAATACCTAAGGATAGCAC
4570	GTGGAATACCTAAGGATAGCACC
4571	TGGAATACCTAAGGATAGCACCG
4572	GGAATACCTAAGGATAGCACCGC
4573	GAATACCTAAGGATAGCACCGCT
4574	AATACCTAAGGATAGCACCGCTT
4575	ATACCTAAGGATAGCACCGCTTT
4576	TACCTAAGGATAGCACCGCTTTT
4577	ACCTAAGGATAGCACCGCTTTTG
4578	CCTAAGGATAGCACCGCTTTTGT
4579	CTAAGGATAGCACCGCTTTTGTT
4580	TAAGGATAGCACCGCTTTTGTTC
4581	AAGGATAGCACCGCTTTTGTTCT
4582	AGGATAGCACCGCTTTTGTTCTC

Fig. 28 cont'd (Sheet 79 of 93)

ID	SEQUENCE
4583	GGATAGCACCGCTTTTGTTCTCG
4584	GATAGCACCGCTTTTGTTCTCGC
4585	ATAGCACCGCTTTTGTTCTCGCA
4586	TAGCACCGCTTTTGTTCTCGCAA
4587	AGCACCGCTTTTGTTCTCGCAAA
4588	GCACCGCTTTTGTTCTCGCAAAA
4589	CACCGCTTTTGTTCTCGCAAAAA
4590	ACCGCTTTTGTTCTCGCAAAAAC
4591	CCGCTTTTGTTCTCGCAAAAACG
4592	CGCTTTTGTTCTCGCAAAAACGT
4593	GCTTTTGTTCTCGCAAAAACGTA
4594	CTTTTGTTCTCGCAAAAACGTAT
4595	TTTTGTTCTCGCAAAAACGTATC
4596	TTTGTTCTCGCAAAAACGTATCT
4597	TTGTTCTCGCAAAAACGTATCTC
4598	TGTTCTCGCAAAAACGTATCTCC
4599	GTTCTCGCAAAAACGTATCTCCT
4600	TTCTCGCAAAAACGTATCTCCTA
4601	TCTCGCAAAAACGTATCTCCTAA
4602	CTCGCAAAAACGTATCTCCTAAT
4603	TCGCAAAAACGTATCTCCTAATT
4604	CGCAAAAACGTATCTCCTAATTT
4605	GCAAAAACGTATCTCCTAATTTG
4606	CAAAAACGTATCTCCTAATTTGA
4607	AAAAACGTATCTCCTAATTTGAG
4608	AAAACGTATCTCCTAATTTGAGG
4609	AAACGTATCTCCTAATTTGAGGC
4610	AACGTATCTCCTAATTTGAGGCT
4611	ACGTATCTCCTAATTTGAGGCTC
4612	CGTATCTCCTAATTTGAGGCTCA
4613	GTATCTCCTAATTTGAGGCTCAG
4614	TATCTCCTAATTTGAGGCTCAGA
4615	ATCTCCTAATTTGAGGCTCAGAT
4616	TCTCCTAATTTGAGGCTCAGATG
4617	CTCCTAATTTGAGGCTCAGATGA
4618	TCCTAATTTGAGGCTCAGATGAA
4619	CCTAATTTGAGGCTCAGATGAAA
4620	CTAATTTGAGGCTCAGATGAAAT
4621	TAATTTGAGGCTCAGATGAAATG
4622	AATTTGAGGCTCAGATGAAATGC
4623	ATTTGAGGCTCAGATGAAATGCA
4624	TTTGAGGCTCAGATGAAATGCAT
4625	TTGAGGCTCAGATGAAATGCATC
4626	TGAGGCTCAGATGAAATGCATCA
4627	GAGGCTCAGATGAAATGCATCAG
4628	AGGCTCAGATGAAATGCATCAGG
4629	GGCTCAGATGAAATGCATCAGGT
4630	GCTCAGATGAAATGCATCAGGTC
4631	CTCAGATGAAATGCATCAGGTCC
4632	TCAGATGAAATGCATCAGGTCCT
4633	CAGATGAAATGCATCAGGTCCTT
4634	AGATGAAATGCATCAGGTCCTTT
4635	GATGAAATGCATCAGGTCCTTTG
4636	ATGAAATGCATCAGGTCCTTTGG
4637	TGAAATGCATCAGGTCCTTTGGG
4638	GAAATGCATCAGGTCCTTTGGGG
4639	AAATGCATCAGGTCCTTTGGGGC
4640	AATGCATCAGGTCCTTTGGGGCA

Fig. 28 cont'd (Sheet 80 of 93)

ID	SEQUENCE
4641	ATGCATCAGGTCCTTTGGGGCAT
4642	TGCATCAGGTCCTTTGGGGCATA
4643	GCATCAGGTCCTTTGGGGCATAG
4644	CATCAGGTCCTTTGGGGCATAGA
4645	ATCAGGTCCTTTGGGGCATAGAT
4646	TCAGGTCCTTTGGGGCATAGATC
4647	CAGGTCCTTTGGGGCATAGATCA
4648	AGGTCCTTTGGGGCATAGATCAG
4649	GGTCCTTTGGGGCATAGATCAGA
4650	GTCCTTTGGGGCATAGATCAGAA
4651	TCCTTTGGGGCATAGATCAGAAG
4652	CCTTTGGGGCATAGATCAGAAGA
4653	CTTTGGGGCATAGATCAGAAGAC
4654	TTTGGGGCATAGATCAGAAGACT
4655	TTGGGGCATAGATCAGAAGACTA
4656	TGGGGCATAGATCAGAAGACTAC
4657	GGGGCATAGATCAGAAGACTACA
4658	GGGCATAGATCAGAAGACTACAA
4659	GGCATAGATCAGAAGACTACAAA
4660	GCATAGATCAGAAGACTACAAAA
4661	CATAGATCAGAAGACTACAAAAA
4662	ATAGATCAGAAGACTACAAAAAT
4663	TAGATCAGAAGACTACAAAAATG
4664	AGATCAGAAGACTACAAAAATGA
4665	GATCAGAAGACTACAAAAATGAA
4666	ATCAGAAGACTACAAAAATGAAG
4667	TCAGAAGACTACAAAAATGAAGC
4668	CAGAAGACTACAAAAATGAAGCT
4669	AGAAGACTACAAAAATGAAGCTG
4670	GAAGACTACAAAAATGAAGCTGC
4671	AAGACTACAAAAATGAAGCTGCT
4672	AGACTACAAAAATGAAGCTGCTC
4673	GACTACAAAAATGAAGCTGCTCT
4674	ACTACAAAAATGAAGCTGCTCTG
4675	CTACAAAAATGAAGCTGCTCTGA
4676	TACAAAAATGAAGCTGCTCTGAA
4677	ACAAAAATGAAGCTGCTCTGAAA
4678	CAAAAATGAAGCTGCTCTGAAAT
4679	AAAAATGAAGCTGCTCTGAAATC
4680	AAAATGAAGCTGCTCTGAAATCT
4681	AAATGAAGCTGCTCTGAAATCTC
4682	AATGAAGCTGCTCTGAAATCTCC
4683	ATGAAGCTGCTCTGAAATCTCCT
4684	TGAAGCTGCTCTGAAATCTCCTT
4685	GAAGCTGCTCTGAAATCTCCTTT
4686	AAGCTGCTCTGAAATCTCCTTTA
4687	AGCTGCTCTGAAATCTCCTTTAG
4688	GCTGCTCTGAAATCTCCTTTAGC
4689	CTGCTCTGAAATCTCCTTTAGCC
4690	TGCTCTGAAATCTCCTTTAGCCA
4691	GCTCTGAAATCTCCTTTAGCCAT
4692	CTCTGAAATCTCCTTTAGCCATC
4693	TCTGAAATCTCCTTTAGCCATCA
4694	CTGAAATCTCCTTTAGCCATCAC
4695	TGAAATCTCCTTTAGCCATCACC
4696	GAAATCTCCTTTAGCCATCACCC
4697	AAATCTCCTTTAGCCATCACCCC
4698	AATCTCCTTTAGCCATCACCCCA

Fig. 28 cont'd (Sheet 81 of 93)

ID	SEQUENCE
4699	ATCTCCTTTAGCCATCACCCCAA
4700	TCTCCTTTAGCCATCACCCCAAC
4701	CTCCTTTAGCCATCACCCCAACC
4702	TCCTTTAGCCATCACCCCAACCC
4703	CCTTTAGCCATCACCCCAACCCC
4704	CTTTAGCCATCACCCCAACCCCC
4705	TTTAGCCATCACCCCAACCCCCC
4706	TTAGCCATCACCCCAACCCCCCA
4707	TAGCCATCACCCCAACCCCCCAA
4708	AGCCATCACCCCAACCCCCCAAA
4709	GCCATCACCCCAACCCCCCAAAA
4710	CCATCACCCCAACCCCCCAAAAT
4711	CATCACCCCAACCCCCCAAAATT
4712	ATCACCCCAACCCCCCAAAATTA
4713	TCACCCCAACCCCCCAAAATTAG
4714	CACCCCAACCCCCCAAAATTAGT
4715	ACCCCAACCCCCCAAAATTAGTT
4716	CCCCAACCCCCCAAAATTAGTTT
4717	CCCAACCCCCCAAAATTAGTTTG
4718	CCAACCCCCCAAAATTAGTTTGT
4719	CAACCCCCCAAAATTAGTTTGTG
4720	AACCCCCCAAAATTAGTTTGTGT
4721	ACCCCCCAAAATTAGTTTGTGTT
4722	CCCCCCAAAATTAGTTTGTGTTA
4723	CCCCCAAAATTAGTTTGTGTTAC
4724	CCCCAAAATTAGTTTGTGTTACT
4725	CCCAAAATTAGTTTGTGTTACTT
4726	CCAAAATTAGTTTGTGTTACTTA
4727	CAAAATTAGTTTGTGTTACTTAT
4728	AAAATTAGTTTGTGTTACTTATG
4729	AAATTAGTTTGTGTTACTTATGG
4730	AATTAGTTTGTGTTACTTATGGA
4731	ATTAGTTTGTGTTACTTATGGAA
4732	TTAGTTTGTGTTACTTATGGAAG
4733	TAGTTTGTGTTACTTATGGAAGA
4734	AGTTTGTGTTACTTATGGAAGAT
4735	GTTTGTGTTACTTATGGAAGATA
4736	TTTGTGTTACTTATGGAAGATAG
4737	TTGTGTTACTTATGGAAGATAGT
4738	TGTGTTACTTATGGAAGATAGTT
4739	GTGTTACTTATGGAAGATAGTTT
4740	TGTTACTTATGGAAGATAGTTTT
4741	GTTACTTATGGAAGATAGTTTTC
4742	TTACTTATGGAAGATAGTTTTCT
4743	TACTTATGGAAGATAGTTTTCTC
4744	ACTTATGGAAGATAGTTTTCTCC
4745	CTTATGGAAGATAGTTTTCTCCT
4746	TTATGGAAGATAGTTTTCTCCTT
4747	TATGGAAGATAGTTTTCTCCTTT
4748	ATGGAAGATAGTTTTCTCCTTTT
4749	TGGAAGATAGTTTTCTCCTTTTA
4750	GGAAGATAGTTTTCTCCTTTTAC
4751	GAAGATAGTTTTCTCCTTTTACT
4752	AAGATAGTTTTCTCCTTTTACTT
4753	AGATAGTTTTCTCCTTTTACTTC
4754	GATAGTTTTCTCCTTTTACTTCA
4755	ATAGTTTTCTCCTTTTACTTCAC
4756	TAGTTTTCTCCTTTTACTTCACT

Fig. 28 cont'd (Sheet 82 of 93)

ID	SEQUENCE
4757	AGTTTTCTCCTTTTACTTCACTT
4758	GTTTTCTCCTTTTACTTCACTTC
4759	TTTTCTCCTTTTACTTCACTTCA
4760	TTTCTCCTTTTACTTCACTTCAA
4761	TTCTCCTTTTACTTCACTTCAAA
4762	TCTCCTTTTACTTCACTTCAAAA
4763	CTCCTTTTACTTCACTTCAAAAG
4764	TCCTTTTACTTCACTTCAAAAGC
4765	CCTTTTACTTCACTTCAAAAGCT
4766	CTTTTACTTCACTTCAAAAGCTT
4767	TTTTACTTCACTTCAAAAGCTTT
4768	TTTACTTCACTTCAAAAGCTTTT
4769	TTACTTCACTTCAAAAGCTTTTT
4770	TACTTCACTTCAAAAGCTTTTTA
4771	ACTTCACTTCAAAAGCTTTTTAC
4772	CTTCACTTCAAAAGCTTTTTACT
4773	TTCACTTCAAAAGCTTTTTACTC
4774	TCACTTCAAAAGCTTTTTACTCA
4775	CACTTCAAAAGCTTTTTACTCAA
4776	ACTTCAAAAGCTTTTTACTCAAA
4777	CTTCAAAAGCTTTTTACTCAAAG
4778	TTCAAAAGCTTTTTACTCAAAGA
4779	TCAAAAGCTTTTTACTCAAAGAG
4780	CAAAAGCTTTTTACTCAAAGAGT
4781	AAAAGCTTTTTACTCAAAGAGTA
4782	AAAGCTTTTTACTCAAAGAGTAT
4783	AAGCTTTTTACTCAAAGAGTATA
4784	AGCTTTTTACTCAAAGAGTATAT
4785	GCTTTTTACTCAAAGAGTATATG
4786	CTTTTTACTCAAAGAGTATATGT
4787	TTTTTACTCAAAGAGTATATGTT
4788	TTTTACTCAAAGAGTATATGTTC
4789	TTTACTCAAAGAGTATATGTTCC
4790	TTACTCAAAGAGTATATGTTCCC
4791	TACTCAAAGAGTATATGTTCCCT
4792	ACTCAAAGAGTATATGTTCCCTC
4793	CTCAAAGAGTATATGTTCCCTCC
4794	TCAAAGAGTATATGTTCCCTCCA
4795	CAAAGAGTATATGTTCCCTCCAG
4796	AAAGAGTATATGTTCCCTCCAGG
4797	AAGAGTATATGTTCCCTCCAGGT
4798	AGAGTATATGTTCCCTCCAGGTC
4799	GAGTATATGTTCCCTCCAGGTCA
4800	AGTATATGTTCCCTCCAGGTCAG
4801	GTATATGTTCCCTCCAGGTCAGC
4802	TATATGTTCCCTCCAGGTCAGCT
4803	ATATGTTCCCTCCAGGTCAGCTG
4804	TATGTTCCCTCCAGGTCAGCTGC
4805	ATGTTCCCTCCAGGTCAGCTGCC
4806	TGTTCCCTCCAGGTCAGCTGCCC
4807	GTTCCCTCCAGGTCAGCTGCCCC
4808	TTCCCTCCAGGTCAGCTGCCCCC
4809	TCCCTCCAGGTCAGCTGCCCCCA
4810	CCCTCCAGGTCAGCTGCCCCCAA
4811	CCTCCAGGTCAGCTGCCCCCAAA
4812	CTCCAGGTCAGCTGCCCCCAAAC
4813	TCCAGGTCAGCTGCCCCCAAACC
4814	CCAGGTCAGCTGCCCCCAAACCC

Fig. 28 cont'd (Sheet 83 of 93)

ID	SEQUENCE
4815	CAGGTCAGCTGCCCCCAAACCCC
4816	AGGTCAGCTGCCCCCAAACCCCC
4817	GGTCAGCTGCCCCCAAACCCCCT
4818	GTCAGCTGCCCCCAAACCCCCTC
4819	TCAGCTGCCCCCAAACCCCCTCC
4820	CAGCTGCCCCCAAACCCCCTCCT
4821	AGCTGCCCCCAAACCCCCTCCTT
4822	GCTGCCCCCAAACCCCCTCCTTA
4823	CTGCCCCCAAACCCCCTCCTTAC
4824	TGCCCCCAAACCCCCTCCTTACG
4825	GCCCCCAAACCCCCTCCTTACGC
4826	CCCCCAAACCCCCTCCTTACGCT
4827	CCCCAAACCCCCTCCTTACGCTT
4828	CCCAAACCCCCTCCTTACGCTTT
4829	CCAAACCCCCTCCTTACGCTTTG
4830	CAAACCCCCTCCTTACGCTTTGT
4831	AAACCCCCTCCTTACGCTTTGTC
4832	AACCCCCTCCTTACGCTTTGTCA
4833	ACCCCCTCCTTACGCTTTGTCAC
4834	CCCCCTCCTTACGCTTTGTCACA
4835	CCCCTCCTTACGCTTTGTCACAC
4836	CCCTCCTTACGCTTTGTCACACA
4837	CCTCCTTACGCTTTGTCACACAA
4838	CTCCTTACGCTTTGTCACACAAA
4839	TCCTTACGCTTTGTCACACAAAA
4840	CCTTACGCTTTGTCACACAAAAA
4841	CTTACGCTTTGTCACACAAAAAG
4842	TTACGCTTTGTCACACAAAAAGT
4843	TACGCTTTGTCACACAAAAAGTG
4844	ACGCTTTGTCACACAAAAAGTGT
4845	CGCTTTGTCACACAAAAAGTGTC
4846	GCTTTGTCACACAAAAAGTGTCT
4847	CTTTGTCACACAAAAAGTGTCTC
4848	TTTGTCACACAAAAAGTGTCTCT
4849	TTGTCACACAAAAAGTGTCTCTG
4850	TGTCACACAAAAAGTGTCTCTGC
4851	GTCACACAAAAAGTGTCTCTGCC
4852	TCACACAAAAAGTGTCTCTGCCT
4853	CACACAAAAAGTGTCTCTGCCTT
4854	ACACAAAAAGTGTCTCTGCCTTG
4855	CACAAAAAGTGTCTCTGCCTTGA
4856	ACAAAAAGTGTCTCTGCCTTGAG
4857	CAAAAAGTGTCTCTGCCTTGAGT
4858	AAAAAGTGTCTCTGCCTTGAGTC
4859	AAAAGTGTCTCTGCCTTGAGTCA
4860	AAAGTGTCTCTGCCTTGAGTCAT
4861	AAGTGTCTCTGCCTTGAGTCATC
4862	AGTGTCTCTGCCTTGAGTCATCT
4863	GTGTCTCTGCCTTGAGTCATCTA
4864	TGTCTCTGCCTTGAGTCATCTAT
4865	GTCTCTGCCTTGAGTCATCTATT
4866	TCTCTGCCTTGAGTCATCTATTC
4867	CTCTGCCTTGAGTCATCTATTCA
4868	TCTGCCTTGAGTCATCTATTCAA
4869	CTGCCTTGAGTCATCTATTCAAG
4870	TGCCTTGAGTCATCTATTCAAGC
4871	GCCTTGAGTCATCTATTCAAGCA
4872	CCTTGAGTCATCTATTCAAGCAC

Fig. 28 cont'd (Sheet 84 of 93)

ID	SEQUENCE
4873	CTTGAGTCATCTATTCAAGCACT
4874	TTGAGTCATCTATTCAAGCACTT
4875	TGAGTCATCTATTCAAGCACTTA
4876	GAGTCATCTATTCAAGCACTTAC
4877	AGTCATCTATTCAAGCACTTACA
4878	GTCATCTATTCAAGCACTTACAG
4879	TCATCTATTCAAGCACTTACAGC
4880	CATCTATTCAAGCACTTACAGCT
4881	ATCTATTCAAGCACTTACAGCTC
4882	TCTATTCAAGCACTTACAGCTCT
4883	CTATTCAAGCACTTACAGCTCTG
4884	TATTCAAGCACTTACAGCTCTGG
4885	ATTCAAGCACTTACAGCTCTGGC
4886	TTCAAGCACTTACAGCTCTGGCC
4887	TCAAGCACTTACAGCTCTGGCCA
4888	CAAGCACTTACAGCTCTGGCCAC
4889	AAGCACTTACAGCTCTGGCCACA
4890	AGCACTTACAGCTCTGGCCACAA
4891	GCACTTACAGCTCTGGCCACAAC
4892	CACTTACAGCTCTGGCCACAACA
4893	ACTTACAGCTCTGGCCACAACAG
4894	CTTACAGCTCTGGCCACAACAGG
4895	TTACAGCTCTGGCCACAACAGGG
4896	TACAGCTCTGGCCACAACAGGGC
4897	ACAGCTCTGGCCACAACAGGGCA
4898	CAGCTCTGGCCACAACAGGGCAT
4899	AGCTCTGGCCACAACAGGGCATT
4900	GCTCTGGCCACAACAGGGCATTT
4901	CTCTGGCCACAACAGGGCATTTT
4902	TCTGGCCACAACAGGGCATTTTA
4903	CTGGCCACAACAGGGCATTTTAC
4904	TGGCCACAACAGGGCATTTTACA
4905	GGCCACAACAGGGCATTTTACAG
4906	GCCACAACAGGGCATTTTACAGG
4907	CCACAACAGGGCATTTTACAGGT
4908	CACAACAGGGCATTTTACAGGTG
4909	ACAACAGGGCATTTTACAGGTGC
4910	CAACAGGGCATTTTACAGGTGCG
4911	AACAGGGCATTTTACAGGTGCGA
4912	ACAGGGCATTTTACAGGTGCGAA
4913	CAGGGCATTTTACAGGTGCGAAT
4914	AGGGCATTTTACAGGTGCGAATG
4915	GGGCATTTTACAGGTGCGAATGA
4916	GGCATTTTACAGGTGCGAATGAC
4917	GCATTTTACAGGTGCGAATGACA
4918	CATTTTACAGGTGCGAATGACAG
4919	ATTTTACAGGTGCGAATGACAGT
4920	TTTTACAGGTGCGAATGACAGTA
4921	TTTACAGGTGCGAATGACAGTAG
4922	TTACAGGTGCGAATGACAGTAGC
4923	TACAGGTGCGAATGACAGTAGCA
4924	ACAGGTGCGAATGACAGTAGCAT
4925	CAGGTGCGAATGACAGTAGCATT
4926	AGGTGCGAATGACAGTAGCATTA
4927	GGTGCGAATGACAGTAGCATTAT
4928	GTGCGAATGACAGTAGCATTATG
4929	TGCGAATGACAGTAGCATTATGA
4930	GCGAATGACAGTAGCATTATGAG

Fig. 28 cont'd (Sheet 85 of 93)

ID	SEQUENCE
4931	CGAATGACAGTAGCATTATGAGT
4932	GAATGACAGTAGCATTATGAGTA
4933	AATGACAGTAGCATTATGAGTAG
4934	ATGACAGTAGCATTATGAGTAGT
4935	TGACAGTAGCATTATGAGTAGTG
4936	GACAGTAGCATTATGAGTAGTGT
4937	ACAGTAGCATTATGAGTAGTGTG
4938	CAGTAGCATTATGAGTAGTGTGG
4939	AGTAGCATTATGAGTAGTGTGGA
4940	GTAGCATTATGAGTAGTGTGGAA
4941	TAGCATTATGAGTAGTGTGGAAT
4942	AGCATTATGAGTAGTGTGGAATT
4943	GCATTATGAGTAGTGTGGAATTC
4944	CATTATGAGTAGTGTGGAATTCA
4945	ATTATGAGTAGTGTGGAATTCAG
4946	TTATGAGTAGTGTGGAATTCAGG
4947	TATGAGTAGTGTGGAATTCAGGT
4948	ATGAGTAGTGTGGAATTCAGGTA
4949	TGAGTAGTGTGGAATTCAGGTAG
4950	GAGTAGTGTGGAATTCAGGTAGT
4951	AGTAGTGTGGAATTCAGGTAGTA
4952	GTAGTGTGGAATTCAGGTAGTAA
4953	TAGTGTGGAATTCAGGTAGTAAA
4954	AGTGTGGAATTCAGGTAGTAAAT
4955	GTGTGGAATTCAGGTAGTAAATA
4956	TGTGGAATTCAGGTAGTAAATAT
4957	GTGGAATTCAGGTAGTAAATATG
4958	TGGAATTCAGGTAGTAAATATGA
4959	GGAATTCAGGTAGTAAATATGAA
4960	GAATTCAGGTAGTAAATATGAAA
4961	AATTCAGGTAGTAAATATGAAAC
4962	ATTCAGGTAGTAAATATGAAACT
4963	TTCAGGTAGTAAATATGAAACTA
4964	TCAGGTAGTAAATATGAAACTAG
4965	CAGGTAGTAAATATGAAACTAGG
4966	AGGTAGTAAATATGAAACTAGGG
4967	GGTAGTAAATATGAAACTAGGGT
4968	GTAGTAAATATGAAACTAGGGTT
4969	TAGTAAATATGAAACTAGGGTTT
4970	AGTAAATATGAAACTAGGGTTTG
4971	GTAAATATGAAACTAGGGTTTGA
4972	TAAATATGAAACTAGGGTTTGAA
4973	AAATATGAAACTAGGGTTTGAAA
4974	AATATGAAACTAGGGTTTGAAAT
4975	ATATGAAACTAGGGTTTGAAATT
4976	TATGAAACTAGGGTTTGAAATTG
4977	ATGAAACTAGGGTTTGAAATTGA
4978	TGAAACTAGGGTTTGAAATTGAT
4979	GAAACTAGGGTTTGAAATTGATA
4980	AAACTAGGGTTTGAAATTGATAA
4981	AACTAGGGTTTGAAATTGATAAT
4982	ACTAGGGTTTGAAATTGATAATG
4983	CTAGGGTTTGAAATTGATAATGC
4984	TAGGGTTTGAAATTGATAATGCT
4985	AGGGTTTGAAATTGATAATGCTT
4986	GGGTTTGAAATTGATAATGCTTT
4987	GGTTTGAAATTGATAATGCTTTC
4988	GTTTGAAATTGATAATGCTTTCA

Fig. 28 cont'd (Sheet 86 of 93)

ID	SEQUENCE
4989	TTTGAAATTGATAATGCTTTCAC
4990	TTGAAATTGATAATGCTTTCACA
4991	TGAAATTGATAATGCTTTCACAA
4992	GAAATTGATAATGCTTTCACAAC
4993	AAATTGATAATGCTTTCACAACA
4994	AATTGATAATGCTTTCACAACAT
4995	ATTGATAATGCTTTCACAACATT
4996	TTGATAATGCTTTCACAACATTT
4997	TGATAATGCTTTCACAACATTTG
4998	GATAATGCTTTCACAACATTTGC
4999	ATAATGCTTTCACAACATTTGCA
5000	TAATGCTTTCACAACATTTGCAG
5001	AATGCTTTCACAACATTTGCAGA
5002	ATGCTTTCACAACATTTGCAGAT
5003	TGCTTTCACAACATTTGCAGATG
5004	GCTTTCACAACATTTGCAGATGT
5005	CTTTCACAACATTTGCAGATGTT
5006	TTTCACAACATTTGCAGATGTTT
5007	TTCACAACATTTGCAGATGTTTT
5008	TCACAACATTTGCAGATGTTTTA
5009	CACAACATTTGCAGATGTTTTAG
5010	ACAACATTTGCAGATGTTTTAGA
5011	CAACATTTGCAGATGTTTTAGAA
5012	AACATTTGCAGATGTTTTAGAAG
5013	ACATTTGCAGATGTTTTAGAAGG
5014	CATTTGCAGATGTTTTAGAAGGA
5015	ATTTGCAGATGTTTTAGAAGGAA
5016	TTTGCAGATGTTTTAGAAGGAAA
5017	TTGCAGATGTTTTAGAAGGAAAA
5018	TGCAGATGTTTTAGAAGGAAAAA
5019	GCAGATGTTTTAGAAGGAAAAAA
5020	CAGATGTTTTAGAAGGAAAAAAG
5021	AGATGTTTTAGAAGGAAAAAAGT
5022	GATGTTTTAGAAGGAAAAAAGTT
5023	ATGTTTTAGAAGGAAAAAAGTTC
5024	TGTTTTAGAAGGAAAAAAGTTCC
5025	GTTTTAGAAGGAAAAAAGTTCCT
5026	TTTTAGAAGGAAAAAAGTTCCTT
5027	TTTAGAAGGAAAAAAGTTCCTTC
5028	TTAGAAGGAAAAAAGTTCCTTCC
5029	TAGAAGGAAAAAAGTTCCTTCCT
5030	AGAAGGAAAAAAGTTCCTTCCTA
5031	GAAGGAAAAAAGTTCCTTCCTAA
5032	AAGGAAAAAAGTTCCTTCCTAAA
5033	AGGAAAAAAGTTCCTTCCTAAAA
5034	GGAAAAAAGTTCCTTCCTAAAAT
5035	GAAAAAAGTTCCTTCCTAAAATA
5036	AAAAAAGTTCCTTCCTAAAATAA
5037	AAAAAGTTCCTTCCTAAAATAAT
5038	AAAAGTTCCTTCCTAAAATAATT
5039	AAAGTTCCTTCCTAAAATAATTT
5040	AAGTTCCTTCCTAAAATAATTTC
5041	AGTTCCTTCCTAAAATAATTTCT
5042	GTTCCTTCCTAAAATAATTTCTC
5043	TTCCTTCCTAAAATAATTTCTCT
5044	TCCTTCCTAAAATAATTTCTCTA
5045	CCTTCCTAAAATAATTTCTCTAC
5046	CTTCCTAAAATAATTTCTCTACA

Fig. 28 cont'd (Sheet 87 of 93)

ID	SEQUENCE
5047	TTCCTAAAATAATTTCTCTACAA
5048	TCCTAAAATAATTTCTCTACAAT
5049	CCTAAAATAATTTCTCTACAATT
5050	CTAAAATAATTTCTCTACAATTG
5051	TAAAATAATTTCTCTACAATTGG
5052	AAAATAATTTCTCTACAATTGGA
5053	AAATAATTTCTCTACAATTGGAA
5054	AATAATTTCTCTACAATTGGAAG
5055	ATAATTTCTCTACAATTGGAAGA
5056	TAATTTCTCTACAATTGGAAGAT
5057	AATTTCTCTACAATTGGAAGATT
5058	ATTTCTCTACAATTGGAAGATTG
5059	TTTCTCTACAATTGGAAGATTGG
5060	TTCTCTACAATTGGAAGATTGGA
5061	TCTCTACAATTGGAAGATTGGAA
5062	CTCTACAATTGGAAGATTGGAAG
5063	TCTACAATTGGAAGATTGGAAGA
5064	CTACAATTGGAAGATTGGAAGAT
5065	TACAATTGGAAGATTGGAAGATT
5066	ACAATTGGAAGATTGGAAGATTC
5067	CAATTGGAAGATTGGAAGATTCA
5068	AATTGGAAGATTGGAAGATTCAG
5069	ATTGGAAGATTGGAAGATTCAGC
5070	TTGGAAGATTGGAAGATTCAGCT
5071	TGGAAGATTGGAAGATTCAGCTA
5072	GGAAGATTGGAAGATTCAGCTAG
5073	GAAGATTGGAAGATTCAGCTAGT
5074	AAGATTGGAAGATTCAGCTAGTT
5075	AGATTGGAAGATTCAGCTAGTTA
5076	GATTGGAAGATTCAGCTAGTTAG
5077	ATTGGAAGATTCAGCTAGTTAGG
5078	TTGGAAGATTCAGCTAGTTAGGA
5079	TGGAAGATTCAGCTAGTTAGGAG
5080	GGAAGATTCAGCTAGTTAGGAGC
5081	GAAGATTCAGCTAGTTAGGAGCC
5082	AAGATTCAGCTAGTTAGGAGCCC
5083	AGATTCAGCTAGTTAGGAGCCCA
5084	GATTCAGCTAGTTAGGAGCCCAC
5085	ATTCAGCTAGTTAGGAGCCCACC
5086	TTCAGCTAGTTAGGAGCCCACCT
5087	TCAGCTAGTTAGGAGCCCACCTT
5088	CAGCTAGTTAGGAGCCCACCTTT
5089	AGCTAGTTAGGAGCCCACCTTTT
5090	GCTAGTTAGGAGCCCACCTTTTT
5091	CTAGTTAGGAGCCCACCTTTTTT
5092	TAGTTAGGAGCCCACCTTTTTTC
5093	AGTTAGGAGCCCACCTTTTTTCC
5094	GTTAGGAGCCCACCTTTTTTCCT
5095	TTAGGAGCCCACCTTTTTTCCTA
5096	TAGGAGCCCACCTTTTTTCCTAA
5097	AGGAGCCCACCTTTTTTCCTAAT
5098	GGAGCCCACCTTTTTTCCTAATC
5099	GAGCCCACCTTTTTTCCTAATCT
5100	AGCCCACCTTTTTTCCTAATCTG
5101	GCCCACCTTTTTTCCTAATCTGT
5102	CCCACCTTTTTTCCTAATCTGTG
5103	CCACCTTTTTTCCTAATCTGTGT
5104	CACCTTTTTTCCTAATCTGTGTG

Fig. 28 cont'd (Sheet 88 of 93)

ID	SEQUENCE
5105	ACCTTTTTTCCTAATCTGTGTGT
5106	CCTTTTTTCCTAATCTGTGTGTG
5107	CTTTTTTCCTAATCTGTGTGTGC
5108	TTTTTTCCTAATCTGTGTGTGCC
5109	TTTTTCCTAATCTGTGTGTGCCC
5110	TTTTCCTAATCTGTGTGTGCCCT
5111	TTTCCTAATCTGTGTGTGCCCTG
5112	TTCCTAATCTGTGTGTGCCCTGT
5113	TCCTAATCTGTGTGTGCCCTGTA
5114	CCTAATCTGTGTGTGCCCTGTAA
5115	CTAATCTGTGTGTGCCCTGTAAC
5116	TAATCTGTGTGTGCCCTGTAACC
5117	AATCTGTGTGTGCCCTGTAACCT
5118	ATCTGTGTGTGCCCTGTAACCTG
5119	TCTGTGTGTGCCCTGTAACCTGA
5120	CTGTGTGTGCCCTGTAACCTGAC
5121	TGTGTGTGCCCTGTAACCTGACT
5122	GTGTGTGCCCTGTAACCTGACTG
5123	TGTGTGCCCTGTAACCTGACTGG
5124	GTGTGCCCTGTAACCTGACTGGT
5125	TGTGCCCTGTAACCTGACTGGTT
5126	GTGCCCTGTAACCTGACTGGTTA
5127	TGCCCTGTAACCTGACTGGTTAA
5128	GCCCTGTAACCTGACTGGTTAAC
5129	CCCTGTAACCTGACTGGTTAACA
5130	CCTGTAACCTGACTGGTTAACAG
5131	CTGTAACCTGACTGGTTAACAGC
5132	TGTAACCTGACTGGTTAACAGCA
5133	GTAACCTGACTGGTTAACAGCAG
5134	TAACCTGACTGGTTAACAGCAGT
5135	AACCTGACTGGTTAACAGCAGTC
5136	ACCTGACTGGTTAACAGCAGTCC
5137	CCTGACTGGTTAACAGCAGTCCT
5138	CTGACTGGTTAACAGCAGTCCTT
5139	TGACTGGTTAACAGCAGTCCTTT
5140	GACTGGTTAACAGCAGTCCTTTG
5141	ACTGGTTAACAGCAGTCCTTTGT
5142	CTGGTTAACAGCAGTCCTTTGTA
5143	TGGTTAACAGCAGTCCTTTGTAA
5144	GGTTAACAGCAGTCCTTTGTAAA
5145	GTTAACAGCAGTCCTTTGTAAAC
5146	TTAACAGCAGTCCTTTGTAAACA
5147	TAACAGCAGTCCTTTGTAAACAG
5148	AACAGCAGTCCTTTGTAAACAGT
5149	ACAGCAGTCCTTTGTAAACAGTG
5150	CAGCAGTCCTTTGTAAACAGTGT
5151	AGCAGTCCTTTGTAAACAGTGTT
5152	GCAGTCCTTTGTAAACAGTGTTT
5153	CAGTCCTTTGTAAACAGTGTTTT
5154	AGTCCTTTGTAAACAGTGTTTTA
5155	GTCCTTTGTAAACAGTGTTTTAA
5156	TCCTTTGTAAACAGTGTTTTAAA
5157	CCTTTGTAAACAGTGTTTTAAAC
5158	CTTTGTAAACAGTGTTTTAAACT
5159	TTTGTAAACAGTGTTTTAAACTC
5160	TTGTAAACAGTGTTTTAAACTCT
5161	TGTAAACAGTGTTTTAAACTCTC
5162	GTAAACAGTGTTTTAAACTCTCC

Fig. 28 cont'd (Sheet 89 of 93)

ID	SEQUENCE
5163	TAAACAGTGTTTTAAACTCTCCT
5164	AAACAGTGTTTTAAACTCTCCTA
5165	AACAGTGTTTTAAACTCTCCTAG
5166	ACAGTGTTTTAAACTCTCCTAGT
5167	CAGTGTTTTAAACTCTCCTAGTC
5168	AGTGTTTTAAACTCTCCTAGTCA
5169	GTGTTTTAAACTCTCCTAGTCAA
5170	TGTTTTAAACTCTCCTAGTCAAT
5171	GTTTTAAACTCTCCTAGTCAATA
5172	TTTTAAACTCTCCTAGTCAATAT
5173	TTTAAACTCTCCTAGTCAATATC
5174	TTAAACTCTCCTAGTCAATATCC
5175	TAAACTCTCCTAGTCAATATCCA
5176	AAACTCTCCTAGTCAATATCCAC
5177	AACTCTCCTAGTCAATATCCACC
5178	ACTCTCCTAGTCAATATCCACCC
5179	CTCTCCTAGTCAATATCCACCCC
5180	TCTCCTAGTCAATATCCACCCCA
5181	CTCCTAGTCAATATCCACCCCAT
5182	TCCTAGTCAATATCCACCCCATC
5183	CCTAGTCAATATCCACCCCATCC
5184	CTAGTCAATATCCACCCCATCCA
5185	TAGTCAATATCCACCCCATCCAA
5186	AGTCAATATCCACCCCATCCAAT
5187	GTCAATATCCACCCCATCCAATT
5188	TCAATATCCACCCCATCCAATTT
5189	CAATATCCACCCCATCCAATTTA
5190	AATATCCACCCCATCCAATTTAT
5191	ATATCCACCCCATCCAATTTATC
5192	TATCCACCCCATCCAATTTATCA
5193	ATCCACCCCATCCAATTTATCAA
5194	TCCACCCCATCCAATTTATCAAG
5195	CCACCCCATCCAATTTATCAAGG
5196	CACCCCATCCAATTTATCAAGGA
5197	ACCCCATCCAATTTATCAAGGAA
5198	CCCCATCCAATTTATCAAGGAAG
5199	CCCATCCAATTTATCAAGGAAGA
5200	CCATCCAATTTATCAAGGAAGAA
5201	CATCCAATTTATCAAGGAAGAAA
5202	ATCCAATTTATCAAGGAAGAAAT
5203	TCCAATTTATCAAGGAAGAAATG
5204	CCAATTTATCAAGGAAGAAATGG
5205	CAATTTATCAAGGAAGAAATGGT
5206	AATTTATCAAGGAAGAAATGGTT
5207	ATTTATCAAGGAAGAAATGGTTC
5208	TTTATCAAGGAAGAAATGGTTCA
5209	TTATCAAGGAAGAAATGGTTCAG
5210	TATCAAGGAAGAAATGGTTCAGA
5211	ATCAAGGAAGAAATGGTTCAGAA
5212	TCAAGGAAGAAATGGTTCAGAAA
5213	CAAGGAAGAAATGGTTCAGAAAA
5214	AAGGAAGAAATGGTTCAGAAAAT
5215	AGGAAGAAATGGTTCAGAAAATA
5216	GGAAGAAATGGTTCAGAAAATAT
5217	GAAGAAATGGTTCAGAAAATATT
5218	AAGAAATGGTTCAGAAAATATTT
5219	AGAAATGGTTCAGAAAATATTTT
5220	GAAATGGTTCAGAAAATATTTTC

Fig. 28 cont'd (Sheet 90 of 93)

ID	SEQUENCE
5221	AAATGGTTCAGAAAATATTTTCA
5222	AATGGTTCAGAAAATATTTTCAG
5223	ATGGTTCAGAAAATATTTTCAGC
5224	TGGTTCAGAAAATATTTTCAGCC
5225	GGTTCAGAAAATATTTTCAGCCT
5226	GTTCAGAAAATATTTTCAGCCTA
5227	TTCAGAAAATATTTTCAGCCTAC
5228	TCAGAAAATATTTTCAGCCTACA
5229	CAGAAAATATTTTCAGCCTACAG
5230	AGAAAATATTTTCAGCCTACAGT
5231	GAAAATATTTTCAGCCTACAGTT
5232	AAAATATTTTCAGCCTACAGTTA
5233	AAATATTTTCAGCCTACAGTTAT
5234	AATATTTTCAGCCTACAGTTATG
5235	ATATTTTCAGCCTACAGTTATGT
5236	TATTTTCAGCCTACAGTTATGTT
5237	ATTTTCAGCCTACAGTTATGTTC
5238	TTTTCAGCCTACAGTTATGTTCA
5239	TTTCAGCCTACAGTTATGTTCAG
5240	TTCAGCCTACAGTTATGTTCAGT
5241	TCAGCCTACAGTTATGTTCAGTC
5242	CAGCCTACAGTTATGTTCAGTCA
5243	AGCCTACAGTTATGTTCAGTCAC
5244	GCCTACAGTTATGTTCAGTCACA
5245	CCTACAGTTATGTTCAGTCACAC
5246	CTACAGTTATGTTCAGTCACACA
5247	TACAGTTATGTTCAGTCACACAC
5248	ACAGTTATGTTCAGTCACACACA
5249	CAGTTATGTTCAGTCACACACAC
5250	AGTTATGTTCAGTCACACACACA
5251	GTTATGTTCAGTCACACACACAT
5252	TTATGTTCAGTCACACACACATA
5253	TATGTTCAGTCACACACACATAC
5254	ATGTTCAGTCACACACACATACA
5255	TGTTCAGTCACACACACATACAA
5256	GTTCAGTCACACACACATACAAA
5257	TTCAGTCACACACACATACAAAA
5258	TCAGTCACACACACATACAAAAT
5259	CAGTCACACACACATACAAAATG
5260	AGTCACACACACATACAAAATGT
5261	GTCACACACACATACAAAATGTT
5262	TCACACACACATACAAAATGTTC
5263	CACACACACATACAAAATGTTCC
5264	ACACACACATACAAAATGTTCCT
5265	CACACACATACAAAATGTTCCTT
5266	ACACACATACAAAATGTTCCTTT
5267	CACACATACAAAATGTTCCTTTT
5268	ACACATACAAAATGTTCCTTTTG
5269	CACATACAAAATGTTCCTTTTGC
5270	ACATACAAAATGTTCCTTTTGCT
5271	CATACAAAATGTTCCTTTTGCTT
5272	ATACAAAATGTTCCTTTTGCTTT
5273	TACAAAATGTTCCTTTTGCTTTT
5274	ACAAAATGTTCCTTTTGCTTTTA
5275	CAAAATGTTCCTTTTGCTTTTAA
5276	AAAATGTTCCTTTTGCTTTTAAA
5277	AAATGTTCCTTTTGCTTTTAAAG
5278	AATGTTCCTTTTGCTTTTAAAGT

Fig. 28 cont'd (Sheet 91 of 93)

ID	SEQUENCE
5279	ATGTTCCTTTTGCTTTTAAAGTA
5280	TGTTCCTTTTGCTTTTAAAGTAA
5281	GTTCCTTTTGCTTTTAAAGTAAT
5282	TTCCTTTTGCTTTTAAAGTAATT
5283	TCCTTTTGCTTTTAAAGTAATTT
5284	CCTTTTGCTTTTAAAGTAATTTT
5285	CTTTTGCTTTTAAAGTAATTTTT
5286	TTTTGCTTTTAAAGTAATTTTTG
5287	TTTGCTTTTAAAGTAATTTTTGA
5288	TTGCTTTTAAAGTAATTTTTGAC
5289	TGCTTTTAAAGTAATTTTTGACT
5290	GCTTTTAAAGTAATTTTTGACTC
5291	CTTTTAAAGTAATTTTTGACTCC
5292	TTTTAAAGTAATTTTTGACTCCC
5293	TTTAAAGTAATTTTTGACTCCCA
5294	TTAAAGTAATTTTTGACTCCCAG
5295	TAAAGTAATTTTTGACTCCCAGA
5296	AAAGTAATTTTTGACTCCCAGAT
5297	AAGTAATTTTTGACTCCCAGATC
5298	AGTAATTTTTGACTCCCAGATCA
5299	GTAATTTTTGACTCCCAGATCAG
5300	TAATTTTTGACTCCCAGATCAGT
5301	AATTTTTGACTCCCAGATCAGTC
5302	ATTTTTGACTCCCAGATCAGTCA
5303	TTTTTGACTCCCAGATCAGTCAG
5304	TTTTGACTCCCAGATCAGTCAGA
5305	TTTGACTCCCAGATCAGTCAGAG
5306	TTGACTCCCAGATCAGTCAGAGC
5307	TGACTCCCAGATCAGTCAGAGCC
5308	GACTCCCAGATCAGTCAGAGCCC
5309	ACTCCCAGATCAGTCAGAGCCCC
5310	CTCCCAGATCAGTCAGAGCCCCT
5311	TCCCAGATCAGTCAGAGCCCCTA
5312	CCCAGATCAGTCAGAGCCCCTAC
5313	CCAGATCAGTCAGAGCCCCTACA
5314	CAGATCAGTCAGAGCCCCTACAG
5315	AGATCAGTCAGAGCCCCTACAGC
5316	GATCAGTCAGAGCCCCTACAGCA
5317	ATCAGTCAGAGCCCCTACAGCAT
5318	TCAGTCAGAGCCCCTACAGCATT
5319	CAGTCAGAGCCCCTACAGCATTG
5320	AGTCAGAGCCCCTACAGCATTGT
5321	GTCAGAGCCCCTACAGCATTGTT
5322	TCAGAGCCCCTACAGCATTGTTA
5323	CAGAGCCCCTACAGCATTGTTAA
5324	AGAGCCCCTACAGCATTGTTAAG
5325	GAGCCCCTACAGCATTGTTAAGA
5326	AGCCCCTACAGCATTGTTAAGAA
5327	GCCCCTACAGCATTGTTAAGAAA
5328	CCCCTACAGCATTGTTAAGAAAG
5329	CCCTACAGCATTGTTAAGAAAGT
5330	CCTACAGCATTGTTAAGAAAGTA
5331	CTACAGCATTGTTAAGAAAGTAT
5332	TACAGCATTGTTAAGAAAGTATT
5333	ACAGCATTGTTAAGAAAGTATTT
5334	CAGCATTGTTAAGAAAGTATTTG
5335	AGCATTGTTAAGAAAGTATTTGA
5336	GCATTGTTAAGAAAGTATTTGAT

Fig. 28 cont'd (Sheet 92 of 93)

ID	SEQUENCE
5337	CATTGTTAAGAAAGTATTTGATT
5338	ATTGTTAAGAAAGTATTTGATTT
5339	TTGTTAAGAAAGTATTTGATTTT
5340	TGTTAAGAAAGTATTTGATTTTT
5341	GTTAAGAAAGTATTTGATTTTTG
5342	TTAAGAAAGTATTTGATTTTTGT
5343	TAAGAAAGTATTTGATTTTTGTC
5344	AAGAAAGTATTTGATTTTTGTCT
5345	AGAAAGTATTTGATTTTTGTCTC
5346	GAAAGTATTTGATTTTTGTCTCA
5347	AAAGTATTTGATTTTTGTCTCAA
5348	AAGTATTTGATTTTTGTCTCAAT
5349	AGTATTTGATTTTTGTCTCAATG
5350	GTATTTGATTTTTGTCTCAATGA
5351	TATTTGATTTTTGTCTCAATGAA
5352	ATTTGATTTTTGTCTCAATGAAA
5353	TTTGATTTTTGTCTCAATGAAAA
5354	TTGATTTTTGTCTCAATGAAAAT
5355	TGATTTTTGTCTCAATGAAAATA
5356	GATTTTTGTCTCAATGAAAATAA
5357	ATTTTTGTCTCAATGAAAATAAA
5358	TTTTTGTCTCAATGAAAATAAAA
5359	TTTTGTCTCAATGAAAATAAAAC
5360	TTTGTCTCAATGAAAATAAAACT
5361	TTGTCTCAATGAAAATAAAACTA
5362	TGTCTCAATGAAAATAAAACTAT
5363	GTCTCAATGAAAATAAAACTATA
5364	TCTCAATGAAAATAAAACTATAT
5365	CTCAATGAAAATAAAACTATATT
5366	TCAATGAAAATAAAACTATATTC
5367	CAATGAAAATAAAACTATATTCA
5368	AATGAAAATAAAACTATATTCAT
5369	ATGAAAATAAAACTATATTCATT
5370	TGAAAATAAAACTATATTCATTT
5371	GAAAATAAAACTATATTCATTTC
5372	AAAATAAAACTATATTCATTTCC
5373	AAATAAAACTATATTCATTTCCA
5374	AATAAAACTATATTCATTTCCAC
5375	ATAAAACTATATTCATTTCCACT
5376	TAAAACTATATTCATTTCCACTC
5377	AAAACTATATTCATTTCCACTCT
5378	AAACTATATTCATTTCCACTCTA
5379	AACTATATTCATTTCCACTCTAA
5380	ACTATATTCATTTCCACTCTAAA
5381	CTATATTCATTTCCACTCTAAAA
5382	TATATTCATTTCCACTCTAAAAA
5383	ATATTCATTTCCACTCTAAAAAA
5384	TATTCATTTCCACTCTAAAAAAA
5385	ATTCATTTCCACTCTAAAAAAAA

ID	SEQUENCE
1	TTTCCAGATTGGGGCTCGGGCCG
2	TTCCAGATTGGGGCTCGGGCCGC
3	GCCGCGCCTCCTCCGGGACCCTC
4	CCGCGCCTCCTCCGGGACCCTCC
5	CGCGCCTCCTCCGGGACCCTCCC
6	GCGCCTCCTCCGGGACCCTCCCC
7	CGCCTCCTCCGGGACCCTCCCCT
8	GCCTCCTCCGGGACCCTCCCCTT
9	CCTCCTCCGGGACCCTCCCCTTG
10	CTCCTCCGGGACCCTCCCCTTGG
11	TCCTCCGGGACCCTCCCCTTGGA
12	CCTCCGGGACCCTCCCCTTGGAC
13	CTCCGGGACCCTCCCCTTGGACC
14	TCCGGGACCCTCCCCTTGGACCG
15	CCGGGACCCTCCCCTTGGACCGA
16	CGGGACCCTCCCCTTGGACCGAG
17	GGGACCCTCCCCTTGGACCGAGC
18	GGACCCTCCCCTTGGACCGAGCC
19	GACCCTCCCCTTGGACCGAGCCG
20	ACCCTCCCCTTGGACCGAGCCGA
21	CCCTCCCCTTGGACCGAGCCGAT
22	CCTCCCCTTGGACCGAGCCGATC
23	CTCCCCTTGGACCGAGCCGATCG
24	TCCCCTTGGACCGAGCCGATCGC
25	CCCCTTGGACCGAGCCGATCGCC
26	CCCTTGGACCGAGCCGATCGCCG
27	CCTTGGACCGAGCCGATCGCCGC
28	CTTGGACCGAGCCGATCGCCGCG
29	TTGGACCGAGCCGATCGCCGCGG
30	GGGCCGGCTGTCCTGGCGCGAAA
31	GGCCGGCTGTCCTGGCGCGAAAA
32	GCCGGCTGTCCTGGCGCGAAAAG
33	CCGGCTGTCCTGGCGCGAAAAGG
34	CGGCTGTCCTGGCGCGAAAAGGT
35	GGCTGTCCTGGCGCGAAAAGGTG
36	GCTGTCCTGGCGCGAAAAGGTGG
37	CTGTCCTGGCGCGAAAAGGTGGA
38	TGTCCTGGCGCGAAAAGGTGGAC
39	GTCCTGGCGCGAAAAGGTGGACA
40	TCCTGGCGCGAAAAGGTGGACAA
41	CCTGGCGCGAAAAGGTGGACAAG
42	CTGGCGCGAAAAGGTGGACAAGT
43	TGGCGCGAAAAGGTGGACAAGTC
44	GGCGCGAAAAGGTGGACAAGTCC
45	GCGCGAAAAGGTGGACAAGTCCT
46	CGCGAAAAGGTGGACAAGTCCTA
47	GCGAAAAGGTGGACAAGTCCTAT
48	CGAAAAGGTGGACAAGTCCTATT

ID	SEQUENCE
49	GAAAAGGTGGACAAGTCCTATTT
50	AAAAGGTGGACAAGTCCTATTTT
51	AAAGGTGGACAAGTCCTATTTTC
52	AAGGTGGACAAGTCCTATTTTCA
53	AGGTGGACAAGTCCTATTTTCAA
54	GGTGGACAAGTCCTATTTTCAAG
55	GTGGACAAGTCCTATTTTCAAGA
56	TGGACAAGTCCTATTTTCAAGAG
57	GGACAAGTCCTATTTTCAAGAGA
58	GACAAGTCCTATTTTCAAGAGAA
59	ATGACTTTTAACAGTTTTGAAGG
60	TGACTTTTAACAGTTTTGAAGGA
61	GACTTTTAACAGTTTTGAAGGAT
62	ACTTTTAACAGTTTTGAAGGATC
63	CTTTTAACAGTTTTGAAGGATCT
64	TTTTAACAGTTTTGAAGGATCTA
65	TTTAACAGTTTTGAAGGATCTAA
66	TTAACAGTTTTGAAGGATCTAAA
67	TAACAGTTTTGAAGGATCTAAAA
68	AACAGTTTTGAAGGATCTAAAAC
69	ACAGTTTTGAAGGATCTAAAACT
70	CAGTTTTGAAGGATCTAAAACTT
71	AGTTTTGAAGGATCTAAAACTTG
72	GTTTTGAAGGATCTAAAACTTGT
73	TTTTGAAGGATCTAAAACTTGTG
74	TTTGAAGGATCTAAAACTTGTGT
75	TTGAAGGATCTAAAACTTGTGTA
76	TGAAGGATCTAAAACTTGTGTAC
77	GAAGGATCTAAAACTTGTGTACC
78	AAGGATCTAAAACTTGTGTACCT
79	AGGATCTAAAACTTGTGTACCTG
80	GGATCTAAAACTTGTGTACCTGC
81	GATCTAAAACTTGTGTACCTGCA
82	ATCTAAAACTTGTGTACCTGCAG
83	TCTAAAACTTGTGTACCTGCAGA
84	CTAAAACTTGTGTACCTGCAGAC
85	TAAAACTTGTGTACCTGCAGACA
86	AAAACTTGTGTACCTGCAGACAT
87	AAACTTGTGTACCTGCAGACATC
88	AACTTGTGTACCTGCAGACATCA
89	ACTTGTGTACCTGCAGACATCAA
90	CTTGTGTACCTGCAGACATCAAT
91	TTGTGTACCTGCAGACATCAATA
92	TGTGTACCTGCAGACATCAATAA
93	GTGTACCTGCAGACATCAATAAG
94	TGTACCTGCAGACATCAATAAGG
95	GTACCTGCAGACATCAATAAGGA
96	TACCTGCAGACATCAATAAGGAA

Fig. 29 cont'd (Sheet 2 of 170)

ID	SEQUENCE
97	ACCTGCAGACATCAATAAGGAAG
98	CCTGCAGACATCAATAAGGAAGA
99	CTGCAGACATCAATAAGGAAGAA
100	TGCAGACATCAATAAGGAAGAAG
101	GCAGACATCAATAAGGAAGAAGA
102	CAGACATCAATAAGGAAGAAGAA
103	AGACATCAATAAGGAAGAAGAAT
104	GACATCAATAAGGAAGAAGAATT
105	ACATCAATAAGGAAGAAGAATTT
106	CATCAATAAGGAAGAAGAATTTG
107	ATCAATAAGGAAGAAGAATTTGT
108	TCAATAAGGAAGAAGAATTTGTA
109	CAATAAGGAAGAAGAATTTGTAG
110	AATAAGGAAGAAGAATTTGTAGA
111	ATAAGGAAGAAGAATTTGTAGAA
112	TAAGGAAGAAGAATTTGTAGAAG
113	AAGGAAGAAGAATTTGTAGAAGA
114	AGGAAGAAGAATTTGTAGAAGAG
115	GGAAGAAGAATTTGTAGAAGAGT
116	GAAGAAGAATTTGTAGAAGAGTT
117	AAGAAGAATTTGTAGAAGAGTTT
118	AGAAGAATTTGTAGAAGAGTTTA
119	GAAGAATTTGTAGAAGAGTTTAA
120	AAGAATTTGTAGAAGAGTTTAAT
121	AGAATTTGTAGAAGAGTTTAATA
122	GAATTTGTAGAAGAGTTTAATAG
123	AATTTGTAGAAGAGTTTAATAGA
124	ATTTGTAGAAGAGTTTAATAGAT
125	TTTGTAGAAGAGTTTAATAGATT
126	TTGTAGAAGAGTTTAATAGATTA
127	TGTAGAAGAGTTTAATAGATTAA
128	GTAGAAGAGTTTAATAGATTAAA
129	TAGAAGAGTTTAATAGATTAAAA
130	AGAAGAGTTTAATAGATTAAAAA
131	GAAGAGTTTAATAGATTAAAAAC
132	AAGAGTTTAATAGATTAAAAACT
133	AGAGTTTAATAGATTAAAAACTT
134	GAGTTTAATAGATTAAAAACTTT
135	AGTTTAATAGATTAAAAACTTTT
136	GTTTAATAGATTAAAAACTTTTG
137	TTTAATAGATTAAAAACTTTTGC
138	TTAATAGATTAAAAACTTTTGCT
139	TAATAGATTAAAAACTTTTGCTA
140	AATAGATTAAAAACTTTTGCTAA
141	ATAGATTAAAAACTTTTGCTAAT
142	TAGATTAAAAACTTTTGCTAATT
143	AGATTAAAAACTTTTGCTAATTT
144	GATTAAAAACTTTTGCTAATTTT

Fig. 29 cont'd (Sheet 3 of 170)

ID	SEQUENCE
145	ATTAAAAACTTTTGCTAATTTTC
146	TTAAAAACTTTTGCTAATTTTCC
147	TAAAAACTTTTGCTAATTTTCCA
148	AAAAACTTTTGCTAATTTTCCAA
149	AAAACTTTTGCTAATTTTCCAAG
150	AAACTTTTGCTAATTTTCCAAGT
151	AACTTTTGCTAATTTTCCAAGTG
152	ACTTTTGCTAATTTTCCAAGTGG
153	CTTTTGCTAATTTTCCAAGTGGT
154	TTTTGCTAATTTTCCAAGTGGTA
155	TTTGCTAATTTTCCAAGTGGTAG
156	TTGCTAATTTTCCAAGTGGTAGT
157	TGCTAATTTTCCAAGTGGTAGTC
158	GCTAATTTTCCAAGTGGTAGTCC
159	CTAATTTTCCAAGTGGTAGTCCT
160	TAATTTTCCAAGTGGTAGTCCTG
161	AATTTTCCAAGTGGTAGTCCTGT
162	ATTTTCCAAGTGGTAGTCCTGTT
163	TTTTCCAAGTGGTAGTCCTGTTT
164	TTTCCAAGTGGTAGTCCTGTTTC
165	TTCCAAGTGGTAGTCCTGTTTCA
166	TCCAAGTGGTAGTCCTGTTTCAG
167	CCAAGTGGTAGTCCTGTTTCAGC
168	CAAGTGGTAGTCCTGTTTCAGCA
169	AAGTGGTAGTCCTGTTTCAGCAT
170	AGTGGTAGTCCTGTTTCAGCATC
171	GTGGTAGTCCTGTTTCAGCATCA
172	TGGTAGTCCTGTTTCAGCATCAA
173	GGTAGTCCTGTTTCAGCATCAAC
174	GTAGTCCTGTTTCAGCATCAACA
175	TAGTCCTGTTTCAGCATCAACAC
176	AGTCCTGTTTCAGCATCAACACT
177	GTCCTGTTTCAGCATCAACACTG
178	TCCTGTTTCAGCATCAACACTGG
179	CCTGTTTCAGCATCAACACTGGC
180	CTGTTTCAGCATCAACACTGGCA
181	TGTTTCAGCATCAACACTGGCAC
182	GTTTCAGCATCAACACTGGCACG
183	TTTCAGCATCAACACTGGCACGA
184	TTCAGCATCAACACTGGCACGAG
185	TCAGCATCAACACTGGCACGAGC
186	CAGCATCAACACTGGCACGAGCA
187	AGCATCAACACTGGCACGAGCAG
188	GCATCAACACTGGCACGAGCAGG
189	CATCAACACTGGCACGAGCAGGG
190	ATCAACACTGGCACGAGCAGGGT
191	TCAACACTGGCACGAGCAGGGTT
192	CAACACTGGCACGAGCAGGGTTT

Fig. 29 cont'd (Sheet 4 of 170)

ID	SEQUENCE
193	AACACTGGCACGAGCAGGGTTTC
194	ACACTGGCACGAGCAGGGTTTCT
195	CACTGGCACGAGCAGGGTTTCTT
196	ACTGGCACGAGCAGGGTTTCTTT
197	CTGGCACGAGCAGGGTTTCTTTA
198	TGGCACGAGCAGGGTTTCTTTAT
199	GGCACGAGCAGGGTTTCTTTATA
200	GCACGAGCAGGGTTTCTTTATAC
201	CACGAGCAGGGTTTCTTTATACT
202	ACGAGCAGGGTTTCTTTATACTG
203	CGAGCAGGGTTTCTTTATACTGG
204	GAGCAGGGTTTCTTTATACTGGT
205	AGCAGGGTTTCTTTATACTGGTG
206	GCAGGGTTTCTTTATACTGGTGA
207	CAGGGTTTCTTTATACTGGTGAA
208	AGGGTTTCTTTATACTGGTGAAG
209	GGGTTTCTTTATACTGGTGAAGG
210	GGTTTCTTTATACTGGTGAAGGA
211	GTTTCTTTATACTGGTGAAGGAG
212	TTTCTTTATACTGGTGAAGGAGA
213	TTCTTTATACTGGTGAAGGAGAT
214	TCTTTATACTGGTGAAGGAGATA
215	CTTTATACTGGTGAAGGAGATAC
216	TTTATACTGGTGAAGGAGATACC
217	TTATACTGGTGAAGGAGATACCG
218	TATACTGGTGAAGGAGATACCGT
219	ATACTGGTGAAGGAGATACCGTG
220	TACTGGTGAAGGAGATACCGTGC
221	ACTGGTGAAGGAGATACCGTGCG
222	CTGGTGAAGGAGATACCGTGCGG
223	TGGTGAAGGAGATACCGTGCGGT
224	GGTGAAGGAGATACCGTGCGGTG
225	GTGAAGGAGATACCGTGCGGTGC
226	TGAAGGAGATACCGTGCGGTGCT
227	GAAGGAGATACCGTGCGGTGCTT
228	AAGGAGATACCGTGCGGTGCTTT
229	AGGAGATACCGTGCGGTGCTTTA
230	GGAGATACCGTGCGGTGCTTTAG
231	GAGATACCGTGCGGTGCTTTAGT
232	AGATACCGTGCGGTGCTTTAGTT
233	GATACCGTGCGGTGCTTTAGTTG
234	ATACCGTGCGGTGCTTTAGTTGT
235	TACCGTGCGGTGCTTTAGTTGTC
236	ACCGTGCGGTGCTTTAGTTGTCA
237	CCGTGCGGTGCTTTAGTTGTCAT
238	CGTGCGGTGCTTTAGTTGTCATG
239	GTGCGGTGCTTTAGTTGTCATGC
240	TGCGGTGCTTTAGTTGTCATGCA

Fig. 29 cont'd (Sheet 5 of 170)

ID	SEQUENCE
241	GCGGTGCTTTAGTTGTCATGCAG
242	CGGTGCTTTAGTTGTCATGCAGC
243	GGTGCTTTAGTTGTCATGCAGCT
244	GTGCTTTAGTTGTCATGCAGCTG
245	TGCTTTAGTTGTCATGCAGCTGT
246	GCTTTAGTTGTCATGCAGCTGTA
247	CTTTAGTTGTCATGCAGCTGTAG
248	TTTAGTTGTCATGCAGCTGTAGA
249	TTAGTTGTCATGCAGCTGTAGAT
250	TAGTTGTCATGCAGCTGTAGATA
251	AGTTGTCATGCAGCTGTAGATAG
252	GTTGTCATGCAGCTGTAGATAGA
253	TTGTCATGCAGCTGTAGATAGAT
254	TGTCATGCAGCTGTAGATAGATG
255	GTCATGCAGCTGTAGATAGATGG
256	TCATGCAGCTGTAGATAGATGGC
257	CATGCAGCTGTAGATAGATGGCA
258	ATGCAGCTGTAGATAGATGGCAA
259	TGCAGCTGTAGATAGATGGCAAT
260	GCAGCTGTAGATAGATGGCAATA
261	CAGCTGTAGATAGATGGCAATAT
262	AGCTGTAGATAGATGGCAATATG
263	GCTGTAGATAGATGGCAATATGG
264	CTGTAGATAGATGGCAATATGGA
265	TGTAGATAGATGGCAATATGGAG
266	GTAGATAGATGGCAATATGGAGA
267	TAGATAGATGGCAATATGGAGAC
268	AGATAGATGGCAATATGGAGACT
269	GATAGATGGCAATATGGAGACTC
270	ATAGATGGCAATATGGAGACTCA
271	TAGATGGCAATATGGAGACTCAG
272	AGATGGCAATATGGAGACTCAGC
273	GATGGCAATATGGAGACTCAGCA
274	ATGGCAATATGGAGACTCAGCAG
275	TGGCAATATGGAGACTCAGCAGT
276	GGCAATATGGAGACTCAGCAGTT
277	GCAATATGGAGACTCAGCAGTTG
278	CAATATGGAGACTCAGCAGTTGG
279	AATATGGAGACTCAGCAGTTGGA
280	ATATGGAGACTCAGCAGTTGGAA
281	TATGGAGACTCAGCAGTTGGAAG
282	ATGGAGACTCAGCAGTTGGAAGA
283	TGGAGACTCAGCAGTTGGAAGAC
284	GGAGACTCAGCAGTTGGAAGACA
285	GAGACTCAGCAGTTGGAAGACAC
286	AGACTCAGCAGTTGGAAGACACA
287	GACTCAGCAGTTGGAAGACACAG
288	ACTCAGCAGTTGGAAGACACAGG

Fig. 29 cont'd (Sheet 6 of 170)

ID	SEQUENCE
289	CTCAGCAGTTGGAAGACACAGGA
290	TCAGCAGTTGGAAGACACAGGAA
291	CAGCAGTTGGAAGACACAGGAAA
292	AGCAGTTGGAAGACACAGGAAAG
293	GCAGTTGGAAGACACAGGAAAGT
294	CAGTTGGAAGACACAGGAAAGTA
295	AGTTGGAAGACACAGGAAAGTAT
296	GTTGGAAGACACAGGAAAGTATC
297	TTGGAAGACACAGGAAAGTATCC
298	TGGAAGACACAGGAAAGTATCCC
299	GGAAGACACAGGAAAGTATCCCC
300	GAAGACACAGGAAAGTATCCCCA
301	AAGACACAGGAAAGTATCCCCAA
302	AGACACAGGAAAGTATCCCCAAA
303	GACACAGGAAAGTATCCCCAAAT
304	ACACAGGAAAGTATCCCCAAATT
305	CACAGGAAAGTATCCCCAAATTG
306	ACAGGAAAGTATCCCCAAATTGC
307	CAGGAAAGTATCCCCAAATTGCA
308	AGGAAAGTATCCCCAAATTGCAG
309	GGAAAGTATCCCCAAATTGCAGA
310	GAAAGTATCCCCAAATTGCAGAT
311	AAAGTATCCCCAAATTGCAGATT
312	AAGTATCCCCAAATTGCAGATTT
313	AGTATCCCCAAATTGCAGATTTA
314	GTATCCCCAAATTGCAGATTTAT
315	TATCCCCAAATTGCAGATTTATC
316	ATCCCCAAATTGCAGATTTATCA
317	TCCCCAAATTGCAGATTTATCAA
318	CCCCAAATTGCAGATTTATCAAC
319	CCCAAATTGCAGATTTATCAACG
320	CCAAATTGCAGATTTATCAACGG
321	CAAATTGCAGATTTATCAACGGC
322	AAATTGCAGATTTATCAACGGCT
323	AATTGCAGATTTATCAACGGCTT
324	ATTGCAGATTTATCAACGGCTTT
325	TTGCAGATTTATCAACGGCTTTT
326	TGCAGATTTATCAACGGCTTTTA
327	GCAGATTTATCAACGGCTTTTAT
328	CAGATTTATCAACGGCTTTTATC
329	AGATTTATCAACGGCTTTTATCT
330	GATTTATCAACGGCTTTTATCTT
331	ATTTATCAACGGCTTTTATCTTG
332	TTTATCAACGGCTTTTATCTTGA
333	TTATCAACGGCTTTTATCTTGAA
334	TATCAACGGCTTTTATCTTGAAA
335	ATCAACGGCTTTTATCTTGAAAA
336	TCAACGGCTTTTATCTTGAAAAT

Fig. 29 cont'd (Sheet 7 of 170)

ID	SEQUENCE
337	CAACGGCTTTTATCTTGAAAATA
338	AACGGCTTTTATCTTGAAAATAG
339	ACGGCTTTTATCTTGAAAATAGT
340	CGGCTTTTATCTTGAAAATAGTG
341	GGCTTTTATCTTGAAAATAGTGC
342	GCTTTTATCTTGAAAATAGTGCC
343	CTTTTATCTTGAAAATAGTGCCA
344	TTTTATCTTGAAAATAGTGCCAC
345	TTTATCTTGAAAATAGTGCCACG
346	TTATCTTGAAAATAGTGCCACGC
347	TATCTTGAAAATAGTGCCACGCA
348	ATCTTGAAAATAGTGCCACGCAG
349	TCTTGAAAATAGTGCCACGCAGT
350	CTTGAAAATAGTGCCACGCAGTC
351	TTGAAAATAGTGCCACGCAGTCT
352	TGAAAATAGTGCCACGCAGTCTA
353	GAAAATAGTGCCACGCAGTCTAC
354	AAAATAGTGCCACGCAGTCTACA
355	AAATAGTGCCACGCAGTCTACAA
356	AATAGTGCCACGCAGTCTACAAA
357	ATAGTGCCACGCAGTCTACAAAT
358	TAGTGCCACGCAGTCTACAAATT
359	AGTGCCACGCAGTCTACAAATTC
360	GTGCCACGCAGTCTACAAATTCT
361	TGCCACGCAGTCTACAAATTCTG
362	GCCACGCAGTCTACAAATTCTGG
363	CCACGCAGTCTACAAATTCTGGT
364	CACGCAGTCTACAAATTCTGGTA
365	ACGCAGTCTACAAATTCTGGTAT
366	CGCAGTCTACAAATTCTGGTATC
367	GCAGTCTACAAATTCTGGTATCC
368	CAGTCTACAAATTCTGGTATCCA
369	AGTCTACAAATTCTGGTATCCAG
370	GTCTACAAATTCTGGTATCCAGA
371	TCTACAAATTCTGGTATCCAGAA
372	CTACAAATTCTGGTATCCAGAAT
373	TACAAATTCTGGTATCCAGAATG
374	ACAAATTCTGGTATCCAGAATGG
375	CAAATTCTGGTATCCAGAATGGT
376	AAATTCTGGTATCCAGAATGGTC
377	AATTCTGGTATCCAGAATGGTCA
378	ATTCTGGTATCCAGAATGGTCAG
379	TTCTGGTATCCAGAATGGTCAGT
380	TCTGGTATCCAGAATGGTCAGTA
381	CTGGTATCCAGAATGGTCAGTAC
382	TGGTATCCAGAATGGTCAGTACA
383	GGTATCCAGAATGGTCAGTACAA
384	GTATCCAGAATGGTCAGTACAAA

Fig. 29 cont'd (Sheet 8 of 170)

ID	SEQUENCE
385	TATCCAGAATGGTCAGTACAAAG
386	ATCCAGAATGGTCAGTACAAAGT
387	TCCAGAATGGTCAGTACAAAGTT
388	CCAGAATGGTCAGTACAAAGTTG
389	CAGAATGGTCAGTACAAAGTTGA
390	AGAATGGTCAGTACAAAGTTGAA
391	GAATGGTCAGTACAAAGTTGAAA
392	AATGGTCAGTACAAAGTTGAAAA
393	ATGGTCAGTACAAAGTTGAAAAC
394	TGGTCAGTACAAAGTTGAAAACT
395	GGTCAGTACAAAGTTGAAAACTA
396	GTCAGTACAAAGTTGAAAACTAT
397	TCAGTACAAAGTTGAAAACTATC
398	CAGTACAAAGTTGAAAACTATCT
399	AGTACAAAGTTGAAAACTATCTG
400	GTACAAAGTTGAAAACTATCTGG
401	TACAAAGTTGAAAACTATCTGGG
402	ACAAAGTTGAAAACTATCTGGGA
403	CAAAGTTGAAAACTATCTGGGAA
404	AAAGTTGAAAACTATCTGGGAAG
405	AAGTTGAAAACTATCTGGGAAGC
406	AGTTGAAAACTATCTGGGAAGCA
407	GTTGAAAACTATCTGGGAAGCAG
408	TTGAAAACTATCTGGGAAGCAGA
409	TGAAAACTATCTGGGAAGCAGAG
410	GAAAACTATCTGGGAAGCAGAGA
411	AAAACTATCTGGGAAGCAGAGAT
412	AAACTATCTGGGAAGCAGAGATC
413	AACTATCTGGGAAGCAGAGATCA
414	ACTATCTGGGAAGCAGAGATCAT
415	CTATCTGGGAAGCAGAGATCATT
416	TATCTGGGAAGCAGAGATCATTT
417	ATCTGGGAAGCAGAGATCATTTT
418	TCTGGGAAGCAGAGATCATTTTG
419	CTGGGAAGCAGAGATCATTTTGC
420	TGGGAAGCAGAGATCATTTTGCC
421	GGGAAGCAGAGATCATTTTGCCT
422	GGAAGCAGAGATCATTTTGCCTT
423	GAAGCAGAGATCATTTTGCCTTA
424	AAGCAGAGATCATTTTGCCTTAG
425	AGCAGAGATCATTTTGCCTTAGA
426	GCAGAGATCATTTTGCCTTAGAC
427	CAGAGATCATTTTGCCTTAGACA
428	AGAGATCATTTTGCCTTAGACAG
429	GAGATCATTTTGCCTTAGACAGG
430	AGATCATTTTGCCTTAGACAGGC
431	GATCATTTTGCCTTAGACAGGCC
432	ATCATTTTGCCTTAGACAGGCCA

Fig. 29 cont'd (Sheet 9 of 170)

ID	SEQUENCE
433	TCATTTTGCCTTAGACAGGCCAT
434	CATTTTGCCTTAGACAGGCCATC
435	ATTTTGCCTTAGACAGGCCATCT
436	TTTTGCCTTAGACAGGCCATCTG
437	TTTGCCTTAGACAGGCCATCTGA
438	TTGCCTTAGACAGGCCATCTGAG
439	TGCCTTAGACAGGCCATCTGAGA
440	GCCTTAGACAGGCCATCTGAGAC
441	CCTTAGACAGGCCATCTGAGACA
442	CTTAGACAGGCCATCTGAGACAC
443	TTAGACAGGCCATCTGAGACACA
444	TAGACAGGCCATCTGAGACACAT
445	AGACAGGCCATCTGAGACACATG
446	GACAGGCCATCTGAGACACATGC
447	ACAGGCCATCTGAGACACATGCA
448	CAGGCCATCTGAGACACATGCAG
449	AGGCCATCTGAGACACATGCAGA
450	GGCCATCTGAGACACATGCAGAC
451	GCCATCTGAGACACATGCAGACT
452	CCATCTGAGACACATGCAGACTA
453	CATCTGAGACACATGCAGACTAT
454	ATCTGAGACACATGCAGACTATC
455	TCTGAGACACATGCAGACTATCT
456	CTGAGACACATGCAGACTATCTT
457	TGAGACACATGCAGACTATCTTT
458	GAGACACATGCAGACTATCTTTT
459	AGACACATGCAGACTATCTTTTG
460	GACACATGCAGACTATCTTTTGA
461	ACACATGCAGACTATCTTTTGAG
462	CACATGCAGACTATCTTTTGAGA
463	ACATGCAGACTATCTTTTGAGAA
464	CATGCAGACTATCTTTTGAGAAC
465	ATGCAGACTATCTTTTGAGAACT
466	TGCAGACTATCTTTTGAGAACTG
467	GCAGACTATCTTTTGAGAACTGG
468	CAGACTATCTTTTGAGAACTGGG
469	AGACTATCTTTTGAGAACTGGGC
470	GACTATCTTTTGAGAACTGGGCA
471	ACTATCTTTTGAGAACTGGGCAG
472	CTATCTTTTGAGAACTGGGCAGG
473	TATCTTTTGAGAACTGGGCAGGT
474	ATCTTTTGAGAACTGGGCAGGTT
475	TCTTTTGAGAACTGGGCAGGTTG
476	CTTTTGAGAACTGGGCAGGTTGT
477	TTTTGAGAACTGGGCAGGTTGTA
478	TTTGAGAACTGGGCAGGTTGTAG
479	TTGAGAACTGGGCAGGTTGTAGA
480	TGAGAACTGGGCAGGTTGTAGAT

Fig. 29 cont'd (Sheet 10 of 170)

ID	SEQUENCE
481	GAGAACTGGGCAGGTTGTAGATA
482	AGAACTGGGCAGGTTGTAGATAT
483	GAACTGGGCAGGTTGTAGATATA
484	AACTGGGCAGGTTGTAGATATAT
485	ACTGGGCAGGTTGTAGATATATC
486	CTGGGCAGGTTGTAGATATATCA
487	TGGGCAGGTTGTAGATATATCAG
488	GGGCAGGTTGTAGATATATCAGA
489	GGCAGGTTGTAGATATATCAGAC
490	GCAGGTTGTAGATATATCAGACA
491	CAGGTTGTAGATATATCAGACAC
492	AGGTTGTAGATATATCAGACACC
493	GGTTGTAGATATATCAGACACCA
494	GTTGTAGATATATCAGACACCAT
495	TTGTAGATATATCAGACACCATA
496	TGTAGATATATCAGACACCATAT
497	GTAGATATATCAGACACCATATA
498	TAGATATATCAGACACCATATAC
499	AGATATATCAGACACCATATACC
500	GATATATCAGACACCATATACCC
501	ATATATCAGACACCATATACCCG
502	TATATCAGACACCATATACCCGA
503	ATATCAGACACCATATACCCGAG
504	TATCAGACACCATATACCCGAGG
505	ATCAGACACCATATACCCGAGGA
506	TCAGACACCATATACCCGAGGAA
507	CAGACACCATATACCCGAGGAAC
508	AGACACCATATACCCGAGGAACC
509	GACACCATATACCCGAGGAACCC
510	ACACCATATACCCGAGGAACCCT
511	CACCATATACCCGAGGAACCCTG
512	ACCATATACCCGAGGAACCCTGC
513	CCATATACCCGAGGAACCCTGCC
514	CATATACCCGAGGAACCCTGCCA
515	ATATACCCGAGGAACCCTGCCAT
516	TATACCCGAGGAACCCTGCCATG
517	ATACCCGAGGAACCCTGCCATGT
518	TACCCGAGGAACCCTGCCATGTA
519	ACCCGAGGAACCCTGCCATGTAT
520	CCCGAGGAACCCTGCCATGTATA
521	CCGAGGAACCCTGCCATGTATAG
522	CGAGGAACCCTGCCATGTATAGT
523	GAGGAACCCTGCCATGTATAGTG
524	AGGAACCCTGCCATGTATAGTGA
525	GGAACCCTGCCATGTATAGTGAA
526	GAACCCTGCCATGTATAGTGAAG
527	AACCCTGCCATGTATAGTGAAGA
528	ACCCTGCCATGTATAGTGAAGAA

Fig. 29 cont'd (Sheet 11 of 170)

ID	SEQUENCE
529	CCCTGCCATGTATAGTGAAGAAG
530	CCTGCCATGTATAGTGAAGAAGC
531	CTGCCATGTATAGTGAAGAAGCT
532	TGCCATGTATAGTGAAGAAGCTA
533	GCCATGTATAGTGAAGAAGCTAG
534	CCATGTATAGTGAAGAAGCTAGA
535	CATGTATAGTGAAGAAGCTAGAT
536	ATGTATAGTGAAGAAGCTAGATT
537	TGTATAGTGAAGAAGCTAGATTA
538	GTATAGTGAAGAAGCTAGATTAA
539	TATAGTGAAGAAGCTAGATTAAA
540	ATAGTGAAGAAGCTAGATTAAAG
541	TAGTGAAGAAGCTAGATTAAAGT
542	AGTGAAGAAGCTAGATTAAAGTC
543	GTGAAGAAGCTAGATTAAAGTCC
544	TGAAGAAGCTAGATTAAAGTCCT
545	GAAGAAGCTAGATTAAAGTCCTT
546	AAGAAGCTAGATTAAAGTCCTTT
547	AGAAGCTAGATTAAAGTCCTTTC
548	GAAGCTAGATTAAAGTCCTTTCA
549	AAGCTAGATTAAAGTCCTTTCAG
550	AGCTAGATTAAAGTCCTTTCAGA
551	GCTAGATTAAAGTCCTTTCAGAA
552	CTAGATTAAAGTCCTTTCAGAAC
553	TAGATTAAAGTCCTTTCAGAACT
554	AGATTAAAGTCCTTTCAGAACTG
555	GATTAAAGTCCTTTCAGAACTGG
556	ATTAAAGTCCTTTCAGAACTGGC
557	TTAAAGTCCTTTCAGAACTGGCC
558	TAAAGTCCTTTCAGAACTGGCCA
559	AAAGTCCTTTCAGAACTGGCCAG
560	AAGTCCTTTCAGAACTGGCCAGA
561	AGTCCTTTCAGAACTGGCCAGAC
562	GTCCTTTCAGAACTGGCCAGACT
563	TCCTTTCAGAACTGGCCAGACTA
564	CCTTTCAGAACTGGCCAGACTAT
565	CTTTCAGAACTGGCCAGACTATG
566	TTTCAGAACTGGCCAGACTATGC
567	TTCAGAACTGGCCAGACTATGCT
568	TCAGAACTGGCCAGACTATGCTC
569	CAGAACTGGCCAGACTATGCTCA
570	AGAACTGGCCAGACTATGCTCAC
571	GAACTGGCCAGACTATGCTCACC
572	AACTGGCCAGACTATGCTCACCT
573	ACTGGCCAGACTATGCTCACCTA
574	CTGGCCAGACTATGCTCACCTAA
575	TGGCCAGACTATGCTCACCTAAC
576	GGCCAGACTATGCTCACCTAACC

Fig. 29 cont'd (Sheet 12 of 170)

ID	SEQUENCE
577	GCCAGACTATGCTCACCTAACCC
578	CCAGACTATGCTCACCTAACCCC
579	CAGACTATGCTCACCTAACCCCA
580	AGACTATGCTCACCTAACCCCAA
581	GACTATGCTCACCTAACCCCAAG
582	ACTATGCTCACCTAACCCCAAGA
583	CTATGCTCACCTAACCCCAAGAG
584	TATGCTCACCTAACCCCAAGAGA
585	ATGCTCACCTAACCCCAAGAGAG
586	TGCTCACCTAACCCCAAGAGAGT
587	GCTCACCTAACCCCAAGAGAGTT
588	CTCACCTAACCCCAAGAGAGTTA
589	TCACCTAACCCCAAGAGAGTTAG
590	CACCTAACCCCAAGAGAGTTAGC
591	ACCTAACCCCAAGAGAGTTAGCA
592	CCTAACCCCAAGAGAGTTAGCAA
593	CTAACCCCAAGAGAGTTAGCAAG
594	TAACCCCAAGAGAGTTAGCAAGT
595	AACCCCAAGAGAGTTAGCAAGTG
596	ACCCCAAGAGAGTTAGCAAGTGC
597	CCCCAAGAGAGTTAGCAAGTGCT
598	CCCAAGAGAGTTAGCAAGTGCTG
599	CCAAGAGAGTTAGCAAGTGCTGG
600	CAAGAGAGTTAGCAAGTGCTGGA
601	AAGAGAGTTAGCAAGTGCTGGAC
602	AGAGAGTTAGCAAGTGCTGGACT
603	GAGAGTTAGCAAGTGCTGGACTC
604	AGAGTTAGCAAGTGCTGGACTCT
605	GAGTTAGCAAGTGCTGGACTCTA
606	AGTTAGCAAGTGCTGGACTCTAC
607	GTTAGCAAGTGCTGGACTCTACT
608	TTAGCAAGTGCTGGACTCTACTA
609	TAGCAAGTGCTGGACTCTACTAC
610	AGCAAGTGCTGGACTCTACTACA
611	GCAAGTGCTGGACTCTACTACAC
612	CAAGTGCTGGACTCTACTACACA
613	AAGTGCTGGACTCTACTACACAG
614	AGTGCTGGACTCTACTACACAGG
615	GTGCTGGACTCTACTACACAGGT
616	TGCTGGACTCTACTACACAGGTA
617	GCTGGACTCTACTACACAGGTAT
618	CTGGACTCTACTACACAGGTATT
619	TGGACTCTACTACACAGGTATTG
620	GGACTCTACTACACAGGTATTGG
621	GACTCTACTACACAGGTATTGGT
622	ACTCTACTACACAGGTATTGGTG
623	CTCTACTACACAGGTATTGGTGA
624	TCTACTACACAGGTATTGGTGAC

Fig. 29 cont'd (Sheet 13 of 170)

ID	SEQUENCE
625	CTACTACACAGGTATTGGTGACC
626	TACTACACAGGTATTGGTGACCA
627	ACTACACAGGTATTGGTGACCAA
628	CTACACAGGTATTGGTGACCAAG
629	TACACAGGTATTGGTGACCAAGT
630	ACACAGGTATTGGTGACCAAGTG
631	CACAGGTATTGGTGACCAAGTGC
632	ACAGGTATTGGTGACCAAGTGCA
633	CAGGTATTGGTGACCAAGTGCAG
634	AGGTATTGGTGACCAAGTGCAGT
635	GGTATTGGTGACCAAGTGCAGTG
636	GTATTGGTGACCAAGTGCAGTGC
637	TATTGGTGACCAAGTGCAGTGCT
638	ATTGGTGACCAAGTGCAGTGCTT
639	TTGGTGACCAAGTGCAGTGCTTT
640	TGGTGACCAAGTGCAGTGCTTTT
641	GGTGACCAAGTGCAGTGCTTTTG
642	GTGACCAAGTGCAGTGCTTTTGT
643	TGACCAAGTGCAGTGCTTTTGTT
644	GACCAAGTGCAGTGCTTTTGTTG
645	ACCAAGTGCAGTGCTTTTGTTGT
646	CCAAGTGCAGTGCTTTTGTTGTG
647	CAAGTGCAGTGCTTTTGTTGTGG
648	AAGTGCAGTGCTTTTGTTGTGGT
649	AGTGCAGTGCTTTTGTTGTGGTG
650	GTGCAGTGCTTTTGTTGTGGTGG
651	TGCAGTGCTTTTGTTGTGGTGGA
652	GCAGTGCTTTTGTTGTGGTGGAA
653	CAGTGCTTTTGTTGTGGTGGAAA
654	AGTGCTTTTGTTGTGGTGGAAAA
655	GTGCTTTTGTTGTGGTGGAAAAC
656	TGCTTTTGTTGTGGTGGAAAACT
657	GCTTTTGTTGTGGTGGAAAACTG
658	CTTTTGTTGTGGTGGAAAACTGA
659	TTTTGTTGTGGTGGAAAACTGAA
660	TTTGTTGTGGTGGAAAACTGAAA
661	TTGTTGTGGTGGAAAACTGAAAA
662	TGTTGTGGTGGAAAACTGAAAAA
663	GTTGTGGTGGAAAACTGAAAAAT
664	TTGTGGTGGAAAACTGAAAAATT
665	TGTGGTGGAAAACTGAAAAATTG
666	GTGGTGGAAAACTGAAAAATTGG
667	TGGTGGAAAACTGAAAAATTGGG
668	GGTGGAAAACTGAAAAATTGGGA
669	GTGGAAAACTGAAAAATTGGGAA
670	TGGAAAACTGAAAAATTGGGAAC
671	GGAAAACTGAAAAATTGGGAACC
672	GAAAACTGAAAAATTGGGAACCT

Fig. 29 cont'd (Sheet 14 of 170)

ID	SEQUENCE
673	AAAACTGAAAAATTGGGAACCTT
674	AAACTGAAAAATTGGGAACCTTG
675	AACTGAAAAATTGGGAACCTTGT
676	ACTGAAAAATTGGGAACCTTGTG
677	CTGAAAAATTGGGAACCTTGTGA
678	TGAAAAATTGGGAACCTTGTGAT
679	GAAAAATTGGGAACCTTGTGATC
680	AAAAATTGGGAACCTTGTGATCG
681	AAAATTGGGAACCTTGTGATCGT
682	AAATTGGGAACCTTGTGATCGTG
683	AATTGGGAACCTTGTGATCGTGC
684	ATTGGGAACCTTGTGATCGTGCC
685	TTGGGAACCTTGTGATCGTGCCT
686	TGGGAACCTTGTGATCGTGCCTG
687	GGGAACCTTGTGATCGTGCCTGG
688	GGAACCTTGTGATCGTGCCTGGT
689	GAACCTTGTGATCGTGCCTGGTC
690	AACCTTGTGATCGTGCCTGGTCA
691	ACCTTGTGATCGTGCCTGGTCAG
692	CCTTGTGATCGTGCCTGGTCAGA
693	CTTGTGATCGTGCCTGGTCAGAA
694	TTGTGATCGTGCCTGGTCAGAAC
695	TGTGATCGTGCCTGGTCAGAACA
696	GTGATCGTGCCTGGTCAGAACAC
697	TGATCGTGCCTGGTCAGAACACA
698	GATCGTGCCTGGTCAGAACACAG
699	ATCGTGCCTGGTCAGAACACAGG
700	TCGTGCCTGGTCAGAACACAGGC
701	CGTGCCTGGTCAGAACACAGGCG
702	GTGCCTGGTCAGAACACAGGCGA
703	TGCCTGGTCAGAACACAGGCGAC
704	GCCTGGTCAGAACACAGGCGACA
705	CCTGGTCAGAACACAGGCGACAC
706	CTGGTCAGAACACAGGCGACACT
707	TGGTCAGAACACAGGCGACACTT
708	GGTCAGAACACAGGCGACACTTT
709	GTCAGAACACAGGCGACACTTTC
710	TCAGAACACAGGCGACACTTTCC
711	CAGAACACAGGCGACACTTTCCT
712	AGAACACAGGCGACACTTTCCTA
713	GAACACAGGCGACACTTTCCTAA
714	AACACAGGCGACACTTTCCTAAT
715	ACACAGGCGACACTTTCCTAATT
716	CACAGGCGACACTTTCCTAATTG
717	ACAGGCGACACTTTCCTAATTGC
718	CAGGCGACACTTTCCTAATTGCT
719	AGGCGACACTTTCCTAATTGCTT
720	GGCGACACTTTCCTAATTGCTTC

Fig. 29 cont'd (Sheet 15 of 170)

ID	SEQUENCE
721	GCGACACTTTCCTAATTGCTTCT
722	CGACACTTTCCTAATTGCTTCTT
723	GACACTTTCCTAATTGCTTCTTT
724	ACACTTTCCTAATTGCTTCTTTG
725	CACTTTCCTAATTGCTTCTTTGT
726	ACTTTCCTAATTGCTTCTTTGTT
727	CTTTCCTAATTGCTTCTTTGTTT
728	TTTCCTAATTGCTTCTTTGTTTT
729	TTCCTAATTGCTTCTTTGTTTTG
730	TCCTAATTGCTTCTTTGTTTTGG
731	CCTAATTGCTTCTTTGTTTTGGG
732	CTAATTGCTTCTTTGTTTTGGGC
733	TAATTGCTTCTTTGTTTTGGGCC
734	AATTGCTTCTTTGTTTTGGGCCG
735	ATTGCTTCTTTGTTTTGGGCCGG
736	TTGCTTCTTTGTTTTGGGCCGGA
737	TGCTTCTTTGTTTTGGGCCGGAA
738	GCTTCTTTGTTTTGGGCCGGAAT
739	CTTCTTTGTTTTGGGCCGGAATC
740	TTCTTTGTTTTGGGCCGGAATCT
741	TCTTTGTTTTGGGCCGGAATCTT
742	CTTTGTTTTGGGCCGGAATCTTA
743	TTTGTTTTGGGCCGGAATCTTAA
744	TTGTTTTGGGCCGGAATCTTAAT
745	TGTTTTGGGCCGGAATCTTAATA
746	GTTTTGGGCCGGAATCTTAATAT
747	TTTTGGGCCGGAATCTTAATATT
748	TTTGGGCCGGAATCTTAATATTC
749	TTGGGCCGGAATCTTAATATTCG
750	TGGGCCGGAATCTTAATATTCGA
751	GGGCCGGAATCTTAATATTCGAA
752	GGCCGGAATCTTAATATTCGAAG
753	GCCGGAATCTTAATATTCGAAGT
754	CCGGAATCTTAATATTCGAAGTG
755	CGGAATCTTAATATTCGAAGTGA
756	GGAATCTTAATATTCGAAGTGAA
757	GAATCTTAATATTCGAAGTGAAT
758	AATCTTAATATTCGAAGTGAATC
759	ATCTTAATATTCGAAGTGAATCT
760	TCTTAATATTCGAAGTGAATCTG
761	CTTAATATTCGAAGTGAATCTGA
762	TTAATATTCGAAGTGAATCTGAT
763	TAATATTCGAAGTGAATCTGATG
764	AATATTCGAAGTGAATCTGATGC
765	ATATTCGAAGTGAATCTGATGCT
766	TATTCGAAGTGAATCTGATGCTG
767	ATTCGAAGTGAATCTGATGCTGT
768	TTCGAAGTGAATCTGATGCTGTG

Fig. 29 cont'd (Sheet 16 of 170)

ID	SEQUENCE
769	TCGAAGTGAATCTGATGCTGTGA
770	CGAAGTGAATCTGATGCTGTGAG
771	GAAGTGAATCTGATGCTGTGAGT
772	AAGTGAATCTGATGCTGTGAGTT
773	AGTGAATCTGATGCTGTGAGTTC
774	GTGAATCTGATGCTGTGAGTTCT
775	TGAATCTGATGCTGTGAGTTCTG
776	GAATCTGATGCTGTGAGTTCTGA
777	AATCTGATGCTGTGAGTTCTGAT
778	ATCTGATGCTGTGAGTTCTGATA
779	TCTGATGCTGTGAGTTCTGATAG
780	CTGATGCTGTGAGTTCTGATAGG
781	TGATGCTGTGAGTTCTGATAGGA
782	GATGCTGTGAGTTCTGATAGGAA
783	ATGCTGTGAGTTCTGATAGGAAT
784	TGCTGTGAGTTCTGATAGGAATT
785	GCTGTGAGTTCTGATAGGAATTT
786	CTGTGAGTTCTGATAGGAATTTC
787	TGTGAGTTCTGATAGGAATTTCC
788	GTGAGTTCTGATAGGAATTTCCC
789	TGAGTTCTGATAGGAATTTCCCA
790	GAGTTCTGATAGGAATTTCCCAA
791	AGTTCTGATAGGAATTTCCCAAA
792	GTTCTGATAGGAATTTCCCAAAT
793	TTCTGATAGGAATTTCCCAAATT
794	TCTGATAGGAATTTCCCAAATTC
795	CTGATAGGAATTTCCCAAATTCA
796	TGATAGGAATTTCCCAAATTCAA
797	GATAGGAATTTCCCAAATTCAAC
798	ATAGGAATTTCCCAAATTCAACA
799	TAGGAATTTCCCAAATTCAACAA
800	AGGAATTTCCCAAATTCAACAAA
801	GGAATTTCCCAAATTCAACAAAT
802	GAATTTCCCAAATTCAACAAATC
803	AATTTCCCAAATTCAACAAATCT
804	ATTTCCCAAATTCAACAAATCTT
805	TTTCCCAAATTCAACAAATCTTC
806	TTCCCAAATTCAACAAATCTTCC
807	TCCCAAATTCAACAAATCTTCCA
808	CCCAAATTCAACAAATCTTCCAA
809	CCAAATTCAACAAATCTTCCAAG
810	CAAATTCAACAAATCTTCCAAGA
811	AAATTCAACAAATCTTCCAAGAA
812	AATTCAACAAATCTTCCAAGAAA
813	ATTCAACAAATCTTCCAAGAAAT
814	TTCAACAAATCTTCCAAGAAATC
815	TCAACAAATCTTCCAAGAAATCC
816	CAACAAATCTTCCAAGAAATCCA

Fig. 29 cont'd (Sheet 17 of 170)

ID	SEQUENCE
817	AACAAATCTTCCAAGAAATCCAT
818	ACAAATCTTCCAAGAAATCCATC
819	CAAATCTTCCAAGAAATCCATCC
820	AAATCTTCCAAGAAATCCATCCA
821	AATCTTCCAAGAAATCCATCCAT
822	ATCTTCCAAGAAATCCATCCATG
823	TCTTCCAAGAAATCCATCCATGG
824	CTTCCAAGAAATCCATCCATGGC
825	TTCCAAGAAATCCATCCATGGCA
826	TCCAAGAAATCCATCCATGGCAG
827	CCAAGAAATCCATCCATGGCAGA
828	CAAGAAATCCATCCATGGCAGAT
829	AAGAAATCCATCCATGGCAGATT
830	AGAAATCCATCCATGGCAGATTA
831	GAAATCCATCCATGGCAGATTAT
832	AAATCCATCCATGGCAGATTATG
833	AATCCATCCATGGCAGATTATGA
834	ATCCATCCATGGCAGATTATGAA
835	TCCATCCATGGCAGATTATGAAG
836	CCATCCATGGCAGATTATGAAGC
837	CATCCATGGCAGATTATGAAGCA
838	ATCCATGGCAGATTATGAAGCAC
839	TCCATGGCAGATTATGAAGCACG
840	CCATGGCAGATTATGAAGCACGG
841	CATGGCAGATTATGAAGCACGGA
842	ATGGCAGATTATGAAGCACGGAT
843	TGGCAGATTATGAAGCACGGATC
844	GGCAGATTATGAAGCACGGATCT
845	GCAGATTATGAAGCACGGATCTT
846	CAGATTATGAAGCACGGATCTTT
847	AGATTATGAAGCACGGATCTTTA
848	GATTATGAAGCACGGATCTTTAC
849	ATTATGAAGCACGGATCTTTACT
850	TTATGAAGCACGGATCTTTACTT
851	TATGAAGCACGGATCTTTACTTT
852	ATGAAGCACGGATCTTTACTTTT
853	TGAAGCACGGATCTTTACTTTTG
854	GAAGCACGGATCTTTACTTTTGG
855	AAGCACGGATCTTTACTTTTGGG
856	AGCACGGATCTTTACTTTTGGGA
857	GCACGGATCTTTACTTTTGGGAC
858	CACGGATCTTTACTTTTGGGACA
859	ACGGATCTTTACTTTTGGGACAT
860	CGGATCTTTACTTTTGGGACATG
861	GGATCTTTACTTTTGGGACATGG
862	GATCTTTACTTTTGGGACATGGA
863	ATCTTTACTTTTGGGACATGGAT
864	TCTTTACTTTTGGGACATGGATA

Fig. 29 cont'd (Sheet 18 of 170)

ID	SEQUENCE
865	CTTTACTTTTGGGACATGGATAT
866	TTTACTTTTGGGACATGGATATA
867	TTACTTTTGGGACATGGATATAC
868	TACTTTTGGGACATGGATATACT
869	ACTTTTGGGACATGGATATACTC
870	CTTTTGGGACATGGATATACTCA
871	TTTTGGGACATGGATATACTCAG
872	TTTGGGACATGGATATACTCAGT
873	TTGGGACATGGATATACTCAGTT
874	TGGGACATGGATATACTCAGTTA
875	GGGACATGGATATACTCAGTTAA
876	GGACATGGATATACTCAGTTAAC
877	GACATGGATATACTCAGTTAACA
878	ACATGGATATACTCAGTTAACAA
879	CATGGATATACTCAGTTAACAAG
880	ATGGATATACTCAGTTAACAAGG
881	TGGATATACTCAGTTAACAAGGA
882	GGATATACTCAGTTAACAAGGAG
883	GATATACTCAGTTAACAAGGAGC
884	ATATACTCAGTTAACAAGGAGCA
885	TATACTCAGTTAACAAGGAGCAG
886	ATACTCAGTTAACAAGGAGCAGC
887	TACTCAGTTAACAAGGAGCAGCT
888	ACTCAGTTAACAAGGAGCAGCTT
889	CTCAGTTAACAAGGAGCAGCTTG
890	TCAGTTAACAAGGAGCAGCTTGC
891	CAGTTAACAAGGAGCAGCTTGCA
892	AGTTAACAAGGAGCAGCTTGCAA
893	GTTAACAAGGAGCAGCTTGCAAG
894	TTAACAAGGAGCAGCTTGCAAGA
895	TAACAAGGAGCAGCTTGCAAGAG
896	AACAAGGAGCAGCTTGCAAGAGC
897	ACAAGGAGCAGCTTGCAAGAGCT
898	CAAGGAGCAGCTTGCAAGAGCTG
899	AAGGAGCAGCTTGCAAGAGCTGG
900	AGGAGCAGCTTGCAAGAGCTGGA
901	GGAGCAGCTTGCAAGAGCTGGAT
902	GAGCAGCTTGCAAGAGCTGGATT
903	AGCAGCTTGCAAGAGCTGGATTT
904	GCAGCTTGCAAGAGCTGGATTTT
905	CAGCTTGCAAGAGCTGGATTTTA
906	AGCTTGCAAGAGCTGGATTTTAT
907	GCTTGCAAGAGCTGGATTTTATG
908	CTTGCAAGAGCTGGATTTTATGC
909	TTGCAAGAGCTGGATTTTATGCT
910	TGCAAGAGCTGGATTTTATGCTT
911	GCAAGAGCTGGATTTTATGCTTT
912	CAAGAGCTGGATTTTATGCTTTA

Fig. 29 cont'd (Sheet 19 of 170)

ID	SEQUENCE
913	AAGAGCTGGATTTTATGCTTTAG
914	AGAGCTGGATTTTATGCTTTAGG
915	GAGCTGGATTTTATGCTTTAGGT
916	AGCTGGATTTTATGCTTTAGGTG
917	GCTGGATTTTATGCTTTAGGTGA
918	CTGGATTTTATGCTTTAGGTGAA
919	TGGATTTTATGCTTTAGGTGAAG
920	GGATTTTATGCTTTAGGTGAAGG
921	GATTTTATGCTTTAGGTGAAGGT
922	ATTTTATGCTTTAGGTGAAGGTG
923	TTTTATGCTTTAGGTGAAGGTGA
924	TTTATGCTTTAGGTGAAGGTGAT
925	TTATGCTTTAGGTGAAGGTGATA
926	TATGCTTTAGGTGAAGGTGATAA
927	ATGCTTTAGGTGAAGGTGATAAA
928	TGCTTTAGGTGAAGGTGATAAAG
929	GCTTTAGGTGAAGGTGATAAAGT
930	CTTTAGGTGAAGGTGATAAAGTA
931	TTTAGGTGAAGGTGATAAAGTAA
932	TTAGGTGAAGGTGATAAAGTAAA
933	TAGGTGAAGGTGATAAAGTAAAG
934	AGGTGAAGGTGATAAAGTAAAGT
935	GGTGAAGGTGATAAAGTAAAGTG
936	GTGAAGGTGATAAAGTAAAGTGC
937	TGAAGGTGATAAAGTAAAGTGCT
938	GAAGGTGATAAAGTAAAGTGCTT
939	AAGGTGATAAAGTAAAGTGCTTT
940	AGGTGATAAAGTAAAGTGCTTTC
941	GGTGATAAAGTAAAGTGCTTTCA
942	GTGATAAAGTAAAGTGCTTTCAC
943	TGATAAAGTAAAGTGCTTTCACT
944	GATAAAGTAAAGTGCTTTCACTG
945	ATAAAGTAAAGTGCTTTCACTGT
946	TAAAGTAAAGTGCTTTCACTGTG
947	AAAGTAAAGTGCTTTCACTGTGG
948	AAGTAAAGTGCTTTCACTGTGGA
949	AGTAAAGTGCTTTCACTGTGGAG
950	GTAAAGTGCTTTCACTGTGGAGG
951	TAAAGTGCTTTCACTGTGGAGGA
952	AAAGTGCTTTCACTGTGGAGGAG
953	AAGTGCTTTCACTGTGGAGGAGG
954	AGTGCTTTCACTGTGGAGGAGGG
955	GTGCTTTCACTGTGGAGGAGGGC
956	TGCTTTCACTGTGGAGGAGGGCT
957	GCTTTCACTGTGGAGGAGGGCTA
958	CTTTCACTGTGGAGGAGGGCTAA
959	TTTCACTGTGGAGGAGGGCTAAC
960	TTCACTGTGGAGGAGGGCTAACT

Fig. 29 cont'd (Sheet 20 of 170)

ID	SEQUENCE
961	TCACTGTGGAGGAGGGCTAACTG
962	CACTGTGGAGGAGGGCTAACTGA
963	ACTGTGGAGGAGGGCTAACTGAT
964	CTGTGGAGGAGGGCTAACTGATT
965	TGTGGAGGAGGGCTAACTGATTG
966	GTGGAGGAGGGCTAACTGATTGG
967	TGGAGGAGGGCTAACTGATTGGA
968	GGAGGAGGGCTAACTGATTGGAA
969	GAGGAGGGCTAACTGATTGGAAG
970	AGGAGGGCTAACTGATTGGAAGC
971	GGAGGGCTAACTGATTGGAAGCC
972	GAGGGCTAACTGATTGGAAGCCC
973	AGGGCTAACTGATTGGAAGCCCA
974	GGGCTAACTGATTGGAAGCCCAG
975	GGCTAACTGATTGGAAGCCCAGT
976	GCTAACTGATTGGAAGCCCAGTG
977	CTAACTGATTGGAAGCCCAGTGA
978	TAACTGATTGGAAGCCCAGTGAA
979	AACTGATTGGAAGCCCAGTGAAG
980	ACTGATTGGAAGCCCAGTGAAGA
981	CTGATTGGAAGCCCAGTGAAGAC
982	TGATTGGAAGCCCAGTGAAGACC
983	GATTGGAAGCCCAGTGAAGACCC
984	ATTGGAAGCCCAGTGAAGACCCT
985	TTGGAAGCCCAGTGAAGACCCTT
986	TGGAAGCCCAGTGAAGACCCTTG
987	GGAAGCCCAGTGAAGACCCTTGG
988	GAAGCCCAGTGAAGACCCTTGGG
989	AAGCCCAGTGAAGACCCTTGGGA
990	AGCCCAGTGAAGACCCTTGGGAA
991	GCCCAGTGAAGACCCTTGGGAAC
992	CCCAGTGAAGACCCTTGGGAACA
993	CCAGTGAAGACCCTTGGGAACAA
994	CAGTGAAGACCCTTGGGAACAAC
995	AGTGAAGACCCTTGGGAACAACA
996	GTGAAGACCCTTGGGAACAACAT
997	TGAAGACCCTTGGGAACAACATG
998	GAAGACCCTTGGGAACAACATGC
999	AAGACCCTTGGGAACAACATGCT
1000	AGACCCTTGGGAACAACATGCTA
1001	GACCCTTGGGAACAACATGCTAA
1002	ACCCTTGGGAACAACATGCTAAA
1003	CCCTTGGGAACAACATGCTAAAT
1004	CCTTGGGAACAACATGCTAAATG
1005	CTTGGGAACAACATGCTAAATGG
1006	TTGGGAACAACATGCTAAATGGT
1007	TGGGAACAACATGCTAAATGGTA
1008	GGGAACAACATGCTAAATGGTAT

Fig. 29 cont'd (Sheet 21 of 170)

ID	SEQUENCE
1009	GGAACAACATGCTAAATGGTATC
1010	GAACAACATGCTAAATGGTATCC
1011	AACAACATGCTAAATGGTATCCA
1012	ACAACATGCTAAATGGTATCCAG
1013	CAACATGCTAAATGGTATCCAGG
1014	AACATGCTAAATGGTATCCAGGG
1015	ACATGCTAAATGGTATCCAGGGT
1016	CATGCTAAATGGTATCCAGGGTG
1017	ATGCTAAATGGTATCCAGGGTGC
1018	TGCTAAATGGTATCCAGGGTGCA
1019	GCTAAATGGTATCCAGGGTGCAA
1020	CTAAATGGTATCCAGGGTGCAAA
1021	TAAATGGTATCCAGGGTGCAAAT
1022	AAATGGTATCCAGGGTGCAAATA
1023	AATGGTATCCAGGGTGCAAATAT
1024	ATGGTATCCAGGGTGCAAATATC
1025	TGGTATCCAGGGTGCAAATATCT
1026	GGTATCCAGGGTGCAAATATCTG
1027	GTATCCAGGGTGCAAATATCTGT
1028	TATCCAGGGTGCAAATATCTGTT
1029	ATCCAGGGTGCAAATATCTGTTA
1030	TCCAGGGTGCAAATATCTGTTAG
1031	CCAGGGTGCAAATATCTGTTAGA
1032	CAGGGTGCAAATATCTGTTAGAA
1033	AGGGTGCAAATATCTGTTAGAAC
1034	GGGTGCAAATATCTGTTAGAACA
1035	GGTGCAAATATCTGTTAGAACAG
1036	GTGCAAATATCTGTTAGAACAGA
1037	TGCAAATATCTGTTAGAACAGAA
1038	GCAAATATCTGTTAGAACAGAAG
1039	CAAATATCTGTTAGAACAGAAGG
1040	AAATATCTGTTAGAACAGAAGGG
1041	AATATCTGTTAGAACAGAAGGGA
1042	ATATCTGTTAGAACAGAAGGGAC
1043	TATCTGTTAGAACAGAAGGGACA
1044	ATCTGTTAGAACAGAAGGGACAA
1045	TCTGTTAGAACAGAAGGGACAAG
1046	CTGTTAGAACAGAAGGGACAAGA
1047	TGTTAGAACAGAAGGGACAAGAA
1048	GTTAGAACAGAAGGGACAAGAAT
1049	TTAGAACAGAAGGGACAAGAATA
1050	TAGAACAGAAGGGACAAGAATAT
1051	AGAACAGAAGGGACAAGAATATA
1052	GAACAGAAGGGACAAGAATATAT
1053	AACAGAAGGGACAAGAATATATA
1054	ACAGAAGGGACAAGAATATATAA
1055	CAGAAGGGACAAGAATATATAAA
1056	AGAAGGGACAAGAATATATAAAC

Fig. 29 cont'd (Sheet 22 of 170)

ID	SEQUENCE
1057	GAAGGGACAAGAATATATAAACA
1058	AAGGGACAAGAATATATAAACAA
1059	AGGGACAAGAATATATAAACAAT
1060	GGGACAAGAATATATAAACAATA
1061	GGACAAGAATATATAAACAATAT
1062	GACAAGAATATATAAACAATATT
1063	ACAAGAATATATAAACAATATTC
1064	CAAGAATATATAAACAATATTCA
1065	AAGAATATATAAACAATATTCAT
1066	AGAATATATAAACAATATTCATT
1067	GAATATATAAACAATATTCATTT
1068	AATATATAAACAATATTCATTTA
1069	ATATATAAACAATATTCATTTAA
1070	TATATAAACAATATTCATTTAAC
1071	ATATAAACAATATTCATTTAACT
1072	TATAAACAATATTCATTTAACTC
1073	ATAAACAATATTCATTTAACTCA
1074	TAAACAATATTCATTTAACTCAT
1075	AAACAATATTCATTTAACTCATT
1076	AACAATATTCATTTAACTCATTC
1077	ACAATATTCATTTAACTCATTCA
1078	CAATATTCATTTAACTCATTCAC
1079	AATATTCATTTAACTCATTCACT
1080	ATATTCATTTAACTCATTCACTT
1081	TATTCATTTAACTCATTCACTTG
1082	ATTCATTTAACTCATTCACTTGA
1083	TTCATTTAACTCATTCACTTGAG
1084	TCATTTAACTCATTCACTTGAGG
1085	CATTTAACTCATTCACTTGAGGA
1086	ATTTAACTCATTCACTTGAGGAG
1087	TTTAACTCATTCACTTGAGGAGT
1088	TTAACTCATTCACTTGAGGAGTG
1089	TAACTCATTCACTTGAGGAGTGT
1090	AACTCATTCACTTGAGGAGTGTC
1091	ACTCATTCACTTGAGGAGTGTCT
1092	CTCATTCACTTGAGGAGTGTCTG
1093	TCATTCACTTGAGGAGTGTCTGG
1094	CATTCACTTGAGGAGTGTCTGGT
1095	ATTCACTTGAGGAGTGTCTGGTA
1096	TTCACTTGAGGAGTGTCTGGTAA
1097	TCACTTGAGGAGTGTCTGGTAAG
1098	CACTTGAGGAGTGTCTGGTAAGA
1099	ACTTGAGGAGTGTCTGGTAAGAA
1100	CTTGAGGAGTGTCTGGTAAGAAC
1101	TTGAGGAGTGTCTGGTAAGAACT
1102	TGAGGAGTGTCTGGTAAGAACTA
1103	GAGGAGTGTCTGGTAAGAACTAC
1104	AGGAGTGTCTGGTAAGAACTACT

Fig. 29 cont'd (Sheet 23 of 170)

ID	SEQUENCE
1105	GGAGTGTCTGGTAAGAACTACTG
1106	GAGTGTCTGGTAAGAACTACTGA
1107	AGTGTCTGGTAAGAACTACTGAG
1108	GTGTCTGGTAAGAACTACTGAGA
1109	TGTCTGGTAAGAACTACTGAGAA
1110	GTCTGGTAAGAACTACTGAGAAA
1111	TCTGGTAAGAACTACTGAGAAAA
1112	CTGGTAAGAACTACTGAGAAAAC
1113	TGGTAAGAACTACTGAGAAAACA
1114	GGTAAGAACTACTGAGAAAACAC
1115	GTAAGAACTACTGAGAAAACACC
1116	TAAGAACTACTGAGAAAACACCA
1117	AAGAACTACTGAGAAAACACCAT
1118	AGAACTACTGAGAAAACACCATC
1119	GAACTACTGAGAAAACACCATCA
1120	AACTACTGAGAAAACACCATCAC
1121	ACTACTGAGAAAACACCATCACT
1122	CTACTGAGAAAACACCATCACTA
1123	TACTGAGAAAACACCATCACTAA
1124	ACTGAGAAAACACCATCACTAAC
1125	CTGAGAAAACACCATCACTAACT
1126	TGAGAAAACACCATCACTAACTA
1127	GAGAAAACACCATCACTAACTAG
1128	AGAAAACACCATCACTAACTAGA
1129	GAAAACACCATCACTAACTAGAA
1130	AAAACACCATCACTAACTAGAAG
1131	AAACACCATCACTAACTAGAAGA
1132	AACACCATCACTAACTAGAAGAA
1133	ACACCATCACTAACTAGAAGAAT
1134	CACCATCACTAACTAGAAGAATT
1135	ACCATCACTAACTAGAAGAATTG
1136	CCATCACTAACTAGAAGAATTGA
1137	CATCACTAACTAGAAGAATTGAT
1138	ATCACTAACTAGAAGAATTGATG
1139	TCACTAACTAGAAGAATTGATGA
1140	CACTAACTAGAAGAATTGATGAT
1141	ACTAACTAGAAGAATTGATGATA
1142	CTAACTAGAAGAATTGATGATAC
1143	TAACTAGAAGAATTGATGATACC
1144	AACTAGAAGAATTGATGATACCA
1145	ACTAGAAGAATTGATGATACCAT
1146	CTAGAAGAATTGATGATACCATC
1147	TAGAAGAATTGATGATACCATCT
1148	AGAAGAATTGATGATACCATCTT
1149	GAAGAATTGATGATACCATCTTC
1150	AAGAATTGATGATACCATCTTCC
1151	AGAATTGATGATACCATCTTCCA
1152	GAATTGATGATACCATCTTCCAA

ID	SEQUENCE
1153	AATTGATGATACCATCTTCCAAA
1154	ATTGATGATACCATCTTCCAAAA
1155	TTGATGATACCATCTTCCAAAAT
1156	TGATGATACCATCTTCCAAAATC
1157	GATGATACCATCTTCCAAAATCC
1158	ATGATACCATCTTCCAAAATCCT
1159	TGATACCATCTTCCAAAATCCTA
1160	GATACCATCTTCCAAAATCCTAT
1161	ATACCATCTTCCAAAATCCTATG
1162	TACCATCTTCCAAAATCCTATGG
1163	ACCATCTTCCAAAATCCTATGGT
1164	CCATCTTCCAAAATCCTATGGTA
1165	CATCTTCCAAAATCCTATGGTAC
1166	ATCTTCCAAAATCCTATGGTACA
1167	TCTTCCAAAATCCTATGGTACAA
1168	CTTCCAAAATCCTATGGTACAAG
1169	TTCCAAAATCCTATGGTACAAGA
1170	TCCAAAATCCTATGGTACAAGAA
1171	CCAAAATCCTATGGTACAAGAAG
1172	CAAAATCCTATGGTACAAGAAGC
1173	AAAATCCTATGGTACAAGAAGCT
1174	AAATCCTATGGTACAAGAAGCTA
1175	AATCCTATGGTACAAGAAGCTAT
1176	ATCCTATGGTACAAGAAGCTATA
1177	TCCTATGGTACAAGAAGCTATAC
1178	CCTATGGTACAAGAAGCTATACG
1179	CTATGGTACAAGAAGCTATACGA
1180	TATGGTACAAGAAGCTATACGAA
1181	ATGGTACAAGAAGCTATACGAAT
1182	TGGTACAAGAAGCTATACGAATG
1183	GGTACAAGAAGCTATACGAATGG
1184	GTACAAGAAGCTATACGAATGGG
1185	TACAAGAAGCTATACGAATGGGG
1186	ACAAGAAGCTATACGAATGGGGT
1187	CAAGAAGCTATACGAATGGGGTT
1188	AAGAAGCTATACGAATGGGGTTC
1189	AGAAGCTATACGAATGGGGTTCA
1190	GAAGCTATACGAATGGGGTTCAG
1191	AAGCTATACGAATGGGGTTCAGT
1192	AGCTATACGAATGGGGTTCAGTT
1193	GCTATACGAATGGGGTTCAGTTT
1194	CTATACGAATGGGGTTCAGTTTC
1195	TATACGAATGGGGTTCAGTTTCA
1196	ATACGAATGGGGTTCAGTTTCAA
1197	TACGAATGGGGTTCAGTTTCAAG
1198	ACGAATGGGGTTCAGTTTCAAGG
1199	CGAATGGGGTTCAGTTTCAAGGA
1200	GAATGGGGTTCAGTTTCAAGGAC

Fig. 29 cont'd (Sheet 25 of 170)

ID	SEQUENCE
1201	AATGGGGTTCAGTTTCAAGGACA
1202	ATGGGGTTCAGTTTCAAGGACAT
1203	TGGGGTTCAGTTTCAAGGACATT
1204	GGGGTTCAGTTTCAAGGACATTA
1205	GGGTTCAGTTTCAAGGACATTAA
1206	GGTTCAGTTTCAAGGACATTAAG
1207	GTTCAGTTTCAAGGACATTAAGA
1208	TTCAGTTTCAAGGACATTAAGAA
1209	TCAGTTTCAAGGACATTAAGAAA
1210	CAGTTTCAAGGACATTAAGAAAA
1211	AGTTTCAAGGACATTAAGAAAAT
1212	GTTTCAAGGACATTAAGAAAATA
1213	TTTCAAGGACATTAAGAAAATAA
1214	TTCAAGGACATTAAGAAAATAAT
1215	TCAAGGACATTAAGAAAATAATG
1216	CAAGGACATTAAGAAAATAATGG
1217	AAGGACATTAAGAAAATAATGGA
1218	AGGACATTAAGAAAATAATGGAG
1219	GGACATTAAGAAAATAATGGAGG
1220	GACATTAAGAAAATAATGGAGGA
1221	ACATTAAGAAAATAATGGAGGAA
1222	CATTAAGAAAATAATGGAGGAAA
1223	ATTAAGAAAATAATGGAGGAAAA
1224	TTAAGAAAATAATGGAGGAAAAA
1225	TAAGAAAATAATGGAGGAAAAAA
1226	AAGAAAATAATGGAGGAAAAAAT
1227	AGAAAATAATGGAGGAAAAAATT
1228	GAAAATAATGGAGGAAAAAATTC
1229	AAAATAATGGAGGAAAAAATTCA
1230	AAATAATGGAGGAAAAAATTCAG
1231	AATAATGGAGGAAAAAATTCAGA
1232	ATAATGGAGGAAAAAATTCAGAT
1233	TAATGGAGGAAAAAATTCAGATA
1234	AATGGAGGAAAAAATTCAGATAT
1235	ATGGAGGAAAAAATTCAGATATC
1236	TGGAGGAAAAAATTCAGATATCT
1237	GGAGGAAAAAATTCAGATATCTG
1238	GAGGAAAAAATTCAGATATCTGG
1239	AGGAAAAAATTCAGATATCTGGG
1240	GGAAAAAATTCAGATATCTGGGA
1241	GAAAAAATTCAGATATCTGGGAG
1242	AAAAAATTCAGATATCTGGGAGC
1243	AAAAATTCAGATATCTGGGAGCA
1244	AAAATTCAGATATCTGGGAGCAA
1245	AAATTCAGATATCTGGGAGCAAC
1246	AATTCAGATATCTGGGAGCAACT
1247	ATTCAGATATCTGGGAGCAACTA
1248	TTCAGATATCTGGGAGCAACTAT

Fig. 29 cont'd (Sheet 26 of 170)

ID	SEQUENCE
1249	TCAGATATCTGGGAGCAACTATA
1250	CAGATATCTGGGAGCAACTATAA
1251	AGATATCTGGGAGCAACTATAAA
1252	GATATCTGGGAGCAACTATAAAT
1253	ATATCTGGGAGCAACTATAAATC
1254	TATCTGGGAGCAACTATAAATCA
1255	ATCTGGGAGCAACTATAAATCAC
1256	TCTGGGAGCAACTATAAATCACT
1257	CTGGGAGCAACTATAAATCACTT
1258	TGGGAGCAACTATAAATCACTTG
1259	GGGAGCAACTATAAATCACTTGA
1260	GGAGCAACTATAAATCACTTGAG
1261	GAGCAACTATAAATCACTTGAGG
1262	AGCAACTATAAATCACTTGAGGT
1263	GCAACTATAAATCACTTGAGGTT
1264	CAACTATAAATCACTTGAGGTTC
1265	AACTATAAATCACTTGAGGTTCT
1266	ACTATAAATCACTTGAGGTTCTG
1267	CTATAAATCACTTGAGGTTCTGG
1268	TATAAATCACTTGAGGTTCTGGT
1269	ATAAATCACTTGAGGTTCTGGTT
1270	TAAATCACTTGAGGTTCTGGTTG
1271	AAATCACTTGAGGTTCTGGTTGC
1272	AATCACTTGAGGTTCTGGTTGCA
1273	ATCACTTGAGGTTCTGGTTGCAG
1274	TCACTTGAGGTTCTGGTTGCAGA
1275	CACTTGAGGTTCTGGTTGCAGAT
1276	ACTTGAGGTTCTGGTTGCAGATC
1277	CTTGAGGTTCTGGTTGCAGATCT
1278	TTGAGGTTCTGGTTGCAGATCTA
1279	TGAGGTTCTGGTTGCAGATCTAG
1280	GAGGTTCTGGTTGCAGATCTAGT
1281	AGGTTCTGGTTGCAGATCTAGTG
1282	GGTTCTGGTTGCAGATCTAGTGA
1283	GTTCTGGTTGCAGATCTAGTGAA
1284	TTCTGGTTGCAGATCTAGTGAAT
1285	TCTGGTTGCAGATCTAGTGAATG
1286	CTGGTTGCAGATCTAGTGAATGC
1287	TGGTTGCAGATCTAGTGAATGCT
1288	GGTTGCAGATCTAGTGAATGCTC
1289	GTTGCAGATCTAGTGAATGCTCA
1290	TTGCAGATCTAGTGAATGCTCAG
1291	TGCAGATCTAGTGAATGCTCAGA
1292	GCAGATCTAGTGAATGCTCAGAA
1293	CAGATCTAGTGAATGCTCAGAAA
1294	AGATCTAGTGAATGCTCAGAAAG
1295	GATCTAGTGAATGCTCAGAAAGA
1296	ATCTAGTGAATGCTCAGAAAGAC

Fig. 29 cont'd (Sheet 27 of 170)

ID	SEQUENCE
1297	TCTAGTGAATGCTCAGAAAGACA
1298	CTAGTGAATGCTCAGAAAGACAG
1299	TAGTGAATGCTCAGAAAGACAGT
1300	AGTGAATGCTCAGAAAGACAGTA
1301	GTGAATGCTCAGAAAGACAGTAT
1302	TGAATGCTCAGAAAGACAGTATG
1303	GAATGCTCAGAAAGACAGTATGC
1304	AATGCTCAGAAAGACAGTATGCA
1305	ATGCTCAGAAAGACAGTATGCAA
1306	TGCTCAGAAAGACAGTATGCAAG
1307	GCTCAGAAAGACAGTATGCAAGA
1308	CTCAGAAAGACAGTATGCAAGAT
1309	TCAGAAAGACAGTATGCAAGATG
1310	CAGAAAGACAGTATGCAAGATGA
1311	AGAAAGACAGTATGCAAGATGAG
1312	GAAAGACAGTATGCAAGATGAGT
1313	AAAGACAGTATGCAAGATGAGTC
1314	AAGACAGTATGCAAGATGAGTCA
1315	AGACAGTATGCAAGATGAGTCAA
1316	GACAGTATGCAAGATGAGTCAAG
1317	ACAGTATGCAAGATGAGTCAAGT
1318	CAGTATGCAAGATGAGTCAAGTC
1319	AGTATGCAAGATGAGTCAAGTCA
1320	GTATGCAAGATGAGTCAAGTCAG
1321	TATGCAAGATGAGTCAAGTCAGA
1322	ATGCAAGATGAGTCAAGTCAGAC
1323	TGCAAGATGAGTCAAGTCAGACT
1324	GCAAGATGAGTCAAGTCAGACTT
1325	CAAGATGAGTCAAGTCAGACTTC
1326	AAGATGAGTCAAGTCAGACTTCA
1327	AGATGAGTCAAGTCAGACTTCAT
1328	GATGAGTCAAGTCAGACTTCATT
1329	ATGAGTCAAGTCAGACTTCATTA
1330	TGAGTCAAGTCAGACTTCATTAC
1331	GAGTCAAGTCAGACTTCATTACA
1332	AGTCAAGTCAGACTTCATTACAG
1333	GTCAAGTCAGACTTCATTACAGA
1334	TCAAGTCAGACTTCATTACAGAA
1335	CAAGTCAGACTTCATTACAGAAA
1336	AAGTCAGACTTCATTACAGAAAG
1337	AGTCAGACTTCATTACAGAAAGA
1338	GTCAGACTTCATTACAGAAAGAG
1339	TCAGACTTCATTACAGAAAGAGA
1340	CAGACTTCATTACAGAAAGAGAT
1341	AGACTTCATTACAGAAAGAGATT
1342	GACTTCATTACAGAAAGAGATTA
1343	ACTTCATTACAGAAAGAGATTAG
1344	CTTCATTACAGAAAGAGATTAGT

Fig. 29 cont'd (Sheet 28 of 170)

ID	SEQUENCE
1345	TTCATTACAGAAAGAGATTAGTA
1346	TCATTACAGAAAGAGATTAGTAC
1347	CATTACAGAAAGAGATTAGTACT
1348	ATTACAGAAAGAGATTAGTACTG
1349	TTACAGAAAGAGATTAGTACTGA
1350	TACAGAAAGAGATTAGTACTGAA
1351	ACAGAAAGAGATTAGTACTGAAG
1352	CAGAAAGAGATTAGTACTGAAGA
1353	AGAAAGAGATTAGTACTGAAGAG
1354	GAAAGAGATTAGTACTGAAGAGC
1355	AAAGAGATTAGTACTGAAGAGCA
1356	AAGAGATTAGTACTGAAGAGCAG
1357	AGAGATTAGTACTGAAGAGCAGC
1358	GAGATTAGTACTGAAGAGCAGCT
1359	AGATTAGTACTGAAGAGCAGCTA
1360	GATTAGTACTGAAGAGCAGCTAA
1361	ATTAGTACTGAAGAGCAGCTAAG
1362	TTAGTACTGAAGAGCAGCTAAGG
1363	TAGTACTGAAGAGCAGCTAAGGC
1364	AGTACTGAAGAGCAGCTAAGGCG
1365	GTACTGAAGAGCAGCTAAGGCGC
1366	TACTGAAGAGCAGCTAAGGCGCC
1367	ACTGAAGAGCAGCTAAGGCGCCT
1368	CTGAAGAGCAGCTAAGGCGCCTG
1369	TGAAGAGCAGCTAAGGCGCCTGC
1370	GAAGAGCAGCTAAGGCGCCTGCA
1371	AAGAGCAGCTAAGGCGCCTGCAA
1372	AGAGCAGCTAAGGCGCCTGCAAG
1373	GAGCAGCTAAGGCGCCTGCAAGA
1374	AGCAGCTAAGGCGCCTGCAAGAG
1375	GCAGCTAAGGCGCCTGCAAGAGG
1376	CAGCTAAGGCGCCTGCAAGAGGA
1377	AGCTAAGGCGCCTGCAAGAGGAG
1378	GCTAAGGCGCCTGCAAGAGGAGA
1379	CTAAGGCGCCTGCAAGAGGAGAA
1380	TAAGGCGCCTGCAAGAGGAGAAG
1381	AAGGCGCCTGCAAGAGGAGAAGC
1382	AGGCGCCTGCAAGAGGAGAAGCT
1383	GGCGCCTGCAAGAGGAGAAGCTT
1384	GCGCCTGCAAGAGGAGAAGCTTT
1385	CGCCTGCAAGAGGAGAAGCTTTG
1386	GCCTGCAAGAGGAGAAGCTTTGC
1387	CCTGCAAGAGGAGAAGCTTTGCA
1388	CTGCAAGAGGAGAAGCTTTGCAA
1389	TGCAAGAGGAGAAGCTTTGCAAA
1390	GCAAGAGGAGAAGCTTTGCAAAA
1391	CAAGAGGAGAAGCTTTGCAAAAT
1392	AAGAGGAGAAGCTTTGCAAAATC

Fig. 29 cont'd (Sheet 29 of 170)

ID	SEQUENCE
1393	AGAGGAGAAGCTTTGCAAAATCT
1394	GAGGAGAAGCTTTGCAAAATCTG
1395	AGGAGAAGCTTTGCAAAATCTGT
1396	GGAGAAGCTTTGCAAAATCTGTA
1397	GAGAAGCTTTGCAAAATCTGTAT
1398	AGAAGCTTTGCAAAATCTGTATG
1399	GAAGCTTTGCAAAATCTGTATGG
1400	AAGCTTTGCAAAATCTGTATGGA
1401	AGCTTTGCAAAATCTGTATGGAT
1402	GCTTTGCAAAATCTGTATGGATA
1403	CTTTGCAAAATCTGTATGGATAG
1404	TTTGCAAAATCTGTATGGATAGA
1405	TTGCAAAATCTGTATGGATAGAA
1406	TGCAAAATCTGTATGGATAGAAA
1407	GCAAAATCTGTATGGATAGAAAT
1408	CAAAATCTGTATGGATAGAAATA
1409	AAAATCTGTATGGATAGAAATAT
1410	AAATCTGTATGGATAGAAATATT
1411	AATCTGTATGGATAGAAATATTG
1412	ATCTGTATGGATAGAAATATTGC
1413	TCTGTATGGATAGAAATATTGCT
1414	CTGTATGGATAGAAATATTGCTA
1415	TGTATGGATAGAAATATTGCTAT
1416	GTATGGATAGAAATATTGCTATC
1417	TATGGATAGAAATATTGCTATCG
1418	ATGGATAGAAATATTGCTATCGT
1419	TGGATAGAAATATTGCTATCGTT
1420	GGATAGAAATATTGCTATCGTTT
1421	GATAGAAATATTGCTATCGTTTT
1422	ATAGAAATATTGCTATCGTTTTT
1423	TAGAAATATTGCTATCGTTTTTG
1424	AGAAATATTGCTATCGTTTTTGT
1425	GAAATATTGCTATCGTTTTTGTT
1426	AAATATTGCTATCGTTTTTGTTC
1427	AATATTGCTATCGTTTTTGTTCC
1428	ATATTGCTATCGTTTTTGTTCCT
1429	TATTGCTATCGTTTTTGTTCCTT
1430	ATTGCTATCGTTTTTGTTCCTTG
1431	TTGCTATCGTTTTTGTTCCTTGT
1432	TGCTATCGTTTTTGTTCCTTGTG
1433	GCTATCGTTTTTGTTCCTTGTGG
1434	CTATCGTTTTTGTTCCTTGTGGA
1435	TATCGTTTTTGTTCCTTGTGGAC
1436	ATCGTTTTTGTTCCTTGTGGACA
1437	TCGTTTTTGTTCCTTGTGGACAT
1438	CGTTTTTGTTCCTTGTGGACATC
1439	GTTTTTGTTCCTTGTGGACATCT
1440	TTTTTGTTCCTTGTGGACATCTA

Fig. 29 cont'd (Sheet 30 of 170)

ID	SEQUENCE
1441	TTTTGTTCCTTGTGGACATCTAG
1442	TTTGTTCCTTGTGGACATCTAGT
1443	TTGTTCCTTGTGGACATCTAGTC
1444	TGTTCCTTGTGGACATCTAGTCA
1445	GTTCCTTGTGGACATCTAGTCAC
1446	TTCCTTGTGGACATCTAGTCACT
1447	TCCTTGTGGACATCTAGTCACTT
1448	CCTTGTGGACATCTAGTCACTTG
1449	CTTGTGGACATCTAGTCACTTGT
1450	TTGTGGACATCTAGTCACTTGTA
1451	TGTGGACATCTAGTCACTTGTAA
1452	GTGGACATCTAGTCACTTGTAAA
1453	TGGACATCTAGTCACTTGTAAAC
1454	GGACATCTAGTCACTTGTAAACA
1455	GACATCTAGTCACTTGTAAACAA
1456	ACATCTAGTCACTTGTAAACAAT
1457	CATCTAGTCACTTGTAAACAATG
1458	ATCTAGTCACTTGTAAACAATGT
1459	TCTAGTCACTTGTAAACAATGTG
1460	CTAGTCACTTGTAAACAATGTGC
1461	TAGTCACTTGTAAACAATGTGCT
1462	AGTCACTTGTAAACAATGTGCTG
1463	GTCACTTGTAAACAATGTGCTGA
1464	TCACTTGTAAACAATGTGCTGAA
1465	CACTTGTAAACAATGTGCTGAAG
1466	ACTTGTAAACAATGTGCTGAAGC
1467	CTTGTAAACAATGTGCTGAAGCA
1468	TTGTAAACAATGTGCTGAAGCAG
1469	TGTAAACAATGTGCTGAAGCAGT
1470	GTAAACAATGTGCTGAAGCAGTT
1471	TAAACAATGTGCTGAAGCAGTTG
1472	AAACAATGTGCTGAAGCAGTTGA
1473	AACAATGTGCTGAAGCAGTTGAC
1474	ACAATGTGCTGAAGCAGTTGACA
1475	CAATGTGCTGAAGCAGTTGACAA
1476	AATGTGCTGAAGCAGTTGACAAG
1477	ATGTGCTGAAGCAGTTGACAAGT
1478	TGTGCTGAAGCAGTTGACAAGTG
1479	GTGCTGAAGCAGTTGACAAGTGT
1480	TGCTGAAGCAGTTGACAAGTGTC
1481	GCTGAAGCAGTTGACAAGTGTCC
1482	CTGAAGCAGTTGACAAGTGTCCC
1483	TGAAGCAGTTGACAAGTGTCCCA
1484	GAAGCAGTTGACAAGTGTCCCAT
1485	AAGCAGTTGACAAGTGTCCCATG
1486	AGCAGTTGACAAGTGTCCCATGT
1487	GCAGTTGACAAGTGTCCCATGTG
1488	CAGTTGACAAGTGTCCCATGTGC

Fig. 29 cont'd (Sheet 31 of 170)

ID	SEQUENCE
1489	AGTTGACAAGTGTCCCATGTGCT
1490	GTTGACAAGTGTCCCATGTGCTA
1491	TTGACAAGTGTCCCATGTGCTAC
1492	TGACAAGTGTCCCATGTGCTACA
1493	GACAAGTGTCCCATGTGCTACAC
1494	ACAAGTGTCCCATGTGCTACACA
1495	CAAGTGTCCCATGTGCTACACAG
1496	AAGTGTCCCATGTGCTACACAGT
1497	AGTGTCCCATGTGCTACACAGTC
1498	GTGTCCCATGTGCTACACAGTCA
1499	TGTCCCATGTGCTACACAGTCAT
1500	GTCCCATGTGCTACACAGTCATT
1501	TCCCATGTGCTACACAGTCATTA
1502	CCCATGTGCTACACAGTCATTAC
1503	CCATGTGCTACACAGTCATTACT
1504	CATGTGCTACACAGTCATTACTT
1505	ATGTGCTACACAGTCATTACTTT
1506	TGTGCTACACAGTCATTACTTTC
1507	GTGCTACACAGTCATTACTTTCA
1508	TGCTACACAGTCATTACTTTCAA
1509	GCTACACAGTCATTACTTTCAAG
1510	CTACACAGTCATTACTTTCAAGC
1511	TACACAGTCATTACTTTCAAGCA
1512	ACACAGTCATTACTTTCAAGCAA
1513	CACAGTCATTACTTTCAAGCAAA
1514	ACAGTCATTACTTTCAAGCAAAA
1515	CAGTCATTACTTTCAAGCAAAAA
1516	AGTCATTACTTTCAAGCAAAAAA
1517	GTCATTACTTTCAAGCAAAAAAT
1518	TCATTACTTTCAAGCAAAAAATT
1519	CATTACTTTCAAGCAAAAAATTT
1520	ATTACTTTCAAGCAAAAAATTTT
1521	TTACTTTCAAGCAAAAAATTTTT
1522	TACTTTCAAGCAAAAAATTTTTA
1523	ACTTTCAAGCAAAAAATTTTTAT
1524	CTTTCAAGCAAAAAATTTTTATG
1525	TTTCAAGCAAAAAATTTTTATGT
1526	TTCAAGCAAAAAATTTTTATGTC
1527	TCAAGCAAAAAATTTTTATGTCT
1528	CAAGCAAAAAATTTTTATGTCTT
1529	AAGCAAAAAATTTTTATGTCTTA
1530	TCTAACTCTATAGTAGGCATGTT
1531	CTAACTCTATAGTAGGCATGTTA
1532	TAACTCTATAGTAGGCATGTTAT
1533	AACTCTATAGTAGGCATGTTATG
1534	ACTCTATAGTAGGCATGTTATGT
1535	CTCTATAGTAGGCATGTTATGTT
1536	TCTATAGTAGGCATGTTATGTTG

Fig. 29 cont'd (Sheet 32 of 170)

ID	SEQUENCE
1537	CTATAGTAGGCATGTTATGTTGT
1538	TATAGTAGGCATGTTATGTTGTT
1539	ATAGTAGGCATGTTATGTTGTTC
1540	TAGTAGGCATGTTATGTTGTTCT
1541	AGTAGGCATGTTATGTTGTTCTT
1542	GTAGGCATGTTATGTTGTTCTTA
1543	TAGGCATGTTATGTTGTTCTTAT
1544	AGGCATGTTATGTTGTTCTTATT
1545	GGCATGTTATGTTGTTCTTATTA
1546	GCATGTTATGTTGTTCTTATTAC
1547	CATGTTATGTTGTTCTTATTACC
1548	ATGTTATGTTGTTCTTATTACCC
1549	TGTTATGTTGTTCTTATTACCCT
1550	GTTATGTTGTTCTTATTACCCTG
1551	TTATGTTGTTCTTATTACCCTGA
1552	TATGTTGTTCTTATTACCCTGAT
1553	ATGTTGTTCTTATTACCCTGATT
1554	TGTTGTTCTTATTACCCTGATTG
1555	GTTGTTCTTATTACCCTGATTGA
1556	TTGTTCTTATTACCCTGATTGAA
1557	TGTTCTTATTACCCTGATTGAAT
1558	GTTCTTATTACCCTGATTGAATG
1559	TTCTTATTACCCTGATTGAATGT
1560	TCTTATTACCCTGATTGAATGTG
1561	CTTATTACCCTGATTGAATGTGT
1562	TTATTACCCTGATTGAATGTGTG
1563	TATTACCCTGATTGAATGTGTGA
1564	ATTACCCTGATTGAATGTGTGAT
1565	TTACCCTGATTGAATGTGTGATG
1566	TACCCTGATTGAATGTGTGATGT
1567	ACCCTGATTGAATGTGTGATGTG
1568	CCCTGATTGAATGTGTGATGTGA
1569	CCTGATTGAATGTGTGATGTGAA
1570	CTGATTGAATGTGTGATGTGAAC
1571	TGATTGAATGTGTGATGTGAACT
1572	GATTGAATGTGTGATGTGAACTG
1573	ATTGAATGTGTGATGTGAACTGA
1574	TTGAATGTGTGATGTGAACTGAC
1575	TGAATGTGTGATGTGAACTGACT
1576	GAATGTGTGATGTGAACTGACTT
1577	AATGTGTGATGTGAACTGACTTT
1578	ATGTGTGATGTGAACTGACTTTA
1579	TGTGTGATGTGAACTGACTTTAA
1580	GTGTGATGTGAACTGACTTTAAG
1581	TGTGATGTGAACTGACTTTAAGT
1582	GTGATGTGAACTGACTTTAAGTA
1583	TGATGTGAACTGACTTTAAGTAA
1584	GATGTGAACTGACTTTAAGTAAT

Fig. 29 cont'd (Sheet 33 of 170)

ID	SEQUENCE
1585	ATGTGAACTGACTTTAAGTAATC
1586	TGTGAACTGACTTTAAGTAATCA
1587	GTGAACTGACTTTAAGTAATCAG
1588	TGAACTGACTTTAAGTAATCAGG
1589	GAACTGACTTTAAGTAATCAGGA
1590	AACTGACTTTAAGTAATCAGGAT
1591	ACTGACTTTAAGTAATCAGGATT
1592	CTGACTTTAAGTAATCAGGATTG
1593	TGACTTTAAGTAATCAGGATTGA
1594	GACTTTAAGTAATCAGGATTGAA
1595	ACTTTAAGTAATCAGGATTGAAT
1596	CTTTAAGTAATCAGGATTGAATT
1597	TTTAAGTAATCAGGATTGAATTC
1598	TTAAGTAATCAGGATTGAATTCC
1599	TAAGTAATCAGGATTGAATTCCA
1600	AAGTAATCAGGATTGAATTCCAT
1601	AGTAATCAGGATTGAATTCCATT
1602	GTAATCAGGATTGAATTCCATTA
1603	TAATCAGGATTGAATTCCATTAG
1604	AATCAGGATTGAATTCCATTAGC
1605	ATCAGGATTGAATTCCATTAGCA
1606	TCAGGATTGAATTCCATTAGCAT
1607	CAGGATTGAATTCCATTAGCATT
1608	AGGATTGAATTCCATTAGCATTT
1609	GGATTGAATTCCATTAGCATTTG
1610	GATTGAATTCCATTAGCATTTGC
1611	ATTGAATTCCATTAGCATTTGCT
1612	TTGAATTCCATTAGCATTTGCTA
1613	TGAATTCCATTAGCATTTGCTAC
1614	GAATTCCATTAGCATTTGCTACC
1615	AATTCCATTAGCATTTGCTACCA
1616	ATTCCATTAGCATTTGCTACCAA
1617	TTCCATTAGCATTTGCTACCAAG
1618	TCCATTAGCATTTGCTACCAAGT
1619	CCATTAGCATTTGCTACCAAGTA
1620	CATTAGCATTTGCTACCAAGTAG
1621	ATTAGCATTTGCTACCAAGTAGG
1622	TTAGCATTTGCTACCAAGTAGGA
1623	TAGCATTTGCTACCAAGTAGGAA
1624	AGCATTTGCTACCAAGTAGGAAA
1625	GCATTTGCTACCAAGTAGGAAAA
1626	CATTTGCTACCAAGTAGGAAAAA
1627	ATTTGCTACCAAGTAGGAAAAAA
1628	TTTGCTACCAAGTAGGAAAAAAA
1629	TTGCTACCAAGTAGGAAAAAAAA
1630	TGCTACCAAGTAGGAAAAAAAAT
1631	GCTACCAAGTAGGAAAAAAAATG
1632	CTACCAAGTAGGAAAAAAAATGT

Fig. 29 cont'd (Sheet 34 of 170)

ID	SEQUENCE
1633	TACCAAGTAGGAAAAAAAATGTA
1634	ACCAAGTAGGAAAAAAAATGTAC
1635	CCAAGTAGGAAAAAAAATGTACA
1636	CAAGTAGGAAAAAAAATGTACAT
1637	AAGTAGGAAAAAAAATGTACATG
1638	AGTAGGAAAAAAAATGTACATGG
1639	GTAGGAAAAAAAATGTACATGGC
1640	TAGGAAAAAAAATGTACATGGCA
1641	AGGAAAAAAAATGTACATGGCAG
1642	GGAAAAAAAATGTACATGGCAGT
1643	GAAAAAAAATGTACATGGCAGTG
1644	AAAAAAAATGTACATGGCAGTGT
1645	AAAAAAATGTACATGGCAGTGTT
1646	AAAAAATGTACATGGCAGTGTTT
1647	AAAAATGTACATGGCAGTGTTTT
1648	AAAATGTACATGGCAGTGTTTTA
1649	AAATGTACATGGCAGTGTTTTAG
1650	AATGTACATGGCAGTGTTTTAGT
1651	ATGTACATGGCAGTGTTTTAGTT
1652	TGTACATGGCAGTGTTTTAGTTG
1653	GTACATGGCAGTGTTTTAGTTGG
1654	TACATGGCAGTGTTTTAGTTGGC
1655	ACATGGCAGTGTTTTAGTTGGCA
1656	CATGGCAGTGTTTTAGTTGGCAA
1657	ATGGCAGTGTTTTAGTTGGCAAT
1658	TGGCAGTGTTTTAGTTGGCAATA
1659	GGCAGTGTTTTAGTTGGCAATAT
1660	GCAGTGTTTTAGTTGGCAATATA
1661	CAGTGTTTTAGTTGGCAATATAA
1662	AGTGTTTTAGTTGGCAATATAAT
1663	GTGTTTTAGTTGGCAATATAATC
1664	TGTTTTAGTTGGCAATATAATCT
1665	GTTTTAGTTGGCAATATAATCTT
1666	TTTTAGTTGGCAATATAATCTTT
1667	TTTAGTTGGCAATATAATCTTTG
1668	TTAGTTGGCAATATAATCTTTGA
1669	TAGTTGGCAATATAATCTTTGAA
1670	AGTTGGCAATATAATCTTTGAAT
1671	GTTGGCAATATAATCTTTGAATT
1672	TTGGCAATATAATCTTTGAATTT
1673	TGGCAATATAATCTTTGAATTTC
1674	GGCAATATAATCTTTGAATTTCT
1675	GCAATATAATCTTTGAATTTCTT
1676	CAATATAATCTTTGAATTTCTTG
1677	AATATAATCTTTGAATTTCTTGA
1678	ATATAATCTTTGAATTTCTTGAT
1679	TATAATCTTTGAATTTCTTGATT
1680	ATAATCTTTGAATTTCTTGATTT

Fig. 29 cont'd (Sheet 35 of 170)

ID	SEQUENCE
1681	TAATCTTTGAATTTCTTGATTTT
1682	AATCTTTGAATTTCTTGATTTTT
1683	ATCTTTGAATTTCTTGATTTTTC
1684	TCTTTGAATTTCTTGATTTTTCA
1685	CTTTGAATTTCTTGATTTTTCAG
1686	TTTGAATTTCTTGATTTTTCAGG
1687	TTGAATTTCTTGATTTTTCAGGG
1688	TGAATTTCTTGATTTTTCAGGGT
1689	GAATTTCTTGATTTTTCAGGGTA
1690	AATTTCTTGATTTTTCAGGGTAT
1691	ATTTCTTGATTTTTCAGGGTATT
1692	TTTCTTGATTTTTCAGGGTATTA
1693	TTCTTGATTTTTCAGGGTATTAG
1694	TCTTGATTTTTCAGGGTATTAGC
1695	CTTGATTTTTCAGGGTATTAGCT
1696	TTGATTTTTCAGGGTATTAGCTG
1697	TGATTTTTCAGGGTATTAGCTGT
1698	GATTTTTCAGGGTATTAGCTGTA
1699	ATTTTTCAGGGTATTAGCTGTAT
1700	TTTTTCAGGGTATTAGCTGTATT
1701	TTTTCAGGGTATTAGCTGTATTA
1702	TTTCAGGGTATTAGCTGTATTAT
1703	TTCAGGGTATTAGCTGTATTATC
1704	TCAGGGTATTAGCTGTATTATCC
1705	CAGGGTATTAGCTGTATTATCCA
1706	AGGGTATTAGCTGTATTATCCAT
1707	GGGTATTAGCTGTATTATCCATT
1708	GGTATTAGCTGTATTATCCATTT
1709	GTATTAGCTGTATTATCCATTTT
1710	TATTAGCTGTATTATCCATTTTT
1711	ATTAGCTGTATTATCCATTTTTT
1712	TTAGCTGTATTATCCATTTTTTT
1713	TAGCTGTATTATCCATTTTTTTT
1714	AGCTGTATTATCCATTTTTTTTA
1715	GCTGTATTATCCATTTTTTTTAC
1716	CTGTATTATCCATTTTTTTTACT
1717	TGTATTATCCATTTTTTTTACTG
1718	GTATTATCCATTTTTTTTACTGT
1719	TATTATCCATTTTTTTTACTGTT
1720	ATTATCCATTTTTTTTACTGTTA
1721	TTATCCATTTTTTTTACTGTTAT
1722	TATCCATTTTTTTTACTGTTATT
1723	ATCCATTTTTTTTACTGTTATTT
1724	TCCATTTTTTTTACTGTTATTTA
1725	CCATTTTTTTTACTGTTATTTAA
1726	CATTTTTTTTACTGTTATTTAAT
1727	ATTTTTTTTACTGTTATTTAATT
1728	TTTTTTTTACTGTTATTTAATTG

Fig. 29 cont'd (Sheet 36 of 170)

ID	SEQUENCE
1729	TTTTTTTACTGTTATTTAATTGA
1730	TTTTTTACTGTTATTTAATTGAA
1731	TTTTTACTGTTATTTAATTGAAA
1732	TTTTACTGTTATTTAATTGAAAC
1733	TTTACTGTTATTTAATTGAAACC
1734	TTACTGTTATTTAATTGAAACCA
1735	TACTGTTATTTAATTGAAACCAT
1736	ACTGTTATTTAATTGAAACCATA
1737	CTGTTATTTAATTGAAACCATAG
1738	TGTTATTTAATTGAAACCATAGA
1739	GTTATTTAATTGAAACCATAGAC
1740	TTATTTAATTGAAACCATAGACT
1741	TATTTAATTGAAACCATAGACTA
1742	ATTTAATTGAAACCATAGACTAA
1743	TTTAATTGAAACCATAGACTAAG
1744	TTAATTGAAACCATAGACTAAGA
1745	TAATTGAAACCATAGACTAAGAA
1746	AATTGAAACCATAGACTAAGAAT
1747	ATTGAAACCATAGACTAAGAATA
1748	TTGAAACCATAGACTAAGAATAA
1749	TGAAACCATAGACTAAGAATAAG
1750	GAAACCATAGACTAAGAATAAGA
1751	AAACCATAGACTAAGAATAAGAA
1752	AACCATAGACTAAGAATAAGAAG
1753	ACCATAGACTAAGAATAAGAAGC
1754	CCATAGACTAAGAATAAGAAGCA
1755	CATAGACTAAGAATAAGAAGCAT
1756	ATAGACTAAGAATAAGAAGCATC
1757	TAGACTAAGAATAAGAAGCATCA
1758	AGACTAAGAATAAGAAGCATCAT
1759	GACTAAGAATAAGAAGCATCATA
1760	ACTAAGAATAAGAAGCATCATAC
1761	CTAAGAATAAGAAGCATCATACT
1762	TAAGAATAAGAAGCATCATACTA
1763	AAGAATAAGAAGCATCATACTAT
1764	AGAATAAGAAGCATCATACTATA
1765	GAATAAGAAGCATCATACTATAA
1766	AATAAGAAGCATCATACTATAAC
1767	ATAAGAAGCATCATACTATAACT
1768	TAAGAAGCATCATACTATAACTG
1769	AAGAAGCATCATACTATAACTGA
1770	AGAAGCATCATACTATAACTGAA
1771	GAAGCATCATACTATAACTGAAC
1772	AAGCATCATACTATAACTGAACA
1773	AGCATCATACTATAACTGAACAC
1774	GCATCATACTATAACTGAACACA
1775	CATCATACTATAACTGAACACAA
1776	ATCATACTATAACTGAACACAAT

Fig. 29 cont'd (Sheet 37 of 170)

ID	SEQUENCE
1777	TCATACTATAACTGAACACAATG
1778	CATACTATAACTGAACACAATGT
1779	ATACTATAACTGAACACAATGTG
1780	TACTATAACTGAACACAATGTGT
1781	ACTATAACTGAACACAATGTGTA
1782	CTATAACTGAACACAATGTGTAT
1783	TATAACTGAACACAATGTGTATT
1784	ATAACTGAACACAATGTGTATTC
1785	TAACTGAACACAATGTGTATTCA
1786	AACTGAACACAATGTGTATTCAT
1787	ACTGAACACAATGTGTATTCATA
1788	CTGAACACAATGTGTATTCATAG
1789	TGAACACAATGTGTATTCATAGT
1790	GAACACAATGTGTATTCATAGTA
1791	AACACAATGTGTATTCATAGTAT
1792	ACACAATGTGTATTCATAGTATA
1793	CACAATGTGTATTCATAGTATAC
1794	ACAATGTGTATTCATAGTATACT
1795	CAATGTGTATTCATAGTATACTG
1796	AATGTGTATTCATAGTATACTGA
1797	ATGTGTATTCATAGTATACTGAT
1798	TGTGTATTCATAGTATACTGATT
1799	GTGTATTCATAGTATACTGATTT
1800	TGTATTCATAGTATACTGATTTA
1801	GTATTCATAGTATACTGATTTAA
1802	TATTCATAGTATACTGATTTAAT
1803	ATTCATAGTATACTGATTTAATT
1804	TTCATAGTATACTGATTTAATTT
1805	TCATAGTATACTGATTTAATTTC
1806	CATAGTATACTGATTTAATTTCT
1807	ATAGTATACTGATTTAATTTCTA
1808	TAGTATACTGATTTAATTTCTAA
1809	AGTATACTGATTTAATTTCTAAG
1810	GTATACTGATTTAATTTCTAAGT
1811	TATACTGATTTAATTTCTAAGTG
1812	ATACTGATTTAATTTCTAAGTGT
1813	TACTGATTTAATTTCTAAGTGTA
1814	ACTGATTTAATTTCTAAGTGTAA
1815	CTGATTTAATTTCTAAGTGTAAG
1816	TGATTTAATTTCTAAGTGTAAGT
1817	GATTTAATTTCTAAGTGTAAGTG
1818	ATTTAATTTCTAAGTGTAAGTGA
1819	TTTAATTTCTAAGTGTAAGTGAA
1820	TTAATTTCTAAGTGTAAGTGAAT
1821	TAATTTCTAAGTGTAAGTGAATT
1822	AATTTCTAAGTGTAAGTGAATTA
1823	ATTTCTAAGTGTAAGTGAATTAA
1824	TTTCTAAGTGTAAGTGAATTAAT

Fig. 29 cont'd (Sheet 38 of 170)

ID	SEQUENCE
1825	TTCTAAGTGTAAGTGAATTAATC
1826	TCTAAGTGTAAGTGAATTAATCA
1827	CTAAGTGTAAGTGAATTAATCAT
1828	TAAGTGTAAGTGAATTAATCATC
1829	AAGTGTAAGTGAATTAATCATCT
1830	AGTGTAAGTGAATTAATCATCTG
1831	GTGTAAGTGAATTAATCATCTGG
1832	TGTAAGTGAATTAATCATCTGGA
1833	GTAAGTGAATTAATCATCTGGAT
1834	TAAGTGAATTAATCATCTGGATT
1835	AAGTGAATTAATCATCTGGATTT
1836	AGTGAATTAATCATCTGGATTTT
1837	GTGAATTAATCATCTGGATTTTT
1838	TGAATTAATCATCTGGATTTTTT
1839	GAATTAATCATCTGGATTTTTTA
1840	AATTAATCATCTGGATTTTTTAT
1841	ATTAATCATCTGGATTTTTTATT
1842	TTAATCATCTGGATTTTTTATTC
1843	TAATCATCTGGATTTTTTATTCT
1844	AATCATCTGGATTTTTTATTCTT
1845	ATCATCTGGATTTTTTATTCTTT
1846	TCATCTGGATTTTTTATTCTTTT
1847	CATCTGGATTTTTTATTCTTTTC
1848	ATCTGGATTTTTTATTCTTTTCA
1849	TCTGGATTTTTTATTCTTTTCAG
1850	CTGGATTTTTTATTCTTTTCAGA
1851	TGGATTTTTTATTCTTTTCAGAT
1852	GGATTTTTTATTCTTTTCAGATA
1853	GATTTTTTATTCTTTTCAGATAG
1854	ATTTTTTATTCTTTTCAGATAGG
1855	TTTTTTATTCTTTTCAGATAGGC
1856	TTTTTATTCTTTTCAGATAGGCT
1857	TTTTATTCTTTTCAGATAGGCTT
1858	TTTATTCTTTTCAGATAGGCTTA
1859	TTATTCTTTTCAGATAGGCTTAA
1860	TATTCTTTTCAGATAGGCTTAAC
1861	ATTCTTTTCAGATAGGCTTAACA
1862	TTCTTTTCAGATAGGCTTAACAA
1863	TCTTTTCAGATAGGCTTAACAAA
1864	CTTTTCAGATAGGCTTAACAAAT
1865	TTTTCAGATAGGCTTAACAAATG
1866	TTTCAGATAGGCTTAACAAATGG
1867	TTCAGATAGGCTTAACAAATGGA
1868	TCAGATAGGCTTAACAAATGGAG
1869	CAGATAGGCTTAACAAATGGAGC
1870	AGATAGGCTTAACAAATGGAGCT
1871	GATAGGCTTAACAAATGGAGCTT
1872	ATAGGCTTAACAAATGGAGCTTT

Fig. 29 cont'd (Sheet 39 of 170)

ID	SEQUENCE
1873	TAGGCTTAACAAATGGAGCTTTC
1874	AGGCTTAACAAATGGAGCTTTCT
1875	GGCTTAACAAATGGAGCTTTCTG
1876	GCTTAACAAATGGAGCTTTCTGT
1877	CTTAACAAATGGAGCTTTCTGTA
1878	TTAACAAATGGAGCTTTCTGTAT
1879	TAACAAATGGAGCTTTCTGTATA
1880	AACAAATGGAGCTTTCTGTATAT
1881	ACAAATGGAGCTTTCTGTATATA
1882	CAAATGGAGCTTTCTGTATATAA
1883	AAATGGAGCTTTCTGTATATAAA
1884	AATGGAGCTTTCTGTATATAAAT
1885	ATGGAGCTTTCTGTATATAAATG
1886	TGGAGCTTTCTGTATATAAATGT
1887	GGAGCTTTCTGTATATAAATGTG
1888	GAGCTTTCTGTATATAAATGTGG
1889	AGCTTTCTGTATATAAATGTGGA
1890	GCTTTCTGTATATAAATGTGGAG
1891	CTTTCTGTATATAAATGTGGAGA
1892	TTTCTGTATATAAATGTGGAGAT
1893	TTCTGTATATAAATGTGGAGATT
1894	TCTGTATATAAATGTGGAGATTA
1895	CTGTATATAAATGTGGAGATTAG
1896	TGTATATAAATGTGGAGATTAGA
1897	GTATATAAATGTGGAGATTAGAG
1898	TATATAAATGTGGAGATTAGAGT
1899	ATATAAATGTGGAGATTAGAGTT
1900	TATAAATGTGGAGATTAGAGTTA
1901	ATAAATGTGGAGATTAGAGTTAA
1902	TAAATGTGGAGATTAGAGTTAAT
1903	AAATGTGGAGATTAGAGTTAATC
1904	AATGTGGAGATTAGAGTTAATCT
1905	ATGTGGAGATTAGAGTTAATCTC
1906	TGTGGAGATTAGAGTTAATCTCC
1907	GTGGAGATTAGAGTTAATCTCCC
1908	TGGAGATTAGAGTTAATCTCCCC
1909	GGAGATTAGAGTTAATCTCCCCA
1910	GAGATTAGAGTTAATCTCCCCAA
1911	AGATTAGAGTTAATCTCCCCAAT
1912	GATTAGAGTTAATCTCCCCAATC
1913	ATTAGAGTTAATCTCCCCAATCA
1914	TTAGAGTTAATCTCCCCAATCAC
1915	TAGAGTTAATCTCCCCAATCACA
1916	AGAGTTAATCTCCCCAATCACAT
1917	GAGTTAATCTCCCCAATCACATA
1918	AGTTAATCTCCCCAATCACATAA
1919	GTTAATCTCCCCAATCACATAAT
1920	TTAATCTCCCCAATCACATAATT

Fig. 29 cont'd (Sheet 40 of 170)

ID	SEQUENCE
1921	TAATCTCCCCAATCACATAATTT
1922	AATCTCCCCAATCACATAATTTG
1923	ATCTCCCCAATCACATAATTTGT
1924	TCTCCCCAATCACATAATTTGTT
1925	CTCCCCAATCACATAATTTGTTT
1926	TCCCCAATCACATAATTTGTTTT
1927	CCCCAATCACATAATTTGTTTTG
1928	CCCAATCACATAATTTGTTTTGT
1929	CCAATCACATAATTTGTTTTGTG
1930	CAATCACATAATTTGTTTTGTGT
1931	AATCACATAATTTGTTTTGTGTG
1932	ATCACATAATTTGTTTTGTGTGA
1933	TCACATAATTTGTTTTGTGTGAA
1934	CACATAATTTGTTTTGTGTGAAA
1935	ACATAATTTGTTTTGTGTGAAAA
1936	CATAATTTGTTTTGTGTGAAAAA
1937	ATAATTTGTTTTGTGTGAAAAAG
1938	TAATTTGTTTTGTGTGAAAAAGG
1939	AATTTGTTTTGTGTGAAAAAGGA
1940	ATTTGTTTTGTGTGAAAAAGGAA
1941	TTTGTTTTGTGTGAAAAAGGAAT
1942	TTGTTTTGTGTGAAAAAGGAATA
1943	TGTTTTGTGTGAAAAAGGAATAA
1944	GTTTTGTGTGAAAAAGGAATAAA
1945	TTTTGTGTGAAAAAGGAATAAAT
1946	TTTGTGTGAAAAAGGAATAAATT
1947	TTGTGTGAAAAAGGAATAAATTG
1948	TGTGTGAAAAAGGAATAAATTGT
1949	GTGTGAAAAAGGAATAAATTGTT
1950	TGTGAAAAAGGAATAAATTGTTC
1951	GTGAAAAAGGAATAAATTGTTCC
1952	TGAAAAAGGAATAAATTGTTCCA
1953	GAAAAAGGAATAAATTGTTCCAT
1954	AAAAAGGAATAAATTGTTCCATG
1955	AAAAGGAATAAATTGTTCCATGC
1956	AAAGGAATAAATTGTTCCATGCT
1957	AAGGAATAAATTGTTCCATGCTG
1958	AGGAATAAATTGTTCCATGCTGG
1959	GGAATAAATTGTTCCATGCTGGT
1960	GAATAAATTGTTCCATGCTGGTG
1961	AATAAATTGTTCCATGCTGGTGG
1962	ATAAATTGTTCCATGCTGGTGGA
1963	TAAATTGTTCCATGCTGGTGGAA
1964	AAATTGTTCCATGCTGGTGGAAA
1965	AATTGTTCCATGCTGGTGGAAAG
1966	ATTGTTCCATGCTGGTGGAAAGA
1967	TTGTTCCATGCTGGTGGAAAGAT
1968	TGTTCCATGCTGGTGGAAAGATA

Fig. 29 cont'd (Sheet 41 of 170)

ID	SEQUENCE
1969	GTTCCATGCTGGTGGAAAGATAG
1970	TTCCATGCTGGTGGAAAGATAGA
1971	TCCATGCTGGTGGAAAGATAGAG
1972	CCATGCTGGTGGAAAGATAGAGA
1973	CATGCTGGTGGAAAGATAGAGAT
1974	ATGCTGGTGGAAAGATAGAGATT
1975	TGCTGGTGGAAAGATAGAGATTG
1976	GCTGGTGGAAAGATAGAGATTGT
1977	CTGGTGGAAAGATAGAGATTGTT
1978	TGGTGGAAAGATAGAGATTGTTT
1979	GGTGGAAAGATAGAGATTGTTTT
1980	GTGGAAAGATAGAGATTGTTTTT
1981	TGGAAAGATAGAGATTGTTTTTA
1982	GGAAAGATAGAGATTGTTTTTAG
1983	GAAAGATAGAGATTGTTTTTAGA
1984	AAAGATAGAGATTGTTTTTAGAG
1985	AAGATAGAGATTGTTTTTAGAGG
1986	AGATAGAGATTGTTTTTAGAGGT
1987	GATAGAGATTGTTTTTAGAGGTT
1988	ATAGAGATTGTTTTTAGAGGTTG
1989	TAGAGATTGTTTTTAGAGGTTGG
1990	AGAGATTGTTTTTAGAGGTTGGT
1991	GAGATTGTTTTTAGAGGTTGGTT
1992	AGATTGTTTTTAGAGGTTGGTTG
1993	GATTGTTTTTAGAGGTTGGTTGT
1994	ATTGTTTTTAGAGGTTGGTTGTT
1995	TTGTTTTTAGAGGTTGGTTGTTG
1996	TGTTTTTAGAGGTTGGTTGTTGT
1997	GTTTTTAGAGGTTGGTTGTTGTG
1998	TTTTTAGAGGTTGGTTGTTGTGT
1999	TTTTAGAGGTTGGTTGTTGTGTT
2000	TTTAGAGGTTGGTTGTTGTGTTT
2001	TTAGAGGTTGGTTGTTGTGTTTT
2002	TAGAGGTTGGTTGTTGTGTTTTA
2003	AGAGGTTGGTTGTTGTGTTTTAG
2004	GAGGTTGGTTGTTGTGTTTTAGG
2005	AGGTTGGTTGTTGTGTTTTAGGA
2006	GGTTGGTTGTTGTGTTTTAGGAT
2007	GTTGGTTGTTGTGTTTTAGGATT
2008	TTGGTTGTTGTGTTTTAGGATTC
2009	TGGTTGTTGTGTTTTAGGATTCT
2010	GGTTGTTGTGTTTTAGGATTCTG
2011	GTTGTTGTGTTTTAGGATTCTGT
2012	TTGTTGTGTTTTAGGATTCTGTC
2013	TGTTGTGTTTTAGGATTCTGTCC
2014	GTTGTGTTTTAGGATTCTGTCCA
2015	TTGTGTTTTAGGATTCTGTCCAT
2016	TGTGTTTTAGGATTCTGTCCATT

Fig. 29 cont'd (Sheet 42 of 170)

ID	SEQUENCE
2017	GTGTTTTAGGATTCTGTCCATTT
2018	TGTTTTAGGATTCTGTCCATTTT
2019	GTTTTAGGATTCTGTCCATTTTC
2020	TTTTAGGATTCTGTCCATTTTCT
2021	TTTAGGATTCTGTCCATTTTCTT
2022	TTAGGATTCTGTCCATTTTCTTT
2023	TAGGATTCTGTCCATTTTCTTTT
2024	AGGATTCTGTCCATTTTCTTTTA
2025	GGATTCTGTCCATTTTCTTTTAA
2026	GATTCTGTCCATTTTCTTTTAAA
2027	ATTCTGTCCATTTTCTTTTAAAG
2028	TTCTGTCCATTTTCTTTTAAAGT
2029	TCTGTCCATTTTCTTTTAAAGTT
2030	CTGTCCATTTTCTTTTAAAGTTA
2031	TGTCCATTTTCTTTTAAAGTTAT
2032	GTCCATTTTCTTTTAAAGTTATA
2033	TCCATTTTCTTTTAAAGTTATAA
2034	CCATTTTCTTTTAAAGTTATAAA
2035	CATTTTCTTTTAAAGTTATAAAC
2036	ATTTTCTTTTAAAGTTATAAACA
2037	TTTTCTTTTAAAGTTATAAACAC
2038	TTTCTTTTAAAGTTATAAACACG
2039	TTCTTTTAAAGTTATAAACACGT
2040	TCTTTTAAAGTTATAAACACGTA
2041	CTTTTAAAGTTATAAACACGTAC
2042	TTTTAAAGTTATAAACACGTACT
2043	TTTAAAGTTATAAACACGTACTT
2044	TTAAAGTTATAAACACGTACTTG
2045	TAAAGTTATAAACACGTACTTGT
2046	AAAGTTATAAACACGTACTTGTG
2047	AAGTTATAAACACGTACTTGTGC
2048	AGTTATAAACACGTACTTGTGCG
2049	GTTATAAACACGTACTTGTGCGA
2050	TTATAAACACGTACTTGTGCGAA
2051	TATAAACACGTACTTGTGCGAAT
2052	ATAAACACGTACTTGTGCGAATT
2053	TAAACACGTACTTGTGCGAATTA
2054	AAACACGTACTTGTGCGAATTAT
2055	AACACGTACTTGTGCGAATTATT
2056	ACACGTACTTGTGCGAATTATTT
2057	CACGTACTTGTGCGAATTATTTT
2058	ACGTACTTGTGCGAATTATTTTT
2059	CGTACTTGTGCGAATTATTTTTT
2060	GTACTTGTGCGAATTATTTTTTT
2061	TACTTGTGCGAATTATTTTTTTA
2062	ACTTGTGCGAATTATTTTTTTAA
2063	CTTGTGCGAATTATTTTTTTAAA
2064	TTGTGCGAATTATTTTTTTAAAG

Fig. 29 cont'd (Sheet 43 of 170)

ID	SEQUENCE
2065	TGTGCGAATTATTTTTTTAAAGT
2066	GTGCGAATTATTTTTTTAAAGTG
2067	TGCGAATTATTTTTTTAAAGTGA
2068	GCGAATTATTTTTTTAAAGTGAT
2069	CGAATTATTTTTTTAAAGTGATT
2070	GAATTATTTTTTTAAAGTGATTT
2071	AATTATTTTTTTAAAGTGATTTG
2072	ATTATTTTTTTAAAGTGATTTGC
2073	TTATTTTTTTAAAGTGATTTGCC
2074	TATTTTTTTAAAGTGATTTGCCA
2075	ATTTTTTTAAAGTGATTTGCCAT
2076	TTTTTTTAAAGTGATTTGCCATT
2077	TTTTTTAAAGTGATTTGCCATTT
2078	TTTTTAAAGTGATTTGCCATTTT
2079	TTTTAAAGTGATTTGCCATTTTT
2080	TTTAAAGTGATTTGCCATTTTTG
2081	TTAAAGTGATTTGCCATTTTTGA
2082	TAAAGTGATTTGCCATTTTTGAA
2083	AAAGTGATTTGCCATTTTTGAAA
2084	AAGTGATTTGCCATTTTTGAAAG
2085	AGTGATTTGCCATTTTTGAAAGC
2086	GTGATTTGCCATTTTTGAAAGCG
2087	TGATTTGCCATTTTTGAAAGCGT
2088	GATTTGCCATTTTTGAAAGCGTA
2089	ATTTGCCATTTTTGAAAGCGTAT
2090	TTTGCCATTTTTGAAAGCGTATT
2091	TTGCCATTTTTGAAAGCGTATTT
2092	TGCCATTTTTGAAAGCGTATTTA
2093	GCCATTTTTGAAAGCGTATTTAA
2094	CCATTTTTGAAAGCGTATTTAAT
2095	CATTTTTGAAAGCGTATTTAATG
2096	ATTTTTGAAAGCGTATTTAATGA
2097	TTTTTGAAAGCGTATTTAATGAT
2098	TTTTGAAAGCGTATTTAATGATA
2099	TTTGAAAGCGTATTTAATGATAG
2100	TTGAAAGCGTATTTAATGATAGA
2101	TGAAAGCGTATTTAATGATAGAA
2102	GAAAGCGTATTTAATGATAGAAT
2103	AAAGCGTATTTAATGATAGAATA
2104	AAGCGTATTTAATGATAGAATAC
2105	AGCGTATTTAATGATAGAATACT
2106	GCGTATTTAATGATAGAATACTA
2107	CGTATTTAATGATAGAATACTAT
2108	GTATTTAATGATAGAATACTATC
2109	TATTTAATGATAGAATACTATCG
2110	ATTTAATGATAGAATACTATCGA
2111	TTTAATGATAGAATACTATCGAG
2112	TTAATGATAGAATACTATCGAGC

Fig. 29 cont'd (Sheet 44 of 170)

ID	SEQUENCE
2113	TAATGATAGAATACTATCGAGCC
2114	AATGATAGAATACTATCGAGCCA
2115	ATGATAGAATACTATCGAGCCAA
2116	TGATAGAATACTATCGAGCCAAC
2117	GATAGAATACTATCGAGCCAACA
2118	ATAGAATACTATCGAGCCAACAT
2119	TAGAATACTATCGAGCCAACATG
2120	AGAATACTATCGAGCCAACATGT
2121	GAATACTATCGAGCCAACATGTA
2122	AATACTATCGAGCCAACATGTAC
2123	ATACTATCGAGCCAACATGTACT
2124	TACTATCGAGCCAACATGTACTG
2125	ACTATCGAGCCAACATGTACTGA
2126	CTATCGAGCCAACATGTACTGAC
2127	TATCGAGCCAACATGTACTGACA
2128	ATCGAGCCAACATGTACTGACAT
2129	TCGAGCCAACATGTACTGACATG
2130	CGAGCCAACATGTACTGACATGG
2131	GAGCCAACATGTACTGACATGGA
2132	AGCCAACATGTACTGACATGGAA
2133	GCCAACATGTACTGACATGGAAA
2134	CCAACATGTACTGACATGGAAAG
2135	CAACATGTACTGACATGGAAAGA
2136	AACATGTACTGACATGGAAAGAT
2137	ACATGTACTGACATGGAAAGATG
2138	CATGTACTGACATGGAAAGATGT
2139	ATGTACTGACATGGAAAGATGTC
2140	TGTACTGACATGGAAAGATGTCA
2141	GTACTGACATGGAAAGATGTCAA
2142	TACTGACATGGAAAGATGTCAAA
2143	ACTGACATGGAAAGATGTCAAAG
2144	CTGACATGGAAAGATGTCAAAGA
2145	TGACATGGAAAGATGTCAAAGAT
2146	GACATGGAAAGATGTCAAAGATA
2147	ACATGGAAAGATGTCAAAGATAT
2148	CATGGAAAGATGTCAAAGATATG
2149	ATGGAAAGATGTCAAAGATATGT
2150	TGGAAAGATGTCAAAGATATGTT
2151	GGAAAGATGTCAAAGATATGTTA
2152	GAAAGATGTCAAAGATATGTTAA
2153	AAAGATGTCAAAGATATGTTAAG
2154	AAGATGTCAAAGATATGTTAAGT
2155	AGATGTCAAAGATATGTTAAGTG
2156	GATGTCAAAGATATGTTAAGTGT
2157	ATGTCAAAGATATGTTAAGTGTA
2158	TGTCAAAGATATGTTAAGTGTAA
2159	GTCAAAGATATGTTAAGTGTAAA
2160	TCAAAGATATGTTAAGTGTAAAA

Fig. 29 cont'd (Sheet 45 of 170)

ID	SEQUENCE
2161	CAAAGATATGTTAAGTGTAAAAT
2162	AAAGATATGTTAAGTGTAAAATG
2163	AAGATATGTTAAGTGTAAAATGC
2164	AGATATGTTAAGTGTAAAATGCA
2165	GATATGTTAAGTGTAAAATGCAA
2166	ATATGTTAAGTGTAAAATGCAAG
2167	TATGTTAAGTGTAAAATGCAAGT
2168	ATGTTAAGTGTAAAATGCAAGTG
2169	TGTTAAGTGTAAAATGCAAGTGG
2170	GTTAAGTGTAAAATGCAAGTGGC
2171	TTAAGTGTAAAATGCAAGTGGCA
2172	TAAGTGTAAAATGCAAGTGGCAA
2173	AAGTGTAAAATGCAAGTGGCAAA
2174	AGTGTAAAATGCAAGTGGCAAAA
2175	GTGTAAAATGCAAGTGGCAAAAC
2176	TGTAAAATGCAAGTGGCAAAACA
2177	GTAAAATGCAAGTGGCAAAACAC
2178	TAAAATGCAAGTGGCAAAACACT
2179	AAAATGCAAGTGGCAAAACACTA
2180	AAATGCAAGTGGCAAAACACTAT
2181	AATGCAAGTGGCAAAACACTATG
2182	ATGCAAGTGGCAAAACACTATGT
2183	TGCAAGTGGCAAAACACTATGTA
2184	GCAAGTGGCAAAACACTATGTAT
2185	CAAGTGGCAAAACACTATGTATA
2186	AAGTGGCAAAACACTATGTATAG
2187	AGTGGCAAAACACTATGTATAGT
2188	GTGGCAAAACACTATGTATAGTC
2189	TGGCAAAACACTATGTATAGTCT
2190	GGCAAAACACTATGTATAGTCTG
2191	GCAAAACACTATGTATAGTCTGA
2192	CAAAACACTATGTATAGTCTGAG
2193	AAAACACTATGTATAGTCTGAGC
2194	AAACACTATGTATAGTCTGAGCC
2195	AACACTATGTATAGTCTGAGCCA
2196	ACACTATGTATAGTCTGAGCCAG
2197	CACTATGTATAGTCTGAGCCAGA
2198	ACTATGTATAGTCTGAGCCAGAT
2199	CTATGTATAGTCTGAGCCAGATC
2200	TATGTATAGTCTGAGCCAGATCA
2201	ATGTATAGTCTGAGCCAGATCAA
2202	TGTATAGTCTGAGCCAGATCAAA
2203	GTATAGTCTGAGCCAGATCAAAG
2204	TATAGTCTGAGCCAGATCAAAGT
2205	ATAGTCTGAGCCAGATCAAAGTA
2206	TAGTCTGAGCCAGATCAAAGTAT
2207	AGTCTGAGCCAGATCAAAGTATG
2208	GTCTGAGCCAGATCAAAGTATGT

Fig. 29 cont'd (Sheet 46 of 170)

ID	SEQUENCE
2209	TCTGAGCCAGATCAAAGTATGTA
2210	CTGAGCCAGATCAAAGTATGTAT
2211	TGAGCCAGATCAAAGTATGTATG
2212	GAGCCAGATCAAAGTATGTATGT
2213	AGCCAGATCAAAGTATGTATGTT
2214	GCCAGATCAAAGTATGTATGTTT
2215	CCAGATCAAAGTATGTATGTTTT
2216	CAGATCAAAGTATGTATGTTTTT
2217	AGATCAAAGTATGTATGTTTTTA
2218	GATCAAAGTATGTATGTTTTTAA
2219	ATCAAAGTATGTATGTTTTTAAT
2220	TCAAAGTATGTATGTTTTTAATA
2221	CAAAGTATGTATGTTTTTAATAT
2222	AAAGTATGTATGTTTTTAATATG
2223	AAGTATGTATGTTTTTAATATGC
2224	AGTATGTATGTTTTTAATATGCA
2225	GTATGTATGTTTTTAATATGCAT
2226	TATGTATGTTTTTAATATGCATA
2227	ATGTATGTTTTTAATATGCATAG
2228	TGTATGTTTTTAATATGCATAGA
2229	GTATGTTTTTAATATGCATAGAA
2230	TATGTTTTTAATATGCATAGAAC
2231	ATGTTTTTAATATGCATAGAACA
2232	TGTTTTTAATATGCATAGAACAA
2233	GTTTTTAATATGCATAGAACAAA
2234	TTTTTAATATGCATAGAACAAAA
2235	TTTTAATATGCATAGAACAAAAG
2236	TTTAATATGCATAGAACAAAAGA
2237	TTAATATGCATAGAACAAAAGAT
2238	TAATATGCATAGAACAAAAGATT
2239	AATATGCATAGAACAAAAGATTT
2240	ATATGCATAGAACAAAAGATTTG
2241	TATGCATAGAACAAAAGATTTGG
2242	ATGCATAGAACAAAAGATTTGGA
2243	TGCATAGAACAAAAGATTTGGAA
2244	GCATAGAACAAAAGATTTGGAAA
2245	CATAGAACAAAAGATTTGGAAAG
2246	ATAGAACAAAAGATTTGGAAAGA
2247	TAGAACAAAAGATTTGGAAAGAT
2248	AGAACAAAAGATTTGGAAAGATA
2249	GAACAAAAGATTTGGAAAGATAT
2250	AACAAAAGATTTGGAAAGATATA
2251	ACAAAAGATTTGGAAAGATATAC
2252	CAAAAGATTTGGAAAGATATACA
2253	AAAAGATTTGGAAAGATATACAC
2254	AAAGATTTGGAAAGATATACACC
2255	AAGATTTGGAAAGATATACACCA
2256	AGATTTGGAAAGATATACACCAA

Fig. 29 cont'd (Sheet 47 of 170)

ID	SEQUENCE
2257	GATTTGGAAAGATATACACCAAA
2258	ATTTGGAAAGATATACACCAAAC
2259	TTTGGAAAGATATACACCAAACT
2260	TTGGAAAGATATACACCAAACTG
2261	TGGAAAGATATACACCAAACTGT
2262	GGAAAGATATACACCAAACTGTT
2263	GAAAGATATACACCAAACTGTTA
2264	AAAGATATACACCAAACTGTTAA
2265	AAGATATACACCAAACTGTTAAA
2266	AGATATACACCAAACTGTTAAAT
2267	GATATACACCAAACTGTTAAATG
2268	ATATACACCAAACTGTTAAATGT
2269	TATACACCAAACTGTTAAATGTG
2270	ATACACCAAACTGTTAAATGTGG
2271	TACACCAAACTGTTAAATGTGGT
2272	ACACCAAACTGTTAAATGTGGTT
2273	CACCAAACTGTTAAATGTGGTTT
2274	ACCAAACTGTTAAATGTGGTTTC
2275	CCAAACTGTTAAATGTGGTTTCT
2276	CAAACTGTTAAATGTGGTTTCTC
2277	AAACTGTTAAATGTGGTTTCTCT
2278	AACTGTTAAATGTGGTTTCTCTT
2279	ACTGTTAAATGTGGTTTCTCTTC
2280	CTGTTAAATGTGGTTTCTCTTCG
2281	TGTTAAATGTGGTTTCTCTTCGG
2282	GTTAAATGTGGTTTCTCTTCGGG
2283	TTAAATGTGGTTTCTCTTCGGGG
2284	TAAATGTGGTTTCTCTTCGGGGA
2285	AAATGTGGTTTCTCTTCGGGGAG
2286	AATGTGGTTTCTCTTCGGGGAGG
2287	ATGTGGTTTCTCTTCGGGGAGGG
2288	TGTGGTTTCTCTTCGGGGAGGGG
2289	GTGGTTTCTCTTCGGGGAGGGGG
2290	TGGTTTCTCTTCGGGGAGGGGGG
2291	GGTTTCTCTTCGGGGAGGGGGGG
2292	GTTTCTCTTCGGGGAGGGGGGGA
2293	TTTCTCTTCGGGGAGGGGGGGAT
2294	TTCTCTTCGGGGAGGGGGGGATT
2295	TCTCTTCGGGGAGGGGGGGATTG
2296	CTCTTCGGGGAGGGGGGGATTGG
2297	TCTTCGGGGAGGGGGGGATTGGG
2298	CTTCGGGGAGGGGGGGATTGGGG
2299	TTCGGGGAGGGGGGGATTGGGGG
2300	TCGGGGAGGGGGGGATTGGGGGA
2301	CGGGGAGGGGGGGATTGGGGGAG
2302	GGGGAGGGGGGGATTGGGGGAGG
2303	GGGAGGGGGGGATTGGGGGAGGG
2304	GGAGGGGGGGATTGGGGGAGGGG

Fig. 29 cont'd (Sheet 48 of 170)

ID	SEQUENCE
2305	GAGGGGGGGATTGGGGGAGGGGC
2306	AGGGGGGGATTGGGGGAGGGGCC
2307	GGGGGGGATTGGGGGAGGGGCCC
2308	GGGGGGATTGGGGGAGGGGCCCC
2309	GGGGGATTGGGGGAGGGGCCCCA
2310	GGGGATTGGGGGAGGGGCCCCAG
2311	GGGATTGGGGGAGGGGCCCCAGA
2312	GGATTGGGGGAGGGGCCCCAGAG
2313	GATTGGGGGAGGGGCCCCAGAGG
2314	ATTGGGGGAGGGGCCCCAGAGGG
2315	TTGGGGGAGGGGCCCCAGAGGGG
2316	TGGGGGAGGGGCCCCAGAGGGGT
2317	GGGGGAGGGGCCCCAGAGGGGTT
2318	GGGGAGGGGCCCCAGAGGGGTTT
2319	GGGAGGGGCCCCAGAGGGGTTTT
2320	GGAGGGGCCCCAGAGGGGTTTTA
2321	GAGGGGCCCCAGAGGGGTTTTAT
2322	AGGGGCCCCAGAGGGGTTTTATA
2323	GGGGCCCCAGAGGGGTTTTATAG
2324	GGGCCCCAGAGGGGTTTTATAGG
2325	GGCCCCAGAGGGGTTTTATAGGG
2326	GCCCCAGAGGGGTTTTATAGGGG
2327	CCCCAGAGGGGTTTTATAGGGGC
2328	CCCAGAGGGGTTTTATAGGGGCC
2329	CCAGAGGGGTTTTATAGGGGCCT
2330	CAGAGGGGTTTTATAGGGGCCTT
2331	AGAGGGGTTTTATAGGGGCCTTT
2332	GAGGGGTTTTATAGGGGCCTTTT
2333	AGGGGTTTTATAGGGGCCTTTTC
2334	GGGGTTTTATAGGGGCCTTTTCA
2335	GGGTTTTATAGGGGCCTTTTCAC
2336	GGTTTTATAGGGGCCTTTTCACT
2337	GTTTTATAGGGGCCTTTTCACTT
2338	TTTTATAGGGGCCTTTTCACTTT
2339	TTTATAGGGGCCTTTTCACTTTC
2340	TTATAGGGGCCTTTTCACTTTCT
2341	TATAGGGGCCTTTTCACTTTCTA
2342	ATAGGGGCCTTTTCACTTTCTAC
2343	TAGGGGCCTTTTCACTTTCTACT
2344	AGGGGCCTTTTCACTTTCTACTT
2345	GGGGCCTTTTCACTTTCTACTTT
2346	GGGCCTTTTCACTTTCTACTTTT
2347	GGCCTTTTCACTTTCTACTTTTT
2348	GCCTTTTCACTTTCTACTTTTTT
2349	CCTTTTCACTTTCTACTTTTTTC
2350	CTTTTCACTTTCTACTTTTTTCA
2351	TTTTCACTTTCTACTTTTTTCAT
2352	TTTCACTTTCTACTTTTTTCATT

Fig. 29 cont'd (Sheet 49 of 170)

ID	SEQUENCE
2353	TTCACTTTCTACTTTTTTCATTT
2354	TCACTTTCTACTTTTTTCATTTT
2355	CACTTTCTACTTTTTTCATTTTG
2356	ACTTTCTACTTTTTTCATTTTGT
2357	CTTTCTACTTTTTTCATTTTGTT
2358	TTTCTACTTTTTTCATTTTGTTC
2359	TTCTACTTTTTTCATTTTGTTCT
2360	TCTACTTTTTTCATTTTGTTCTG
2361	CTACTTTTTTCATTTTGTTCTGT
2362	TACTTTTTTCATTTTGTTCTGTT
2363	ACTTTTTTCATTTTGTTCTGTTC
2364	CTTTTTTCATTTTGTTCTGTTCG
2365	TTTTTTCATTTTGTTCTGTTCGA
2366	TTTTTCATTTTGTTCTGTTCGAA
2367	TTTTCATTTTGTTCTGTTCGAAT
2368	TTTCATTTTGTTCTGTTCGAATT
2369	TTCATTTTGTTCTGTTCGAATTT
2370	TCATTTTGTTCTGTTCGAATTTT
2371	CATTTTGTTCTGTTCGAATTTTT
2372	ATTTTGTTCTGTTCGAATTTTTT
2373	TTTTGTTCTGTTCGAATTTTTTA
2374	TTTGTTCTGTTCGAATTTTTTAT
2375	TTGTTCTGTTCGAATTTTTTATA
2376	TGTTCTGTTCGAATTTTTTATAA
2377	GTTCTGTTCGAATTTTTTATAAG
2378	TTCTGTTCGAATTTTTTATAAGT
2379	TCTGTTCGAATTTTTTATAAGTA
2380	CTGTTCGAATTTTTTATAAGTAT
2381	TGTTCGAATTTTTTATAAGTATG
2382	GTTCGAATTTTTTATAAGTATGT
2383	TTCGAATTTTTTATAAGTATGTA
2384	TCGAATTTTTTATAAGTATGTAT
2385	CGAATTTTTTATAAGTATGTATT
2386	GAATTTTTTATAAGTATGTATTA
2387	AATTTTTTATAAGTATGTATTAC
2388	ATTTTTTATAAGTATGTATTACT
2389	TTTTTTATAAGTATGTATTACTT
2390	TTTTTATAAGTATGTATTACTTT
2391	TTTTATAAGTATGTATTACTTTT
2392	TTTATAAGTATGTATTACTTTTG
2393	TTATAAGTATGTATTACTTTTGT
2394	TATAAGTATGTATTACTTTTGTA
2395	ATAAGTATGTATTACTTTTGTAA
2396	TAAGTATGTATTACTTTTGTAAT
2397	AAGTATGTATTACTTTTGTAATC
2398	AGTATGTATTACTTTTGTAATCA
2399	GTATGTATTACTTTTGTAATCAG
2400	TATGTATTACTTTTGTAATCAGA

Fig. 29 cont'd (Sheet 50 of 170)

ID	SEQUENCE
2401	ATGTATTACTTTTGTAATCAGAA
2402	TGTATTACTTTTGTAATCAGAAT
2403	GTATTACTTTTGTAATCAGAATT
2404	TATTACTTTTGTAATCAGAATTT
2405	ATTACTTTTGTAATCAGAATTTT
2406	TTACTTTTGTAATCAGAATTTTT
2407	TACTTTTGTAATCAGAATTTTTA
2408	ACTTTTGTAATCAGAATTTTTAG
2409	CTTTTGTAATCAGAATTTTTAGA
2410	TTTTGTAATCAGAATTTTTAGAA
2411	TTTGTAATCAGAATTTTTAGAAA
2412	TTGTAATCAGAATTTTTAGAAAG
2413	TGTAATCAGAATTTTTAGAAAGT
2414	GTAATCAGAATTTTTAGAAAGTA
2415	TAATCAGAATTTTTAGAAAGTAT
2416	AATCAGAATTTTTAGAAAGTATT
2417	ATCAGAATTTTTAGAAAGTATTT
2418	TCAGAATTTTTAGAAAGTATTTT
2419	CAGAATTTTTAGAAAGTATTTTG
2420	AGAATTTTTAGAAAGTATTTTGC
2421	GAATTTTTAGAAAGTATTTTGCT
2422	AATTTTTAGAAAGTATTTTGCTG
2423	ATTTTTAGAAAGTATTTTGCTGA
2424	TTTTTAGAAAGTATTTTGCTGAT
2425	TTTTAGAAAGTATTTTGCTGATT
2426	TTTAGAAAGTATTTTGCTGATTT
2427	TTAGAAAGTATTTTGCTGATTTA
2428	TAGAAAGTATTTTGCTGATTTAA
2429	AGAAAGTATTTTGCTGATTTAAA
2430	GAAAGTATTTTGCTGATTTAAAG
2431	AAAGTATTTTGCTGATTTAAAGG
2432	AAGTATTTTGCTGATTTAAAGGC
2433	AGTATTTTGCTGATTTAAAGGCT
2434	GTATTTTGCTGATTTAAAGGCTT
2435	TATTTTGCTGATTTAAAGGCTTA
2436	ATTTTGCTGATTTAAAGGCTTAG
2437	TTTTGCTGATTTAAAGGCTTAGG
2438	TTTGCTGATTTAAAGGCTTAGGC
2439	TTGCTGATTTAAAGGCTTAGGCA
2440	TGCTGATTTAAAGGCTTAGGCAT
2441	GCTGATTTAAAGGCTTAGGCATG
2442	CTGATTTAAAGGCTTAGGCATGT
2443	TGATTTAAAGGCTTAGGCATGTT
2444	GATTTAAAGGCTTAGGCATGTTC
2445	ATTTAAAGGCTTAGGCATGTTCA
2446	TTTAAAGGCTTAGGCATGTTCAA
2447	TTAAAGGCTTAGGCATGTTCAAA
2448	TAAAGGCTTAGGCATGTTCAAAC

Fig. 29 cont'd (Sheet 51 of 170)

ID	SEQUENCE
2449	AAAGGCTTAGGCATGTTCAAACG
2450	AAGGCTTAGGCATGTTCAAACGC
2451	AGGCTTAGGCATGTTCAAACGCC
2452	GGCTTAGGCATGTTCAAACGCCT
2453	GCTTAGGCATGTTCAAACGCCTG
2454	CTTAGGCATGTTCAAACGCCTGC
2455	TTAGGCATGTTCAAACGCCTGCA
2456	TAGGCATGTTCAAACGCCTGCAA
2457	AGGCATGTTCAAACGCCTGCAAA
2458	GGCATGTTCAAACGCCTGCAAAA
2459	GCATGTTCAAACGCCTGCAAAAC
2460	CATGTTCAAACGCCTGCAAAACT
2461	ATGTTCAAACGCCTGCAAAACTA
2462	TGTTCAAACGCCTGCAAAACTAC
2463	GTTCAAACGCCTGCAAAACTACT
2464	TTCAAACGCCTGCAAAACTACTT
2465	TCAAACGCCTGCAAAACTACTTA
2466	CAAACGCCTGCAAAACTACTTAT
2467	AAACGCCTGCAAAACTACTTATC
2468	AACGCCTGCAAAACTACTTATCA
2469	ACGCCTGCAAAACTACTTATCAC
2470	CGCCTGCAAAACTACTTATCACT
2471	GCCTGCAAAACTACTTATCACTC
2472	CCTGCAAAACTACTTATCACTCA
2473	CTGCAAAACTACTTATCACTCAG
2474	TGCAAAACTACTTATCACTCAGC
2475	GCAAAACTACTTATCACTCAGCT
2476	CAAAACTACTTATCACTCAGCTT
2477	AAAACTACTTATCACTCAGCTTT
2478	AAACTACTTATCACTCAGCTTTA
2479	AACTACTTATCACTCAGCTTTAG
2480	ACTACTTATCACTCAGCTTTAGT
2481	CTACTTATCACTCAGCTTTAGTT
2482	TACTTATCACTCAGCTTTAGTTT
2483	ACTTATCACTCAGCTTTAGTTTT
2484	CTTATCACTCAGCTTTAGTTTTT
2485	TTATCACTCAGCTTTAGTTTTTC
2486	TATCACTCAGCTTTAGTTTTTCT
2487	ATCACTCAGCTTTAGTTTTTCTA
2488	TCACTCAGCTTTAGTTTTTCTAA
2489	CACTCAGCTTTAGTTTTTCTAAT
2490	ACTCAGCTTTAGTTTTTCTAATC
2491	CTCAGCTTTAGTTTTTCTAATCC
2492	TCAGCTTTAGTTTTTCTAATCCA
2493	CAGCTTTAGTTTTTCTAATCCAA
2494	AGCTTTAGTTTTTCTAATCCAAG
2495	GCTTTAGTTTTTCTAATCCAAGA
2496	CTTTAGTTTTTCTAATCCAAGAA

Fig. 29 cont'd (Sheet 52 of 170)

ID	SEQUENCE
2497	TTTAGTTTTTCTAATCCAAGAAG
2498	TTAGTTTTTCTAATCCAAGAAGG
2499	TAGTTTTTCTAATCCAAGAAGGC
2500	AGTTTTTCTAATCCAAGAAGGCA
2501	GTTTTTCTAATCCAAGAAGGCAG
2502	TTTTTCTAATCCAAGAAGGCAGG
2503	TTTTCTAATCCAAGAAGGCAGGG
2504	TTTCTAATCCAAGAAGGCAGGGC
2505	TTCTAATCCAAGAAGGCAGGGCA
2506	TCTAATCCAAGAAGGCAGGGCAG
2507	CTAATCCAAGAAGGCAGGGCAGT
2508	TAATCCAAGAAGGCAGGGCAGTT
2509	AATCCAAGAAGGCAGGGCAGTTA
2510	ATCCAAGAAGGCAGGGCAGTTAA
2511	TCCAAGAAGGCAGGGCAGTTAAC
2512	CCAAGAAGGCAGGGCAGTTAACC
2513	CAAGAAGGCAGGGCAGTTAACCT
2514	AAGAAGGCAGGGCAGTTAACCTT
2515	AGAAGGCAGGGCAGTTAACCTTT
2516	GAAGGCAGGGCAGTTAACCTTTT
2517	AAGGCAGGGCAGTTAACCTTTTT
2518	AGGCAGGGCAGTTAACCTTTTTG
2519	GGCAGGGCAGTTAACCTTTTTGG
2520	GCAGGGCAGTTAACCTTTTTGGT
2521	CAGGGCAGTTAACCTTTTTGGTG
2522	AGGGCAGTTAACCTTTTTGGTGC
2523	GGGCAGTTAACCTTTTTGGTGCC
2524	GGCAGTTAACCTTTTTGGTGCCA
2525	GCAGTTAACCTTTTTGGTGCCAA
2526	CAGTTAACCTTTTTGGTGCCAAT
2527	AGTTAACCTTTTTGGTGCCAATG
2528	GTTAACCTTTTTGGTGCCAATGT
2529	TTAACCTTTTTGGTGCCAATGTG
2530	TAACCTTTTTGGTGCCAATGTGA
2531	AACCTTTTTGGTGCCAATGTGAA
2532	ACCTTTTTGGTGCCAATGTGAAA
2533	CCTTTTTGGTGCCAATGTGAAAT
2534	CTTTTTGGTGCCAATGTGAAATG
2535	TTTTTGGTGCCAATGTGAAATGT
2536	TTTTGGTGCCAATGTGAAATGTA
2537	TTTGGTGCCAATGTGAAATGTAA
2538	TTGGTGCCAATGTGAAATGTAAA
2539	TGGTGCCAATGTGAAATGTAAAT
2540	GGTGCCAATGTGAAATGTAAATG
2541	GTGCCAATGTGAAATGTAAATGA
2542	TGCCAATGTGAAATGTAAATGAT
2543	GCCAATGTGAAATGTAAATGATT
2544	CCAATGTGAAATGTAAATGATTT

Fig. 29 cont'd (Sheet 53 of 170)

ID	SEQUENCE
2545	CAATGTGAAATGTAAATGATTTT
2546	AATGTGAAATGTAAATGATTTTA
2547	ATGTGAAATGTAAATGATTTTAT
2548	TGTGAAATGTAAATGATTTTATG
2549	GTGAAATGTAAATGATTTTATGT
2550	TGAAATGTAAATGATTTTATGTT
2551	GAAATGTAAATGATTTTATGTTT
2552	AAATGTAAATGATTTTATGTTTT
2553	AATGTAAATGATTTTATGTTTTT
2554	ATGTAAATGATTTTATGTTTTTC
2555	TGTAAATGATTTTATGTTTTTCC
2556	GTAAATGATTTTATGTTTTTCCT
2557	TAAATGATTTTATGTTTTTCCTG
2558	AAATGATTTTATGTTTTTCCTGC
2559	AATGATTTTATGTTTTTCCTGCT
2560	ATGATTTTATGTTTTTCCTGCTT
2561	TGATTTTATGTTTTTCCTGCTTT
2562	GATTTTATGTTTTTCCTGCTTTG
2563	ATTTTATGTTTTTCCTGCTTTGT
2564	TTTTATGTTTTTCCTGCTTTGTG
2565	TTTATGTTTTTCCTGCTTTGTGG
2566	TTATGTTTTTCCTGCTTTGTGGA
2567	TATGTTTTTCCTGCTTTGTGGAT
2568	ATGTTTTTCCTGCTTTGTGGATG
2569	TGTTTTTCCTGCTTTGTGGATGA
2570	GTTTTTCCTGCTTTGTGGATGAA
2571	TTTTTCCTGCTTTGTGGATGAAA
2572	TTTTCCTGCTTTGTGGATGAAAA
2573	TTTCCTGCTTTGTGGATGAAAAA
2574	TTCCTGCTTTGTGGATGAAAAAT
2575	TCCTGCTTTGTGGATGAAAAATA
2576	CCTGCTTTGTGGATGAAAAATAT
2577	CTGCTTTGTGGATGAAAAATATT
2578	TGCTTTGTGGATGAAAAATATTT
2579	GCTTTGTGGATGAAAAATATTTC
2580	CTTTGTGGATGAAAAATATTTCT
2581	TTTGTGGATGAAAAATATTTCTG
2582	TTGTGGATGAAAAATATTTCTGA
2583	TGTGGATGAAAAATATTTCTGAG
2584	GTGGATGAAAAATATTTCTGAGT
2585	TGGATGAAAAATATTTCTGAGTG
2586	GGATGAAAAATATTTCTGAGTGG
2587	GATGAAAAATATTTCTGAGTGGT
2588	ATGAAAAATATTTCTGAGTGGTA
2589	TGAAAAATATTTCTGAGTGGTAG
2590	GAAAAATATTTCTGAGTGGTAGT
2591	AAAAATATTTCTGAGTGGTAGTT
2592	AAAATATTTCTGAGTGGTAGTTT

Fig. 29 cont'd (Sheet 54 of 170)

ID	SEQUENCE
2593	AAATATTTCTGAGTGGTAGTTTT
2594	AATATTTCTGAGTGGTAGTTTTT
2595	ATATTTCTGAGTGGTAGTTTTTT
2596	TATTTCTGAGTGGTAGTTTTTTG
2597	ATTTCTGAGTGGTAGTTTTTTGA
2598	TTTCTGAGTGGTAGTTTTTTGAC
2599	TTCTGAGTGGTAGTTTTTTGACA
2600	TCTGAGTGGTAGTTTTTTGACAG
2601	CTGAGTGGTAGTTTTTTGACAGG
2602	TGAGTGGTAGTTTTTTGACAGGT
2603	GAGTGGTAGTTTTTTGACAGGTA
2604	AGTGGTAGTTTTTTGACAGGTAG
2605	GTGGTAGTTTTTTGACAGGTAGA
2606	TGGTAGTTTTTTGACAGGTAGAC
2607	GGTAGTTTTTTGACAGGTAGACC
2608	GTAGTTTTTTGACAGGTAGACCA
2609	TAGTTTTTTGACAGGTAGACCAT
2610	AGTTTTTTGACAGGTAGACCATG
2611	GTTTTTTGACAGGTAGACCATGT
2612	TTTTTTGACAGGTAGACCATGTC
2613	TTTTTGACAGGTAGACCATGTCT
2614	TTTTGACAGGTAGACCATGTCTT
2615	TTTGACAGGTAGACCATGTCTTA
2616	TTGACAGGTAGACCATGTCTTAT
2617	TGACAGGTAGACCATGTCTTATC
2618	GACAGGTAGACCATGTCTTATCT
2619	ACAGGTAGACCATGTCTTATCTT
2620	CAGGTAGACCATGTCTTATCTTG
2621	AGGTAGACCATGTCTTATCTTGT
2622	GGTAGACCATGTCTTATCTTGTT
2623	GTAGACCATGTCTTATCTTGTTT
2624	TAGACCATGTCTTATCTTGTTTC
2625	AGACCATGTCTTATCTTGTTTCA
2626	GACCATGTCTTATCTTGTTTCAA
2627	ACCATGTCTTATCTTGTTTCAAA
2628	CCATGTCTTATCTTGTTTCAAAA
2629	CATGTCTTATCTTGTTTCAAAAT
2630	ATGTCTTATCTTGTTTCAAAATA
2631	TGTCTTATCTTGTTTCAAAATAA
2632	GTCTTATCTTGTTTCAAAATAAG
2633	TCTTATCTTGTTTCAAAATAAGT
2634	CTTATCTTGTTTCAAAATAAGTA
2635	TTATCTTGTTTCAAAATAAGTAT
2636	TATCTTGTTTCAAAATAAGTATT
2637	ATCTTGTTTCAAAATAAGTATTT
2638	TCTTGTTTCAAAATAAGTATTTC
2639	CTTGTTTCAAAATAAGTATTTCT
2640	TTGTTTCAAAATAAGTATTTCTG

Fig. 29 cont'd (Sheet 55 of 170)

ID	SEQUENCE
2641	TGTTTCAAAATAAGTATTTCTGA
2642	GTTTCAAAATAAGTATTTCTGAT
2643	TTTCAAAATAAGTATTTCTGATT
2644	TTCAAAATAAGTATTTCTGATTT
2645	TCAAAATAAGTATTTCTGATTTT
2646	CAAAATAAGTATTTCTGATTTTG
2647	AAAATAAGTATTTCTGATTTTGT
2648	AAATAAGTATTTCTGATTTTGTA
2649	AATAAGTATTTCTGATTTTGTAA
2650	ATAAGTATTTCTGATTTTGTAAA
2651	TAAGTATTTCTGATTTTGTAAAA
2652	AAGTATTTCTGATTTTGTAAAAT
2653	AGTATTTCTGATTTTGTAAAATG
2654	GTATTTCTGATTTTGTAAAATGA
2655	TATTTCTGATTTTGTAAAATGAA
2656	ATTTCTGATTTTGTAAAATGAAA
2657	TTTCTGATTTTGTAAAATGAAAT
2658	TTCTGATTTTGTAAAATGAAATA
2659	TCTGATTTTGTAAAATGAAATAT
2660	CTGATTTTGTAAAATGAAATATA
2661	TGATTTTGTAAAATGAAATATAA
2662	GATTTTGTAAAATGAAATATAAA
2663	ATTTTGTAAAATGAAATATAAAA
2664	TTTTGTAAAATGAAATATAAAAT
2665	TTTGTAAAATGAAATATAAAATA
2666	TTGTAAAATGAAATATAAAATAT
2667	TGTAAAATGAAATATAAAATATG
2668	GTAAAATGAAATATAAAATATGT
2669	TAAAATGAAATATAAAATATGTC
2670	AAAATGAAATATAAAATATGTCT
2671	AAATGAAATATAAAATATGTCTC
2672	AATGAAATATAAAATATGTCTCA
2673	ATGAAATATAAAATATGTCTCAG
2674	TGAAATATAAAATATGTCTCAGA
2675	GAAATATAAAATATGTCTCAGAT
2676	AAATATAAAATATGTCTCAGATC
2677	AATATAAAATATGTCTCAGATCT
2678	ATATAAAATATGTCTCAGATCTT
2679	TATAAAATATGTCTCAGATCTTC
2680	ATAAAATATGTCTCAGATCTTCC
2681	TAAAATATGTCTCAGATCTTCCA
2682	AAAATATGTCTCAGATCTTCCAA
2683	AAATATGTCTCAGATCTTCCAAT
2684	AATATGTCTCAGATCTTCCAATT
2685	ATATGTCTCAGATCTTCCAATTA
2686	TATGTCTCAGATCTTCCAATTAA
2687	ATGTCTCAGATCTTCCAATTAAT
2688	TGTCTCAGATCTTCCAATTAATT

Fig. 29 cont'd (Sheet 56 of 170)

ID	SEQUENCE
2689	GTCTCAGATCTTCCAATTAATTA
2690	TCTCAGATCTTCCAATTAATTAG
2691	CTCAGATCTTCCAATTAATTAGT
2692	TCAGATCTTCCAATTAATTAGTA
2693	CAGATCTTCCAATTAATTAGTAA
2694	AGATCTTCCAATTAATTAGTAAG
2695	GATCTTCCAATTAATTAGTAAGG
2696	ATCTTCCAATTAATTAGTAAGGA
2697	TCTTCCAATTAATTAGTAAGGAT
2698	CTTCCAATTAATTAGTAAGGATT
2699	TTCCAATTAATTAGTAAGGATTC
2700	TCCAATTAATTAGTAAGGATTCA
2701	CCAATTAATTAGTAAGGATTCAT
2702	CAATTAATTAGTAAGGATTCATC
2703	AATTAATTAGTAAGGATTCATCC
2704	ATTAATTAGTAAGGATTCATCCT
2705	TTAATTAGTAAGGATTCATCCTT
2706	TAATTAGTAAGGATTCATCCTTA
2707	AATTAGTAAGGATTCATCCTTAA
2708	ATTAGTAAGGATTCATCCTTAAT
2709	TTAGTAAGGATTCATCCTTAATC
2710	TAGTAAGGATTCATCCTTAATCC
2711	AGTAAGGATTCATCCTTAATCCT
2712	GTAAGGATTCATCCTTAATCCTT
2713	TAAGGATTCATCCTTAATCCTTG
2714	AAGGATTCATCCTTAATCCTTGC
2715	AGGATTCATCCTTAATCCTTGCT
2716	GGATTCATCCTTAATCCTTGCTA
2717	GATTCATCCTTAATCCTTGCTAG
2718	ATTCATCCTTAATCCTTGCTAGT
2719	TTCATCCTTAATCCTTGCTAGTT
2720	TCATCCTTAATCCTTGCTAGTTT
2721	CATCCTTAATCCTTGCTAGTTTA
2722	ATCCTTAATCCTTGCTAGTTTAA
2723	TCCTTAATCCTTGCTAGTTTAAG
2724	CCTTAATCCTTGCTAGTTTAAGC
2725	CTTAATCCTTGCTAGTTTAAGCC
2726	TTAATCCTTGCTAGTTTAAGCCT
2727	TAATCCTTGCTAGTTTAAGCCTG
2728	AATCCTTGCTAGTTTAAGCCTGC
2729	ATCCTTGCTAGTTTAAGCCTGCC
2730	TCCTTGCTAGTTTAAGCCTGCCT
2731	CCTTGCTAGTTTAAGCCTGCCTA
2732	CTTGCTAGTTTAAGCCTGCCTAA
2733	TTGCTAGTTTAAGCCTGCCTAAG
2734	TGCTAGTTTAAGCCTGCCTAAGT
2735	GCTAGTTTAAGCCTGCCTAAGTC
2736	CTAGTTTAAGCCTGCCTAAGTCA

Fig. 29 cont'd (Sheet 57 of 170)

ID	SEQUENCE
2737	TAGTTTAAGCCTGCCTAAGTCAC
2738	AGTTTAAGCCTGCCTAAGTCACT
2739	GTTTAAGCCTGCCTAAGTCACTT
2740	TTTAAGCCTGCCTAAGTCACTTT
2741	TTAAGCCTGCCTAAGTCACTTTA
2742	TAAGCCTGCCTAAGTCACTTTAC
2743	AAGCCTGCCTAAGTCACTTTACT
2744	AGCCTGCCTAAGTCACTTTACTA
2745	GCCTGCCTAAGTCACTTTACTAA
2746	CCTGCCTAAGTCACTTTACTAAA
2747	CTGCCTAAGTCACTTTACTAAAA
2748	TGCCTAAGTCACTTTACTAAAAG
2749	GCCTAAGTCACTTTACTAAAAGA
2750	CCTAAGTCACTTTACTAAAAGAT
2751	CTAAGTCACTTTACTAAAAGATC
2752	TAAGTCACTTTACTAAAAGATCT
2753	AAGTCACTTTACTAAAAGATCTT
2754	AGTCACTTTACTAAAAGATCTTT
2755	GTCACTTTACTAAAAGATCTTTG
2756	TCACTTTACTAAAAGATCTTTGT
2757	CACTTTACTAAAAGATCTTTGTT
2758	ACTTTACTAAAAGATCTTTGTTA
2759	CTTTACTAAAAGATCTTTGTTAA
2760	TTTACTAAAAGATCTTTGTTAAC
2761	TTACTAAAAGATCTTTGTTAACT
2762	TACTAAAAGATCTTTGTTAACTC
2763	ACTAAAAGATCTTTGTTAACTCA
2764	CTAAAAGATCTTTGTTAACTCAG
2765	TAAAAGATCTTTGTTAACTCAGT
2766	AAAAGATCTTTGTTAACTCAGTA
2767	AAAGATCTTTGTTAACTCAGTAT
2768	AAGATCTTTGTTAACTCAGTATT
2769	AGATCTTTGTTAACTCAGTATTT
2770	GATCTTTGTTAACTCAGTATTTT
2771	ATCTTTGTTAACTCAGTATTTTA
2772	TCTTTGTTAACTCAGTATTTTAA
2773	CTTTGTTAACTCAGTATTTTAAA
2774	TTTGTTAACTCAGTATTTTAAAC
2775	TTGTTAACTCAGTATTTTAAACA
2776	TGTTAACTCAGTATTTTAAACAT
2777	GTTAACTCAGTATTTTAAACATC
2778	TTAACTCAGTATTTTAAACATCT
2779	TAACTCAGTATTTTAAACATCTG
2780	AACTCAGTATTTTAAACATCTGT
2781	ACTCAGTATTTTAAACATCTGTC
2782	CTCAGTATTTTAAACATCTGTCA
2783	TCAGTATTTTAAACATCTGTCAG
2784	CAGTATTTTAAACATCTGTCAGC

Fig. 29 cont'd (Sheet 58 of 170)

ID	SEQUENCE
2785	AGTATTTTAAACATCTGTCAGCT
2786	GTATTTTAAACATCTGTCAGCTT
2787	TATTTTAAACATCTGTCAGCTTA
2788	ATTTTAAACATCTGTCAGCTTAT
2789	TTTTAAACATCTGTCAGCTTATG
2790	TTTAAACATCTGTCAGCTTATGT
2791	TTAAACATCTGTCAGCTTATGTA
2792	TAAACATCTGTCAGCTTATGTAG
2793	AAACATCTGTCAGCTTATGTAGG
2794	AACATCTGTCAGCTTATGTAGGT
2795	ACATCTGTCAGCTTATGTAGGTA
2796	CATCTGTCAGCTTATGTAGGTAA
2797	ATCTGTCAGCTTATGTAGGTAAA
2798	TCTGTCAGCTTATGTAGGTAAAA
2799	CTGTCAGCTTATGTAGGTAAAAG
2800	TGTCAGCTTATGTAGGTAAAAGT
2801	GTCAGCTTATGTAGGTAAAAGTA
2802	TCAGCTTATGTAGGTAAAAGTAG
2803	CAGCTTATGTAGGTAAAAGTAGA
2804	AGCTTATGTAGGTAAAAGTAGAA
2805	GCTTATGTAGGTAAAAGTAGAAG
2806	CTTATGTAGGTAAAAGTAGAAGC
2807	TTATGTAGGTAAAAGTAGAAGCA
2808	TATGTAGGTAAAAGTAGAAGCAT
2809	ATGTAGGTAAAAGTAGAAGCATG
2810	TGTAGGTAAAAGTAGAAGCATGT
2811	GTAGGTAAAAGTAGAAGCATGTT
2812	TAGGTAAAAGTAGAAGCATGTTT
2813	AGGTAAAAGTAGAAGCATGTTTG
2814	GGTAAAAGTAGAAGCATGTTTGT
2815	GTAAAAGTAGAAGCATGTTTGTA
2816	TAAAAGTAGAAGCATGTTTGTAC
2817	AAAAGTAGAAGCATGTTTGTACA
2818	AAAGTAGAAGCATGTTTGTACAC
2819	AAGTAGAAGCATGTTTGTACACT
2820	AGTAGAAGCATGTTTGTACACTG
2821	GTAGAAGCATGTTTGTACACTGC
2822	TAGAAGCATGTTTGTACACTGCT
2823	AGAAGCATGTTTGTACACTGCTT
2824	GAAGCATGTTTGTACACTGCTTG
2825	AAGCATGTTTGTACACTGCTTGT
2826	AGCATGTTTGTACACTGCTTGTA
2827	GCATGTTTGTACACTGCTTGTAG
2828	CATGTTTGTACACTGCTTGTAGT
2829	ATGTTTGTACACTGCTTGTAGTT
2830	TGTTTGTACACTGCTTGTAGTTA
2831	GTTTGTACACTGCTTGTAGTTAT
2832	TTTGTACACTGCTTGTAGTTATA

Fig. 29 cont'd (Sheet 59 of 170)

ID	SEQUENCE
2833	TTGTACACTGCTTGTAGTTATAG
2834	TGTACACTGCTTGTAGTTATAGT
2835	GTACACTGCTTGTAGTTATAGTG
2836	TACACTGCTTGTAGTTATAGTGA
2837	ACACTGCTTGTAGTTATAGTGAC
2838	CACTGCTTGTAGTTATAGTGACA
2839	ACTGCTTGTAGTTATAGTGACAG
2840	CTGCTTGTAGTTATAGTGACAGC
2841	TGCTTGTAGTTATAGTGACAGCT
2842	GCTTGTAGTTATAGTGACAGCTT
2843	CTTGTAGTTATAGTGACAGCTTT
2844	TTGTAGTTATAGTGACAGCTTTC
2845	TGTAGTTATAGTGACAGCTTTCC
2846	GTAGTTATAGTGACAGCTTTCCA
2847	TAGTTATAGTGACAGCTTTCCAT
2848	AGTTATAGTGACAGCTTTCCATG
2849	GTTATAGTGACAGCTTTCCATGT
2850	TTATAGTGACAGCTTTCCATGTT
2851	TATAGTGACAGCTTTCCATGTTG
2852	ATAGTGACAGCTTTCCATGTTGA
2853	TAGTGACAGCTTTCCATGTTGAG
2854	AGTGACAGCTTTCCATGTTGAGA
2855	GTGACAGCTTTCCATGTTGAGAT
2856	TGACAGCTTTCCATGTTGAGATT
2857	GACAGCTTTCCATGTTGAGATTC
2858	ACAGCTTTCCATGTTGAGATTCT
2859	CAGCTTTCCATGTTGAGATTCTC
2860	AGCTTTCCATGTTGAGATTCTCA
2861	GCTTTCCATGTTGAGATTCTCAT
2862	CTTTCCATGTTGAGATTCTCATA
2863	TTTCCATGTTGAGATTCTCATAT
2864	TTCCATGTTGAGATTCTCATATC
2865	TCCATGTTGAGATTCTCATATCA
2866	CCATGTTGAGATTCTCATATCAT
2867	CATGTTGAGATTCTCATATCATC
2868	ATGTTGAGATTCTCATATCATCT
2869	TGTTGAGATTCTCATATCATCTT
2870	GTTGAGATTCTCATATCATCTTG
2871	TTGAGATTCTCATATCATCTTGT
2872	TGAGATTCTCATATCATCTTGTA
2873	GAGATTCTCATATCATCTTGTAT
2874	AGATTCTCATATCATCTTGTATC
2875	GATTCTCATATCATCTTGTATCT
2876	ATTCTCATATCATCTTGTATCTT
2877	TTCTCATATCATCTTGTATCTTA
2878	TCTCATATCATCTTGTATCTTAA
2879	CTCATATCATCTTGTATCTTAAA
2880	TCATATCATCTTGTATCTTAAAG

Fig. 29 cont'd (Sheet 60 of 170)

ID	SEQUENCE
2881	CATATCATCTTGTATCTTAAAGT
2882	ATATCATCTTGTATCTTAAAGTT
2883	TATCATCTTGTATCTTAAAGTTT
2884	ATCATCTTGTATCTTAAAGTTTC
2885	TCATCTTGTATCTTAAAGTTTCA
2886	CATCTTGTATCTTAAAGTTTCAT
2887	ATCTTGTATCTTAAAGTTTCATG
2888	TCTTGTATCTTAAAGTTTCATGT
2889	CTTGTATCTTAAAGTTTCATGTG
2890	TTGTATCTTAAAGTTTCATGTGA
2891	TGTATCTTAAAGTTTCATGTGAG
2892	GTATCTTAAAGTTTCATGTGAGT
2893	TATCTTAAAGTTTCATGTGAGTT
2894	ATCTTAAAGTTTCATGTGAGTTT
2895	TCTTAAAGTTTCATGTGAGTTTT
2896	CTTAAAGTTTCATGTGAGTTTTT
2897	TTAAAGTTTCATGTGAGTTTTTA
2898	TAAAGTTTCATGTGAGTTTTTAC
2899	AAAGTTTCATGTGAGTTTTTACC
2900	AAGTTTCATGTGAGTTTTTACCG
2901	AGTTTCATGTGAGTTTTTACCGT
2902	GTTTCATGTGAGTTTTTACCGTT
2903	TTTCATGTGAGTTTTTACCGTTA
2904	TTCATGTGAGTTTTTACCGTTAG
2905	TCATGTGAGTTTTTACCGTTAGG
2906	CATGTGAGTTTTTACCGTTAGGA
2907	ATGTGAGTTTTTACCGTTAGGAT
2908	TGTGAGTTTTTACCGTTAGGATG
2909	GTGAGTTTTTACCGTTAGGATGA
2910	TGAGTTTTTACCGTTAGGATGAT
2911	GAGTTTTTACCGTTAGGATGATT
2912	AGTTTTTACCGTTAGGATGATTA
2913	GTTTTTACCGTTAGGATGATTAA
2914	TTTTTACCGTTAGGATGATTAAG
2915	TTTTACCGTTAGGATGATTAAGA
2916	TTTACCGTTAGGATGATTAAGAT
2917	TTACCGTTAGGATGATTAAGATG
2918	TACCGTTAGGATGATTAAGATGT
2919	ACCGTTAGGATGATTAAGATGTA
2920	CCGTTAGGATGATTAAGATGTAT
2921	CGTTAGGATGATTAAGATGTATA
2922	GTTAGGATGATTAAGATGTATAT
2923	TTAGGATGATTAAGATGTATATA
2924	TAGGATGATTAAGATGTATATAG
2925	AGGATGATTAAGATGTATATAGG
2926	GGATGATTAAGATGTATATAGGA
2927	GATGATTAAGATGTATATAGGAC
2928	ATGATTAAGATGTATATAGGACA

Fig. 29 cont'd (Sheet 61 of 170)

ID	SEQUENCE
2929	TGATTAAGATGTATATAGGACAA
2930	GATTAAGATGTATATAGGACAAA
2931	ATTAAGATGTATATAGGACAAAA
2932	TTAAGATGTATATAGGACAAAAT
2933	TAAGATGTATATAGGACAAAATG
2934	AAGATGTATATAGGACAAAATGT
2935	AGATGTATATAGGACAAAATGTT
2936	GATGTATATAGGACAAAATGTTA
2937	ATGTATATAGGACAAAATGTTAA
2938	TGTATATAGGACAAAATGTTAAG
2939	GTATATAGGACAAAATGTTAAGT
2940	TATATAGGACAAAATGTTAAGTC
2941	ATATAGGACAAAATGTTAAGTCT
2942	TATAGGACAAAATGTTAAGTCTT
2943	ATAGGACAAAATGTTAAGTCTTT
2944	TAGGACAAAATGTTAAGTCTTTC
2945	AGGACAAAATGTTAAGTCTTTCC
2946	GGACAAAATGTTAAGTCTTTCCT
2947	GACAAAATGTTAAGTCTTTCCTC
2948	ACAAAATGTTAAGTCTTTCCTCT
2949	CAAAATGTTAAGTCTTTCCTCTA
2950	AAAATGTTAAGTCTTTCCTCTAC
2951	AAATGTTAAGTCTTTCCTCTACC
2952	AATGTTAAGTCTTTCCTCTACCT
2953	ATGTTAAGTCTTTCCTCTACCTA
2954	TGTTAAGTCTTTCCTCTACCTAC
2955	GTTAAGTCTTTCCTCTACCTACA
2956	TTAAGTCTTTCCTCTACCTACAT
2957	TAAGTCTTTCCTCTACCTACATT
2958	AAGTCTTTCCTCTACCTACATTT
2959	AGTCTTTCCTCTACCTACATTTG
2960	GTCTTTCCTCTACCTACATTTGT
2961	TCTTTCCTCTACCTACATTTGTT
2962	CTTTCCTCTACCTACATTTGTTT
2963	TTTCCTCTACCTACATTTGTTTT
2964	TTCCTCTACCTACATTTGTTTTC
2965	TCCTCTACCTACATTTGTTTTCT
2966	CCTCTACCTACATTTGTTTTCTT
2967	CTCTACCTACATTTGTTTTCTTG
2968	TCTACCTACATTTGTTTTCTTGG
2969	CTACCTACATTTGTTTTCTTGGC
2970	TACCTACATTTGTTTTCTTGGCT
2971	ACCTACATTTGTTTTCTTGGCTA
2972	CCTACATTTGTTTTCTTGGCTAG
2973	CTACATTTGTTTTCTTGGCTAGT
2974	TACATTTGTTTTCTTGGCTAGTA
2975	ACATTTGTTTTCTTGGCTAGTAA
2976	CATTTGTTTTCTTGGCTAGTAAT

Fig. 29 cont'd (Sheet 62 of 170)

ID	SEQUENCE
2977	ATTTGTTTTCTTGGCTAGTAATA
2978	TTTGTTTTCTTGGCTAGTAATAG
2979	TTGTTTTCTTGGCTAGTAATAGT
2980	TGTTTTCTTGGCTAGTAATAGTA
2981	GTTTTCTTGGCTAGTAATAGTAG
2982	TTTTCTTGGCTAGTAATAGTAGT
2983	TTTCTTGGCTAGTAATAGTAGTA
2984	TTCTTGGCTAGTAATAGTAGTAG
2985	TCTTGGCTAGTAATAGTAGTAGA
2986	CTTGGCTAGTAATAGTAGTAGAT
2987	TTGGCTAGTAATAGTAGTAGATA
2988	TGGCTAGTAATAGTAGTAGATAC
2989	GGCTAGTAATAGTAGTAGATACT
2990	GCTAGTAATAGTAGTAGATACTT
2991	CTAGTAATAGTAGTAGATACTTC
2992	TAGTAATAGTAGTAGATACTTCT
2993	AGTAATAGTAGTAGATACTTCTG
2994	GTAATAGTAGTAGATACTTCTGA
2995	TAATAGTAGTAGATACTTCTGAA
2996	AATAGTAGTAGATACTTCTGAAA
2997	ATAGTAGTAGATACTTCTGAAAT
2998	TAGTAGTAGATACTTCTGAAATA
2999	AGTAGTAGATACTTCTGAAATAA
3000	GTAGTAGATACTTCTGAAATAAA
3001	TAGTAGATACTTCTGAAATAAAT
3002	AGTAGATACTTCTGAAATAAATG
3003	GTAGATACTTCTGAAATAAATGT
3004	TAGATACTTCTGAAATAAATGTT
3005	AGATACTTCTGAAATAAATGTTC
3006	GATACTTCTGAAATAAATGTTCT
3007	ATACTTCTGAAATAAATGTTCTC
3008	TACTTCTGAAATAAATGTTCTCT
3009	ACTTCTGAAATAAATGTTCTCTC
3010	CTTCTGAAATAAATGTTCTCTCA
3011	TTCTGAAATAAATGTTCTCTCAA
3012	TCTGAAATAAATGTTCTCTCAAG
3013	CTGAAATAAATGTTCTCTCAAGA
3014	TGAAATAAATGTTCTCTCAAGAT
3015	GAAATAAATGTTCTCTCAAGATC
3016	AAATAAATGTTCTCTCAAGATCC
3017	AATAAATGTTCTCTCAAGATCCT
3018	ATAAATGTTCTCTCAAGATCCTT
3019	TAAATGTTCTCTCAAGATCCTTA
3020	AAATGTTCTCTCAAGATCCTTAA
3021	AATGTTCTCTCAAGATCCTTAAA
3022	ATGTTCTCTCAAGATCCTTAAAA
3023	TGTTCTCTCAAGATCCTTAAAAC
3024	GTTCTCTCAAGATCCTTAAAACC

Fig. 29 cont'd (Sheet 63 of 170)

ID	SEQUENCE
3025	TTCTCTCAAGATCCTTAAAACCT
3026	TCTCTCAAGATCCTTAAAACCTC
3027	CTCTCAAGATCCTTAAAACCTCT
3028	TCTCAAGATCCTTAAAACCTCTT
3029	CTCAAGATCCTTAAAACCTCTTG
3030	TCAAGATCCTTAAAACCTCTTGG
3031	CAAGATCCTTAAAACCTCTTGGA
3032	AAGATCCTTAAAACCTCTTGGAA
3033	AGATCCTTAAAACCTCTTGGAAA
3034	GATCCTTAAAACCTCTTGGAAAT
3035	ATCCTTAAAACCTCTTGGAAATT
3036	TCCTTAAAACCTCTTGGAAATTA
3037	CCTTAAAACCTCTTGGAAATTAT
3038	CTTAAAACCTCTTGGAAATTATA
3039	TTAAAACCTCTTGGAAATTATAA
3040	TAAAACCTCTTGGAAATTATAAA
3041	AAAACCTCTTGGAAATTATAAAA
3042	AAACCTCTTGGAAATTATAAAAA
3043	AACCTCTTGGAAATTATAAAAAT
3044	ACCTCTTGGAAATTATAAAAATA
3045	CCTCTTGGAAATTATAAAAATAT
3046	CTCTTGGAAATTATAAAAATATT
3047	TCTTGGAAATTATAAAAATATTG
3048	CTTGGAAATTATAAAAATATTGG
3049	TTGGAAATTATAAAAATATTGGC
3050	TGGAAATTATAAAAATATTGGCA
3051	GGAAATTATAAAAATATTGGCAA
3052	GAAATTATAAAAATATTGGCAAG
3053	AAATTATAAAAATATTGGCAAGA
3054	AATTATAAAAATATTGGCAAGAA
3055	ATTATAAAAATATTGGCAAGAAA
3056	TTATAAAAATATTGGCAAGAAAA
3057	TATAAAAATATTGGCAAGAAAAG
3058	ATAAAAATATTGGCAAGAAAAGA
3059	TAAAAATATTGGCAAGAAAAGAA
3060	AAAAATATTGGCAAGAAAAGAAG
3061	AAAATATTGGCAAGAAAAGAAGA
3062	AAATATTGGCAAGAAAAGAAGAA
3063	AATATTGGCAAGAAAAGAAGAAT
3064	ATATTGGCAAGAAAAGAAGAATA
3065	TATTGGCAAGAAAAGAAGAATAG
3066	ATTGGCAAGAAAAGAAGAATAGT
3067	TTGGCAAGAAAAGAAGAATAGTT
3068	TGGCAAGAAAAGAAGAATAGTTG
3069	GGCAAGAAAAGAAGAATAGTTGT
3070	GCAAGAAAAGAAGAATAGTTGTT
3071	CAAGAAAAGAAGAATAGTTGTTT
3072	AAGAAAAGAAGAATAGTTGTTTA

Fig. 29 cont'd (Sheet 64 of 170)

ID	SEQUENCE
3073	AGAAAAGAAGAATAGTTGTTTAA
3074	GAAAAGAAGAATAGTTGTTTAAA
3075	AAAAGAAGAATAGTTGTTTAAAT
3076	AAAGAAGAATAGTTGTTTAAATA
3077	AAGAAGAATAGTTGTTTAAATAT
3078	AGAAGAATAGTTGTTTAAATATT
3079	GAAGAATAGTTGTTTAAATATTT
3080	AAGAATAGTTGTTTAAATATTTT
3081	AGAATAGTTGTTTAAATATTTTT
3082	GAATAGTTGTTTAAATATTTTTT
3083	AATAGTTGTTTAAATATTTTTTA
3084	ATAGTTGTTTAAATATTTTTTAA
3085	TAGTTGTTTAAATATTTTTTAAA
3086	AGTTGTTTAAATATTTTTTAAAA
3087	GTTGTTTAAATATTTTTTAAAAA
3088	TTGTTTAAATATTTTTTAAAAAA
3089	TGTTTAAATATTTTTTAAAAAAC
3090	GTTTAAATATTTTTTAAAAAACA
3091	TTTAAATATTTTTTAAAAAACAC
3092	TTAAATATTTTTTAAAAAACACT
3093	TAAATATTTTTTAAAAAACACTT
3094	AAATATTTTTTAAAAAACACTTG
3095	AATATTTTTTAAAAAACACTTGA
3096	ATATTTTTTAAAAAACACTTGAA
3097	TATTTTTTAAAAAACACTTGAAT
3098	ATTTTTTAAAAAACACTTGAATA
3099	TTTTTTAAAAAACACTTGAATAA
3100	TTTTTAAAAAACACTTGAATAAG
3101	TTTTAAAAAACACTTGAATAAGA
3102	TTTAAAAAACACTTGAATAAGAA
3103	TTAAAAAACACTTGAATAAGAAT
3104	TAAAAAACACTTGAATAAGAATC
3105	AAAAAACACTTGAATAAGAATCA
3106	AAAAACACTTGAATAAGAATCAG
3107	AAAACACTTGAATAAGAATCAGT
3108	AAACACTTGAATAAGAATCAGTA
3109	AACACTTGAATAAGAATCAGTAG
3110	ACACTTGAATAAGAATCAGTAGG
3111	CACTTGAATAAGAATCAGTAGGG
3112	ACTTGAATAAGAATCAGTAGGGT
3113	CTTGAATAAGAATCAGTAGGGTA
3114	TTGAATAAGAATCAGTAGGGTAT
3115	TGAATAAGAATCAGTAGGGTATA
3116	GAATAAGAATCAGTAGGGTATAA
3117	AATAAGAATCAGTAGGGTATAAA
3118	ATAAGAATCAGTAGGGTATAAAC
3119	TAAGAATCAGTAGGGTATAAACT
3120	AAGAATCAGTAGGGTATAAACTA

Fig. 29 cont'd (Sheet 65 of 170)

ID	SEQUENCE
3121	AGAATCAGTAGGGTATAAACTAG
3122	GAATCAGTAGGGTATAAACTAGA
3123	AATCAGTAGGGTATAAACTAGAA
3124	ATCAGTAGGGTATAAACTAGAAG
3125	TCAGTAGGGTATAAACTAGAAGT
3126	CAGTAGGGTATAAACTAGAAGTT
3127	AGTAGGGTATAAACTAGAAGTTT
3128	GTAGGGTATAAACTAGAAGTTTA
3129	TAGGGTATAAACTAGAAGTTTAA
3130	AGGGTATAAACTAGAAGTTTAAA
3131	GGGTATAAACTAGAAGTTTAAAA
3132	GGTATAAACTAGAAGTTTAAAAA
3133	GTATAAACTAGAAGTTTAAAAAT
3134	TATAAACTAGAAGTTTAAAAATG
3135	ATAAACTAGAAGTTTAAAAATGC
3136	TAAACTAGAAGTTTAAAAATGCT
3137	AAACTAGAAGTTTAAAAATGCTT
3138	AACTAGAAGTTTAAAAATGCTTC
3139	ACTAGAAGTTTAAAAATGCTTCA
3140	CTAGAAGTTTAAAAATGCTTCAT
3141	TAGAAGTTTAAAAATGCTTCATA
3142	AGAAGTTTAAAAATGCTTCATAG
3143	GAAGTTTAAAAATGCTTCATAGA
3144	AAGTTTAAAAATGCTTCATAGAA
3145	AGTTTAAAAATGCTTCATAGAAC
3146	GTTTAAAAATGCTTCATAGAACG
3147	TTTAAAAATGCTTCATAGAACGT
3148	TTAAAAATGCTTCATAGAACGTC
3149	TAAAAATGCTTCATAGAACGTCC
3150	AAAAATGCTTCATAGAACGTCCA
3151	AAAATGCTTCATAGAACGTCCAG
3152	AAATGCTTCATAGAACGTCCAGG
3153	AATGCTTCATAGAACGTCCAGGG
3154	ATGCTTCATAGAACGTCCAGGGT
3155	TGCTTCATAGAACGTCCAGGGTT
3156	GCTTCATAGAACGTCCAGGGTTT
3157	CTTCATAGAACGTCCAGGGTTTA
3158	TTCATAGAACGTCCAGGGTTTAC
3159	TCATAGAACGTCCAGGGTTTACA
3160	CATAGAACGTCCAGGGTTTACAT
3161	ATAGAACGTCCAGGGTTTACATT
3162	TAGAACGTCCAGGGTTTACATTA
3163	AGAACGTCCAGGGTTTACATTAC
3164	GAACGTCCAGGGTTTACATTACA
3165	AACGTCCAGGGTTTACATTACAA
3166	ACGTCCAGGGTTTACATTACAAG
3167	CGTCCAGGGTTTACATTACAAGA
3168	GTCCAGGGTTTACATTACAAGAT

Fig. 29 cont'd (Sheet 66 of 170)

ID	SEQUENCE
3169	TCCAGGGTTTACATTACAAGATT
3170	CCAGGGTTTACATTACAAGATTC
3171	CAGGGTTTACATTACAAGATTCT
3172	AGGGTTTACATTACAAGATTCTC
3173	GGGTTTACATTACAAGATTCTCA
3174	GGTTTACATTACAAGATTCTCAC
3175	GTTTACATTACAAGATTCTCACA
3176	TTTACATTACAAGATTCTCACAA
3177	TTACATTACAAGATTCTCACAAC
3178	TACATTACAAGATTCTCACAACA
3179	ACATTACAAGATTCTCACAACAA
3180	CATTACAAGATTCTCACAACAAA
3181	ATTACAAGATTCTCACAACAAAC
3182	TTACAAGATTCTCACAACAAACC
3183	TACAAGATTCTCACAACAAACCT
3184	ACAAGATTCTCACAACAAACCTA
3185	CAAGATTCTCACAACAAACCTAT
3186	AAGATTCTCACAACAAACCTATT
3187	AGATTCTCACAACAAACCTATTG
3188	GATTCTCACAACAAACCTATTGT
3189	ATTCTCACAACAAACCTATTGTA
3190	TTCTCACAACAAACCTATTGTAG
3191	TCTCACAACAAACCTATTGTAGA
3192	CTCACAACAAACCTATTGTAGAG
3193	TCACAACAAACCTATTGTAGAGG
3194	CACAACAAACCTATTGTAGAGGT
3195	ACAACAAACCTATTGTAGAGGTG
3196	CAACAAACCTATTGTAGAGGTGA
3197	AACAAACCTATTGTAGAGGTGAG
3198	ACAAACCTATTGTAGAGGTGAGT
3199	CAAACCTATTGTAGAGGTGAGTA
3200	AAACCTATTGTAGAGGTGAGTAA
3201	AACCTATTGTAGAGGTGAGTAAG
3202	ACCTATTGTAGAGGTGAGTAAGG
3203	CCTATTGTAGAGGTGAGTAAGGC
3204	CTATTGTAGAGGTGAGTAAGGCA
3205	TATTGTAGAGGTGAGTAAGGCAT
3206	ATTGTAGAGGTGAGTAAGGCATG
3207	TTGTAGAGGTGAGTAAGGCATGT
3208	TGTAGAGGTGAGTAAGGCATGTT
3209	GTAGAGGTGAGTAAGGCATGTTA
3210	TAGAGGTGAGTAAGGCATGTTAC
3211	AGAGGTGAGTAAGGCATGTTACT
3212	GAGGTGAGTAAGGCATGTTACTA
3213	AGGTGAGTAAGGCATGTTACTAC
3214	GGTGAGTAAGGCATGTTACTACA
3215	GTGAGTAAGGCATGTTACTACAG
3216	TGAGTAAGGCATGTTACTACAGA

Fig. 29 cont'd (Sheet 67 of 170)

ID	SEQUENCE
3217	GAGTAAGGCATGTTACTACAGAG
3218	AGTAAGGCATGTTACTACAGAGG
3219	GTAAGGCATGTTACTACAGAGGA
3220	TAAGGCATGTTACTACAGAGGAA
3221	AAGGCATGTTACTACAGAGGAAA
3222	AGGCATGTTACTACAGAGGAAAG
3223	GGCATGTTACTACAGAGGAAAGT
3224	GCATGTTACTACAGAGGAAAGTT
3225	CATGTTACTACAGAGGAAAGTTT
3226	ATGTTACTACAGAGGAAAGTTTG
3227	TGTTACTACAGAGGAAAGTTTGA
3228	GTTACTACAGAGGAAAGTTTGAG
3229	TTACTACAGAGGAAAGTTTGAGA
3230	TACTACAGAGGAAAGTTTGAGAG
3231	ACTACAGAGGAAAGTTTGAGAGT
3232	CTACAGAGGAAAGTTTGAGAGTA
3233	TACAGAGGAAAGTTTGAGAGTAA
3234	ACAGAGGAAAGTTTGAGAGTAAA
3235	CAGAGGAAAGTTTGAGAGTAAAA
3236	AGAGGAAAGTTTGAGAGTAAAAC
3237	GAGGAAAGTTTGAGAGTAAAACT
3238	AGGAAAGTTTGAGAGTAAAACTG
3239	GGAAAGTTTGAGAGTAAAACTGT
3240	GAAAGTTTGAGAGTAAAACTGTA
3241	AAAGTTTGAGAGTAAAACTGTAA
3242	AAGTTTGAGAGTAAAACTGTAAA
3243	AGTTTGAGAGTAAAACTGTAAAA
3244	GTTTGAGAGTAAAACTGTAAAAA
3245	TTTGAGAGTAAAACTGTAAAAAA
3246	TTGAGAGTAAAACTGTAAAAAAT
3247	TGAGAGTAAAACTGTAAAAAATT
3248	GAGAGTAAAACTGTAAAAAATTA
3249	AGAGTAAAACTGTAAAAAATTAT
3250	GAGTAAAACTGTAAAAAATTATA
3251	AGTAAAACTGTAAAAAATTATAT
3252	GTAAAACTGTAAAAAATTATATT
3253	TAAAACTGTAAAAAATTATATTT
3254	AAAACTGTAAAAAATTATATTTT
3255	AAACTGTAAAAAATTATATTTTT
3256	AACTGTAAAAAATTATATTTTTG
3257	ACTGTAAAAAATTATATTTTTGT
3258	CTGTAAAAAATTATATTTTTGTT
3259	TGTAAAAAATTATATTTTTGTTG
3260	GTAAAAAATTATATTTTTGTTGT
3261	TAAAAAATTATATTTTTGTTGTA
3262	AAAAAATTATATTTTTGTTGTAC
3263	AAAAATTATATTTTTGTTGTACT
3264	AAAATTATATTTTTGTTGTACTT

Fig. 29 cont'd (Sheet 68 of 170)

ID	SEQUENCE
3265	AAATTATATTTTTGTTGTACTTT
3266	AATTATATTTTTGTTGTACTTTC
3267	ATTATATTTTTGTTGTACTTTCT
3268	TTATATTTTTGTTGTACTTTCTA
3269	TATATTTTTGTTGTACTTTCTAA
3270	ATATTTTTGTTGTACTTTCTAAG
3271	TATTTTTGTTGTACTTTCTAAGA
3272	ATTTTTGTTGTACTTTCTAAGAG
3273	TTTTTGTTGTACTTTCTAAGAGA
3274	TTTTGTTGTACTTTCTAAGAGAA
3275	TTTGTTGTACTTTCTAAGAGAAA
3276	TTGTTGTACTTTCTAAGAGAAAG
3277	TGTTGTACTTTCTAAGAGAAAGA
3278	GTTGTACTTTCTAAGAGAAAGAG
3279	TTGTACTTTCTAAGAGAAAGAGT
3280	TGTACTTTCTAAGAGAAAGAGTA
3281	GTACTTTCTAAGAGAAAGAGTAT
3282	TACTTTCTAAGAGAAAGAGTATT
3283	ACTTTCTAAGAGAAAGAGTATTG
3284	CTTTCTAAGAGAAAGAGTATTGT
3285	TTTCTAAGAGAAAGAGTATTGTT
3286	TTCTAAGAGAAAGAGTATTGTTA
3287	TCTAAGAGAAAGAGTATTGTTAT
3288	CTAAGAGAAAGAGTATTGTTATG
3289	TAAGAGAAAGAGTATTGTTATGT
3290	AAGAGAAAGAGTATTGTTATGTT
3291	AGAGAAAGAGTATTGTTATGTTC
3292	GAGAAAGAGTATTGTTATGTTCT
3293	AGAAAGAGTATTGTTATGTTCTC
3294	GAAAGAGTATTGTTATGTTCTCC
3295	AAAGAGTATTGTTATGTTCTCCT
3296	AAGAGTATTGTTATGTTCTCCTA
3297	AGAGTATTGTTATGTTCTCCTAA
3298	GAGTATTGTTATGTTCTCCTAAC
3299	AGTATTGTTATGTTCTCCTAACT
3300	GTATTGTTATGTTCTCCTAACTT
3301	TATTGTTATGTTCTCCTAACTTC
3302	ATTGTTATGTTCTCCTAACTTCT
3303	TTGTTATGTTCTCCTAACTTCTG
3304	TGTTATGTTCTCCTAACTTCTGT
3305	GTTATGTTCTCCTAACTTCTGTT
3306	TTATGTTCTCCTAACTTCTGTTG
3307	TATGTTCTCCTAACTTCTGTTGA
3308	ATGTTCTCCTAACTTCTGTTGAT
3309	TGTTCTCCTAACTTCTGTTGATT
3310	GTTCTCCTAACTTCTGTTGATTA
3311	TTCTCCTAACTTCTGTTGATTAC
3312	TCTCCTAACTTCTGTTGATTACT

Fig. 29 cont'd (Sheet 69 of 170)

ID	SEQUENCE
3313	CTCCTAACTTCTGTTGATTACTA
3314	TCCTAACTTCTGTTGATTACTAC
3315	CCTAACTTCTGTTGATTACTACT
3316	CTAACTTCTGTTGATTACTACTT
3317	TAACTTCTGTTGATTACTACTTT
3318	AACTTCTGTTGATTACTACTTTA
3319	ACTTCTGTTGATTACTACTTTAA
3320	CTTCTGTTGATTACTACTTTAAG
3321	TTCTGTTGATTACTACTTTAAGT
3322	TCTGTTGATTACTACTTTAAGTG
3323	CTGTTGATTACTACTTTAAGTGA
3324	TGTTGATTACTACTTTAAGTGAT
3325	GTTGATTACTACTTTAAGTGATA
3326	TTGATTACTACTTTAAGTGATAT
3327	TGATTACTACTTTAAGTGATATT
3328	GATTACTACTTTAAGTGATATTC
3329	ATTACTACTTTAAGTGATATTCA
3330	TTACTACTTTAAGTGATATTCAT
3331	TACTACTTTAAGTGATATTCATT
3332	ACTACTTTAAGTGATATTCATTT
3333	CTACTTTAAGTGATATTCATTTA
3334	TACTTTAAGTGATATTCATTTAA
3335	ACTTTAAGTGATATTCATTTAAA
3336	CTTTAAGTGATATTCATTTAAAA
3337	TTTAAGTGATATTCATTTAAAAC
3338	TTAAGTGATATTCATTTAAAACA
3339	TAAGTGATATTCATTTAAAACAT
3340	AAGTGATATTCATTTAAAACATT
3341	AGTGATATTCATTTAAAACATTG
3342	GTGATATTCATTTAAAACATTGC
3343	TGATATTCATTTAAAACATTGCA
3344	GATATTCATTTAAAACATTGCAA
3345	ATATTCATTTAAAACATTGCAAA
3346	TATTCATTTAAAACATTGCAAAT
3347	ATTCATTTAAAACATTGCAAATT
3348	TTCATTTAAAACATTGCAAATTT
3349	TCATTTAAAACATTGCAAATTTA
3350	CATTTAAAACATTGCAAATTTAT
3351	ATTTAAAACATTGCAAATTTATT
3352	TTTAAAACATTGCAAATTTATTT
3353	TTAAAACATTGCAAATTTATTTT
3354	TAAAACATTGCAAATTTATTTTA
3355	AAAACATTGCAAATTTATTTTAT
3356	AAACATTGCAAATTTATTTTATT
3357	AACATTGCAAATTTATTTTATTT
3358	ACATTGCAAATTTATTTTATTTA
3359	CATTGCAAATTTATTTTATTTAT
3360	ATTGCAAATTTATTTTATTTATT

Fig. 29 cont'd (Sheet 70 of 170)

ID	SEQUENCE
3361	TTGCAAATTTATTTTATTTATTT
3362	TGCAAATTTATTTTATTTATTTA
3363	GCAAATTTATTTTATTTATTTAA
3364	CAAATTTATTTTATTTATTTAAT
3365	AAATTTATTTTATTTATTTAATT
3366	AATTTATTTTATTTATTTAATTT
3367	ATTTATTTTATTTATTTAATTTT
3368	TTTATTTTATTTATTTAATTTTC
3369	TTATTTTATTTATTTAATTTTCT
3370	TATTTTATTTATTTAATTTTCTT
3371	ATTTTATTTATTTAATTTTCTTT
3372	TTTTATTTATTTAATTTTCTTTT
3373	TTTATTTATTTAATTTTCTTTTT
3374	TTATTTATTTAATTTTCTTTTTG
3375	TATTTATTTAATTTTCTTTTTGA
3376	ATTTATTTAATTTTCTTTTTGAG
3377	TTTATTTAATTTTCTTTTTGAGA
3378	TTATTTAATTTTCTTTTTGAGAT
3379	TATTTAATTTTCTTTTTGAGATG
3380	ATTTAATTTTCTTTTTGAGATGG
3381	TTTAATTTTCTTTTTGAGATGGA
3382	TTAATTTTCTTTTTGAGATGGAG
3383	TAATTTTCTTTTTGAGATGGAGT
3384	AATTTTCTTTTTGAGATGGAGTC
3385	ATTTTCTTTTTGAGATGGAGTCT
3386	TTTTCTTTTTGAGATGGAGTCTT
3387	TTTCTTTTTGAGATGGAGTCTTG
3388	TTCTTTTTGAGATGGAGTCTTGC
3389	TCTTTTTGAGATGGAGTCTTGCT
3390	CTTTTTGAGATGGAGTCTTGCTT
3391	TTTTTGAGATGGAGTCTTGCTTG
3392	TTTTGAGATGGAGTCTTGCTTGT
3393	TTTGAGATGGAGTCTTGCTTGTC
3394	TTGAGATGGAGTCTTGCTTGTCA
3395	TGAGATGGAGTCTTGCTTGTCAC
3396	GAGATGGAGTCTTGCTTGTCACC
3397	AGATGGAGTCTTGCTTGTCACCC
3398	GATGGAGTCTTGCTTGTCACCCA
3399	ATGGAGTCTTGCTTGTCACCCAG
3400	TGGAGTCTTGCTTGTCACCCAGG
3401	GGAGTCTTGCTTGTCACCCAGGC
3402	GAGTCTTGCTTGTCACCCAGGCT
3403	AGTCTTGCTTGTCACCCAGGCTG
3404	GTCTTGCTTGTCACCCAGGCTGG
3405	TCTTGCTTGTCACCCAGGCTGGA
3406	CTTGCTTGTCACCCAGGCTGGAG
3407	TTGCTTGTCACCCAGGCTGGAGT
3408	TGCTTGTCACCCAGGCTGGAGTG

Fig. 29 cont'd (Sheet 71 of 170)

ID	SEQUENCE
3409	GCTTGTCACCCAGGCTGGAGTGC
3410	CTTGTCACCCAGGCTGGAGTGCA
3411	TTGTCACCCAGGCTGGAGTGCAG
3412	TGTCACCCAGGCTGGAGTGCAGT
3413	GTCACCCAGGCTGGAGTGCAGTG
3414	TCACCCAGGCTGGAGTGCAGTGG
3415	CACCCAGGCTGGAGTGCAGTGGA
3416	ACCCAGGCTGGAGTGCAGTGGAG
3417	CCCAGGCTGGAGTGCAGTGGAGT
3418	CCAGGCTGGAGTGCAGTGGAGTG
3419	CAGGCTGGAGTGCAGTGGAGTGA
3420	AGGCTGGAGTGCAGTGGAGTGAT
3421	GGCTGGAGTGCAGTGGAGTGATC
3422	GCTGGAGTGCAGTGGAGTGATCT
3423	CTGGAGTGCAGTGGAGTGATCTC
3424	TGGAGTGCAGTGGAGTGATCTCT
3425	GGAGTGCAGTGGAGTGATCTCTG
3426	GAGTGCAGTGGAGTGATCTCTGC
3427	AGTGCAGTGGAGTGATCTCTGCT
3428	GTGCAGTGGAGTGATCTCTGCTC
3429	TGCAGTGGAGTGATCTCTGCTCA
3430	GCAGTGGAGTGATCTCTGCTCAC
3431	CAGTGGAGTGATCTCTGCTCACT
3432	AGTGGAGTGATCTCTGCTCACTG
3433	GTGGAGTGATCTCTGCTCACTGC
3434	TGGAGTGATCTCTGCTCACTGCA
3435	GGAGTGATCTCTGCTCACTGCAA
3436	GAGTGATCTCTGCTCACTGCAAC
3437	AGTGATCTCTGCTCACTGCAACC
3438	GTGATCTCTGCTCACTGCAACCT
3439	TGATCTCTGCTCACTGCAACCTC
3440	GATCTCTGCTCACTGCAACCTCC
3441	ATCTCTGCTCACTGCAACCTCCG
3442	TCTCTGCTCACTGCAACCTCCGC
3443	CTCTGCTCACTGCAACCTCCGCC
3444	TCTGCTCACTGCAACCTCCGCCT
3445	CTGCTCACTGCAACCTCCGCCTT
3446	TGCTCACTGCAACCTCCGCCTTC
3447	GCTCACTGCAACCTCCGCCTTCT
3448	CTCACTGCAACCTCCGCCTTCTG
3449	TCACTGCAACCTCCGCCTTCTGG
3450	CACTGCAACCTCCGCCTTCTGGG
3451	ACTGCAACCTCCGCCTTCTGGGT
3452	CTGCAACCTCCGCCTTCTGGGTT
3453	TGCAACCTCCGCCTTCTGGGTTC
3454	GCAACCTCCGCCTTCTGGGTTCA
3455	CAACCTCCGCCTTCTGGGTTCAA
3456	AACCTCCGCCTTCTGGGTTCAAG

Fig. 29 cont'd (Sheet 72 of 170)

ID	SEQUENCE
3457	ACCTCCGCCTTCTGGGTTCAAGC
3458	CCTCCGCCTTCTGGGTTCAAGCG
3459	CTCCGCCTTCTGGGTTCAAGCGA
3460	TCCGCCTTCTGGGTTCAAGCGAT
3461	CCGCCTTCTGGGTTCAAGCGATT
3462	CGCCTTCTGGGTTCAAGCGATTC
3463	GCCTTCTGGGTTCAAGCGATTCT
3464	CCTTCTGGGTTCAAGCGATTCTC
3465	CTTCTGGGTTCAAGCGATTCTCG
3466	TTCTGGGTTCAAGCGATTCTCGT
3467	TCTGGGTTCAAGCGATTCTCGTG
3468	CTGGGTTCAAGCGATTCTCGTGC
3469	TGGGTTCAAGCGATTCTCGTGCC
3470	GGGTTCAAGCGATTCTCGTGCCT
3471	GGTTCAAGCGATTCTCGTGCCTC
3472	GTTCAAGCGATTCTCGTGCCTCA
3473	TTCAAGCGATTCTCGTGCCTCAG
3474	TCAAGCGATTCTCGTGCCTCAGC
3475	CAAGCGATTCTCGTGCCTCAGCT
3476	AAGCGATTCTCGTGCCTCAGCTT
3477	AGCGATTCTCGTGCCTCAGCTTC
3478	GCGATTCTCGTGCCTCAGCTTCC
3479	CGATTCTCGTGCCTCAGCTTCCT
3480	GATTCTCGTGCCTCAGCTTCCTG
3481	ATTCTCGTGCCTCAGCTTCCTGA
3482	TTCTCGTGCCTCAGCTTCCTGAG
3483	TCTCGTGCCTCAGCTTCCTGAGT
3484	CTCGTGCCTCAGCTTCCTGAGTA
3485	TCGTGCCTCAGCTTCCTGAGTAG
3486	CGTGCCTCAGCTTCCTGAGTAGC
3487	GTGCCTCAGCTTCCTGAGTAGCT
3488	TGCCTCAGCTTCCTGAGTAGCTG
3489	GCCTCAGCTTCCTGAGTAGCTGG
3490	CCTCAGCTTCCTGAGTAGCTGGA
3491	CTCAGCTTCCTGAGTAGCTGGAA
3492	TCAGCTTCCTGAGTAGCTGGAAT
3493	CAGCTTCCTGAGTAGCTGGAATT
3494	AGCTTCCTGAGTAGCTGGAATTA
3495	GCTTCCTGAGTAGCTGGAATTAC
3496	CTTCCTGAGTAGCTGGAATTACA
3497	TTCCTGAGTAGCTGGAATTACAG
3498	TCCTGAGTAGCTGGAATTACAGG
3499	CCTGAGTAGCTGGAATTACAGGC
3500	CTGAGTAGCTGGAATTACAGGCA
3501	TGAGTAGCTGGAATTACAGGCAG
3502	GAGTAGCTGGAATTACAGGCAGG
3503	AGTAGCTGGAATTACAGGCAGGT
3504	GTAGCTGGAATTACAGGCAGGTG

Fig. 29 cont'd (Sheet 73 of 170)

ID	SEQUENCE
3505	TAGCTGGAATTACAGGCAGGTGC
3506	AGCTGGAATTACAGGCAGGTGCC
3507	GCTGGAATTACAGGCAGGTGCCA
3508	CTGGAATTACAGGCAGGTGCCAC
3509	TGGAATTACAGGCAGGTGCCACC
3510	GGAATTACAGGCAGGTGCCACCA
3511	GAATTACAGGCAGGTGCCACCAT
3512	AATTACAGGCAGGTGCCACCATG
3513	ATTACAGGCAGGTGCCACCATGC
3514	TTACAGGCAGGTGCCACCATGCC
3515	TACAGGCAGGTGCCACCATGCCC
3516	ACAGGCAGGTGCCACCATGCCCG
3517	CAGGCAGGTGCCACCATGCCCGA
3518	AGGCAGGTGCCACCATGCCCGAC
3519	GGCAGGTGCCACCATGCCCGACT
3520	GCAGGTGCCACCATGCCCGACTA
3521	CAGGTGCCACCATGCCCGACTAA
3522	AGGTGCCACCATGCCCGACTAAT
3523	GGTGCCACCATGCCCGACTAATT
3524	GTGCCACCATGCCCGACTAATTT
3525	TGCCACCATGCCCGACTAATTTT
3526	GCCACCATGCCCGACTAATTTTT
3527	CCACCATGCCCGACTAATTTTTT
3528	CACCATGCCCGACTAATTTTTTT
3529	ACCATGCCCGACTAATTTTTTTT
3530	TTTTTTTTATTTTTAGTAGAGAC
3531	TTTTTTTATTTTTAGTAGAGACG
3532	TTTTTTATTTTTAGTAGAGACGG
3533	TTTTTATTTTTAGTAGAGACGGG
3534	TTTTATTTTTAGTAGAGACGGGG
3535	TTTATTTTTAGTAGAGACGGGGT
3536	TTATTTTTAGTAGAGACGGGGTT
3537	TATTTTTAGTAGAGACGGGGTTT
3538	ATTTTTAGTAGAGACGGGGTTTC
3539	TTTTTAGTAGAGACGGGGTTTCA
3540	TTTTAGTAGAGACGGGGTTTCAC
3541	TTTAGTAGAGACGGGGTTTCACC
3542	TTAGTAGAGACGGGGTTTCACCA
3543	TAGTAGAGACGGGGTTTCACCAT
3544	AGTAGAGACGGGGTTTCACCATG
3545	GTAGAGACGGGGTTTCACCATGT
3546	TAGAGACGGGGTTTCACCATGTT
3547	AGAGACGGGGTTTCACCATGTTG
3548	GAGACGGGGTTTCACCATGTTGG
3549	AGACGGGGTTTCACCATGTTGGC
3550	GACGGGGTTTCACCATGTTGGCC
3551	ACGGGGTTTCACCATGTTGGCCA
3552	CGGGGTTTCACCATGTTGGCCAG

Fig. 29 cont'd (Sheet 74 of 170)

ID	SEQUENCE
3553	GGGGTTTCACCATGTTGGCCAGG
3554	GGGTTTCACCATGTTGGCCAGGC
3555	GGTTTCACCATGTTGGCCAGGCT
3556	GTTTCACCATGTTGGCCAGGCTG
3557	TTTCACCATGTTGGCCAGGCTGG
3558	TTCACCATGTTGGCCAGGCTGGT
3559	TCACCATGTTGGCCAGGCTGGTA
3560	CACCATGTTGGCCAGGCTGGTAT
3561	ACCATGTTGGCCAGGCTGGTATC
3562	CCATGTTGGCCAGGCTGGTATCA
3563	CATGTTGGCCAGGCTGGTATCAA
3564	ATGTTGGCCAGGCTGGTATCAAA
3565	TGTTGGCCAGGCTGGTATCAAAC
3566	GTTGGCCAGGCTGGTATCAAACT
3567	TTGGCCAGGCTGGTATCAAACTC
3568	TGGCCAGGCTGGTATCAAACTCC
3569	GGCCAGGCTGGTATCAAACTCCT
3570	GCCAGGCTGGTATCAAACTCCTG
3571	CCAGGCTGGTATCAAACTCCTGA
3572	CAGGCTGGTATCAAACTCCTGAC
3573	AGGCTGGTATCAAACTCCTGACC
3574	GGCTGGTATCAAACTCCTGACCT
3575	GCTGGTATCAAACTCCTGACCTC
3576	CTGGTATCAAACTCCTGACCTCA
3577	TGGTATCAAACTCCTGACCTCAA
3578	GGTATCAAACTCCTGACCTCAAG
3579	GTATCAAACTCCTGACCTCAAGA
3580	TATCAAACTCCTGACCTCAAGAG
3581	ATCAAACTCCTGACCTCAAGAGA
3582	TCAAACTCCTGACCTCAAGAGAT
3583	CAAACTCCTGACCTCAAGAGATC
3584	AAACTCCTGACCTCAAGAGATCC
3585	AACTCCTGACCTCAAGAGATCCA
3586	ACTCCTGACCTCAAGAGATCCAC
3587	CTCCTGACCTCAAGAGATCCACT
3588	TCCTGACCTCAAGAGATCCACTC
3589	CCTGACCTCAAGAGATCCACTCG
3590	CTGACCTCAAGAGATCCACTCGC
3591	TGACCTCAAGAGATCCACTCGCC
3592	GACCTCAAGAGATCCACTCGCCT
3593	ACCTCAAGAGATCCACTCGCCTT
3594	CCTCAAGAGATCCACTCGCCTTG
3595	CTCAAGAGATCCACTCGCCTTGC
3596	TCAAGAGATCCACTCGCCTTGCC
3597	CAAGAGATCCACTCGCCTTGCCC
3598	AAGAGATCCACTCGCCTTGCCCT
3599	AGAGATCCACTCGCCTTGCCCTC
3600	GAGATCCACTCGCCTTGCCCTCC

Fig. 29 cont'd (Sheet 75 of 170)

ID	SEQUENCE
3601	AGATCCACTCGCCTTGCCCTCCC
3602	GATCCACTCGCCTTGCCCTCCCA
3603	ATCCACTCGCCTTGCCCTCCCAA
3604	TCCACTCGCCTTGCCCTCCCAAA
3605	CCACTCGCCTTGCCCTCCCAAAG
3606	CACTCGCCTTGCCCTCCCAAAGT
3607	ACTCGCCTTGCCCTCCCAAAGTG
3608	CTCGCCTTGCCCTCCCAAAGTGC
3609	TCGCCTTGCCCTCCCAAAGTGCT
3610	CGCCTTGCCCTCCCAAAGTGCTG
3611	GCCTTGCCCTCCCAAAGTGCTGG
3612	CCTTGCCCTCCCAAAGTGCTGGG
3613	CTTGCCCTCCCAAAGTGCTGGGA
3614	TTGCCCTCCCAAAGTGCTGGGAT
3615	TGCCCTCCCAAAGTGCTGGGATT
3616	GCCCTCCCAAAGTGCTGGGATTA
3617	CCCTCCCAAAGTGCTGGGATTAC
3618	CCTCCCAAAGTGCTGGGATTACA
3619	CTCCCAAAGTGCTGGGATTACAG
3620	TCCCAAAGTGCTGGGATTACAGG
3621	CCCAAAGTGCTGGGATTACAGGC
3622	CCAAAGTGCTGGGATTACAGGCT
3623	CAAAGTGCTGGGATTACAGGCTT
3624	AAAGTGCTGGGATTACAGGCTTG
3625	AAGTGCTGGGATTACAGGCTTGA
3626	AGTGCTGGGATTACAGGCTTGAG
3627	GTGCTGGGATTACAGGCTTGAGC
3628	TGCTGGGATTACAGGCTTGAGCC
3629	GCTGGGATTACAGGCTTGAGCCA
3630	CTGGGATTACAGGCTTGAGCCAC
3631	TGGGATTACAGGCTTGAGCCACC
3632	GGGATTACAGGCTTGAGCCACCA
3633	GGATTACAGGCTTGAGCCACCAC
3634	GATTACAGGCTTGAGCCACCACG
3635	ATTACAGGCTTGAGCCACCACGC
3636	TTACAGGCTTGAGCCACCACGCC
3637	TACAGGCTTGAGCCACCACGCCC
3638	ACAGGCTTGAGCCACCACGCCCG
3639	CAGGCTTGAGCCACCACGCCCGG
3640	AGGCTTGAGCCACCACGCCCGGC
3641	GGCTTGAGCCACCACGCCCGGCT
3642	GCTTGAGCCACCACGCCCGGCTA
3643	CTTGAGCCACCACGCCCGGCTAA
3644	TTGAGCCACCACGCCCGGCTAAA
3645	TGAGCCACCACGCCCGGCTAAAA
3646	GAGCCACCACGCCCGGCTAAAAC
3647	AGCCACCACGCCCGGCTAAAACA
3648	GCCACCACGCCCGGCTAAAACAT

Fig. 29 cont'd (Sheet 76 of 170)

ID	SEQUENCE
3649	CCACCACGCCCGGCTAAAACATT
3650	CACCACGCCCGGCTAAAACATTG
3651	ACCACGCCCGGCTAAAACATTGC
3652	CCACGCCCGGCTAAAACATTGCA
3653	CACGCCCGGCTAAAACATTGCAA
3654	ACGCCCGGCTAAAACATTGCAAA
3655	CGCCCGGCTAAAACATTGCAAAT
3656	GCCCGGCTAAAACATTGCAAATT
3657	CCCGGCTAAAACATTGCAAATTT
3658	CCGGCTAAAACATTGCAAATTTA
3659	CGGCTAAAACATTGCAAATTTAA
3660	GGCTAAAACATTGCAAATTTAAA
3661	GCTAAAACATTGCAAATTTAAAT
3662	CTAAAACATTGCAAATTTAAATG
3663	TAAAACATTGCAAATTTAAATGA
3664	AAAACATTGCAAATTTAAATGAG
3665	AAACATTGCAAATTTAAATGAGA
3666	AACATTGCAAATTTAAATGAGAG
3667	ACATTGCAAATTTAAATGAGAGT
3668	CATTGCAAATTTAAATGAGAGTT
3669	ATTGCAAATTTAAATGAGAGTTT
3670	TTGCAAATTTAAATGAGAGTTTT
3671	TGCAAATTTAAATGAGAGTTTTA
3672	GCAAATTTAAATGAGAGTTTTAA
3673	CAAATTTAAATGAGAGTTTTAAA
3674	AAATTTAAATGAGAGTTTTAAAA
3675	AATTTAAATGAGAGTTTTAAAAA
3676	ATTTAAATGAGAGTTTTAAAAAT
3677	TTTAAATGAGAGTTTTAAAAATT
3678	TTAAATGAGAGTTTTAAAAATTA
3679	TAAATGAGAGTTTTAAAAATTAA
3680	AAATGAGAGTTTTAAAAATTAAA
3681	AATGAGAGTTTTAAAAATTAAAT
3682	ATGAGAGTTTTAAAAATTAAATA
3683	TGAGAGTTTTAAAAATTAAATAA
3684	GAGAGTTTTAAAAATTAAATAAT
3685	AGAGTTTTAAAAATTAAATAATG
3686	GAGTTTTAAAAATTAAATAATGA
3687	AGTTTTAAAAATTAAATAATGAC
3688	GTTTTAAAAATTAAATAATGACT
3689	TTTTAAAAATTAAATAATGACTG
3690	TTTAAAAATTAAATAATGACTGC
3691	TTAAAAATTAAATAATGACTGCC
3692	TAAAAATTAAATAATGACTGCCC
3693	AAAAATTAAATAATGACTGCCCT
3694	AAAATTAAATAATGACTGCCCTG
3695	AAATTAAATAATGACTGCCCTGT
3696	AATTAAATAATGACTGCCCTGTT

Fig. 29 cont'd (Sheet 77 of 170)

ID	SEQUENCE
3697	ATTAAATAATGACTGCCCTGTTT
3698	TTAAATAATGACTGCCCTGTTTC
3699	TAAATAATGACTGCCCTGTTTCT
3700	AAATAATGACTGCCCTGTTTCTG
3701	AATAATGACTGCCCTGTTTCTGT
3702	ATAATGACTGCCCTGTTTCTGTT
3703	TAATGACTGCCCTGTTTCTGTTT
3704	AATGACTGCCCTGTTTCTGTTTT
3705	ATGACTGCCCTGTTTCTGTTTTA
3706	TGACTGCCCTGTTTCTGTTTTAG
3707	GACTGCCCTGTTTCTGTTTTAGT
3708	ACTGCCCTGTTTCTGTTTTAGTA
3709	CTGCCCTGTTTCTGTTTTAGTAT
3710	TGCCCTGTTTCTGTTTTAGTATG
3711	GCCCTGTTTCTGTTTTAGTATGT
3712	CCCTGTTTCTGTTTTAGTATGTA
3713	CCTGTTTCTGTTTTAGTATGTAA
3714	CTGTTTCTGTTTTAGTATGTAAA
3715	TGTTTCTGTTTTAGTATGTAAAT
3716	GTTTCTGTTTTAGTATGTAAATC
3717	TTTCTGTTTTAGTATGTAAATCC
3718	TTCTGTTTTAGTATGTAAATCCT
3719	TCTGTTTTAGTATGTAAATCCTC
3720	CTGTTTTAGTATGTAAATCCTCA
3721	TGTTTTAGTATGTAAATCCTCAG
3722	GTTTTAGTATGTAAATCCTCAGT
3723	TTTTAGTATGTAAATCCTCAGTT
3724	TTTAGTATGTAAATCCTCAGTTC
3725	TTAGTATGTAAATCCTCAGTTCT
3726	TAGTATGTAAATCCTCAGTTCTT
3727	AGTATGTAAATCCTCAGTTCTTC
3728	GTATGTAAATCCTCAGTTCTTCA
3729	TATGTAAATCCTCAGTTCTTCAC
3730	ATGTAAATCCTCAGTTCTTCACC
3731	TGTAAATCCTCAGTTCTTCACCT
3732	GTAAATCCTCAGTTCTTCACCTT
3733	TAAATCCTCAGTTCTTCACCTTT
3734	AAATCCTCAGTTCTTCACCTTTG
3735	AATCCTCAGTTCTTCACCTTTGC
3736	ATCCTCAGTTCTTCACCTTTGCA
3737	TCCTCAGTTCTTCACCTTTGCAC
3738	CCTCAGTTCTTCACCTTTGCACT
3739	CTCAGTTCTTCACCTTTGCACTG
3740	TCAGTTCTTCACCTTTGCACTGT
3741	CAGTTCTTCACCTTTGCACTGTC
3742	AGTTCTTCACCTTTGCACTGTCT
3743	GTTCTTCACCTTTGCACTGTCTG
3744	TTCTTCACCTTTGCACTGTCTGC

Fig. 29 cont'd (Sheet 78 of 170)

ID	SEQUENCE
3745	TCTTCACCTTTGCACTGTCTGCC
3746	CTTCACCTTTGCACTGTCTGCCA
3747	TTCACCTTTGCACTGTCTGCCAC
3748	TCACCTTTGCACTGTCTGCCACT
3749	CACCTTTGCACTGTCTGCCACTT
3750	ACCTTTGCACTGTCTGCCACTTA
3751	CCTTTGCACTGTCTGCCACTTAG
3752	CTTTGCACTGTCTGCCACTTAGT
3753	TTTGCACTGTCTGCCACTTAGTT
3754	TTGCACTGTCTGCCACTTAGTTT
3755	TGCACTGTCTGCCACTTAGTTTG
3756	GCACTGTCTGCCACTTAGTTTGG
3757	CACTGTCTGCCACTTAGTTTGGT
3758	ACTGTCTGCCACTTAGTTTGGTT
3759	CTGTCTGCCACTTAGTTTGGTTA
3760	TGTCTGCCACTTAGTTTGGTTAT
3761	GTCTGCCACTTAGTTTGGTTATA
3762	TCTGCCACTTAGTTTGGTTATAT
3763	CTGCCACTTAGTTTGGTTATATA
3764	TGCCACTTAGTTTGGTTATATAG
3765	GCCACTTAGTTTGGTTATATAGT
3766	CCACTTAGTTTGGTTATATAGTC
3767	CACTTAGTTTGGTTATATAGTCA
3768	ACTTAGTTTGGTTATATAGTCAT
3769	CTTAGTTTGGTTATATAGTCATT
3770	TTAGTTTGGTTATATAGTCATTA
3771	TAGTTTGGTTATATAGTCATTAA
3772	AGTTTGGTTATATAGTCATTAAC
3773	GTTTGGTTATATAGTCATTAACT
3774	TTTGGTTATATAGTCATTAACTT
3775	TTGGTTATATAGTCATTAACTTG
3776	TGGTTATATAGTCATTAACTTGA
3777	GGTTATATAGTCATTAACTTGAA
3778	GTTATATAGTCATTAACTTGAAT
3779	TTATATAGTCATTAACTTGAATT
3780	TATATAGTCATTAACTTGAATTT
3781	ATATAGTCATTAACTTGAATTTG
3782	TATAGTCATTAACTTGAATTTGG
3783	ATAGTCATTAACTTGAATTTGGT
3784	TAGTCATTAACTTGAATTTGGTC
3785	AGTCATTAACTTGAATTTGGTCT
3786	GTCATTAACTTGAATTTGGTCTG
3787	TCATTAACTTGAATTTGGTCTGT
3788	CATTAACTTGAATTTGGTCTGTA
3789	ATTAACTTGAATTTGGTCTGTAT
3790	TTAACTTGAATTTGGTCTGTATA
3791	TAACTTGAATTTGGTCTGTATAG
3792	AACTTGAATTTGGTCTGTATAGT

Fig. 29 cont'd (Sheet 79 of 170)

ID	SEQUENCE
3793	ACTTGAATTTGGTCTGTATAGTC
3794	CTTGAATTTGGTCTGTATAGTCT
3795	TTGAATTTGGTCTGTATAGTCTA
3796	TGAATTTGGTCTGTATAGTCTAG
3797	GAATTTGGTCTGTATAGTCTAGA
3798	AATTTGGTCTGTATAGTCTAGAC
3799	ATTTGGTCTGTATAGTCTAGACT
3800	TTTGGTCTGTATAGTCTAGACTT
3801	TTGGTCTGTATAGTCTAGACTTT
3802	TGGTCTGTATAGTCTAGACTTTA
3803	GGTCTGTATAGTCTAGACTTTAA
3804	GTCTGTATAGTCTAGACTTTAAA
3805	TCTGTATAGTCTAGACTTTAAAT
3806	CTGTATAGTCTAGACTTTAAATT
3807	TGTATAGTCTAGACTTTAAATTT
3808	GTATAGTCTAGACTTTAAATTTA
3809	TATAGTCTAGACTTTAAATTTAA
3810	ATAGTCTAGACTTTAAATTTAAA
3811	TAGTCTAGACTTTAAATTTAAAG
3812	AGTCTAGACTTTAAATTTAAAGT
3813	GTCTAGACTTTAAATTTAAAGTT
3814	TCTAGACTTTAAATTTAAAGTTT
3815	CTAGACTTTAAATTTAAAGTTTT
3816	TAGACTTTAAATTTAAAGTTTTC
3817	AGACTTTAAATTTAAAGTTTTCT
3818	GACTTTAAATTTAAAGTTTTCTA
3819	ACTTTAAATTTAAAGTTTTCTAC
3820	CTTTAAATTTAAAGTTTTCTACA
3821	TTTAAATTTAAAGTTTTCTACAA
3822	TTAAATTTAAAGTTTTCTACAAG
3823	TAAATTTAAAGTTTTCTACAAGG
3824	AAATTTAAAGTTTTCTACAAGGG
3825	AATTTAAAGTTTTCTACAAGGGG
3826	ATTTAAAGTTTTCTACAAGGGGA
3827	TTTAAAGTTTTCTACAAGGGGAG
3828	TTAAAGTTTTCTACAAGGGGAGA
3829	TAAAGTTTTCTACAAGGGGAGAA
3830	AAAGTTTTCTACAAGGGGAGAAA
3831	AAGTTTTCTACAAGGGGAGAAAA
3832	AGTTTTCTACAAGGGGAGAAAAG
3833	GTTTTCTACAAGGGGAGAAAAGT
3834	TTTTCTACAAGGGGAGAAAAGTG
3835	TTTCTACAAGGGGAGAAAAGTGT
3836	TTCTACAAGGGGAGAAAAGTGTT
3837	TCTACAAGGGGAGAAAAGTGTTA
3838	CTACAAGGGGAGAAAAGTGTTAA
3839	TACAAGGGGAGAAAAGTGTTAAA
3840	ACAAGGGGAGAAAAGTGTTAAAA

Fig. 29 cont'd (Sheet 80 of 170)

ID	SEQUENCE
3841	CAAGGGGAGAAAAGTGTTAAAAT
3842	AAGGGGAGAAAAGTGTTAAAATT
3843	AGGGGAGAAAAGTGTTAAAATTT
3844	GGGGAGAAAAGTGTTAAAATTTT
3845	GGGAGAAAAGTGTTAAAATTTTT
3846	GGAGAAAAGTGTTAAAATTTTTA
3847	GAGAAAAGTGTTAAAATTTTTAA
3848	AGAAAAGTGTTAAAATTTTTAAA
3849	GAAAAGTGTTAAAATTTTTAAAA
3850	AAAAGTGTTAAAATTTTTAAAAT
3851	AAAGTGTTAAAATTTTTAAAATA
3852	AAGTGTTAAAATTTTTAAAATAT
3853	AGTGTTAAAATTTTTAAAATATG
3854	GTGTTAAAATTTTTAAAATATGT
3855	TGTTAAAATTTTTAAAATATGTT
3856	GTTAAAATTTTTAAAATATGTTT
3857	TTAAAATTTTTAAAATATGTTTT
3858	TAAAATTTTTAAAATATGTTTTC
3859	AAAATTTTTAAAATATGTTTTCC
3860	AAATTTTTAAAATATGTTTTCCA
3861	AATTTTTAAAATATGTTTTCCAG
3862	ATTTTTAAAATATGTTTTCCAGG
3863	TTTTTAAAATATGTTTTCCAGGA
3864	TTTTAAAATATGTTTTCCAGGAC
3865	TTTAAAATATGTTTTCCAGGACA
3866	TTAAAATATGTTTTCCAGGACAC
3867	TAAAATATGTTTTCCAGGACACT
3868	AAAATATGTTTTCCAGGACACTT
3869	AAATATGTTTTCCAGGACACTTC
3870	AATATGTTTTCCAGGACACTTCA
3871	ATATGTTTTCCAGGACACTTCAC
3872	TATGTTTTCCAGGACACTTCACT
3873	ATGTTTTCCAGGACACTTCACTT
3874	TGTTTTCCAGGACACTTCACTTC
3875	GTTTTCCAGGACACTTCACTTCC
3876	TTTTCCAGGACACTTCACTTCCA
3877	TTTCCAGGACACTTCACTTCCAA
3878	TTCCAGGACACTTCACTTCCAAG
3879	TCCAGGACACTTCACTTCCAAGT
3880	CCAGGACACTTCACTTCCAAGTC
3881	CAGGACACTTCACTTCCAAGTCA
3882	AGGACACTTCACTTCCAAGTCAG
3883	GGACACTTCACTTCCAAGTCAGG
3884	GACACTTCACTTCCAAGTCAGGT
3885	ACACTTCACTTCCAAGTCAGGTA
3886	CACTTCACTTCCAAGTCAGGTAG
3887	ACTTCACTTCCAAGTCAGGTAGG
3888	CTTCACTTCCAAGTCAGGTAGGT

Fig. 29 cont'd (Sheet 81 of 170)

ID	SEQUENCE
3889	TTCACTTCCAAGTCAGGTAGGTA
3890	TCACTTCCAAGTCAGGTAGGTAG
3891	CACTTCCAAGTCAGGTAGGTAGT
3892	ACTTCCAAGTCAGGTAGGTAGTT
3893	CTTCCAAGTCAGGTAGGTAGTTC
3894	TTCCAAGTCAGGTAGGTAGTTCA
3895	TCCAAGTCAGGTAGGTAGTTCAA
3896	CCAAGTCAGGTAGGTAGTTCAAT
3897	CAAGTCAGGTAGGTAGTTCAATC
3898	AAGTCAGGTAGGTAGTTCAATCT
3899	AGTCAGGTAGGTAGTTCAATCTA
3900	GTCAGGTAGGTAGTTCAATCTAG
3901	TCAGGTAGGTAGTTCAATCTAGT
3902	CAGGTAGGTAGTTCAATCTAGTT
3903	AGGTAGGTAGTTCAATCTAGTTG
3904	GGTAGGTAGTTCAATCTAGTTGT
3905	GTAGGTAGTTCAATCTAGTTGTT
3906	TAGGTAGTTCAATCTAGTTGTTA
3907	AGGTAGTTCAATCTAGTTGTTAG
3908	GGTAGTTCAATCTAGTTGTTAGC
3909	GTAGTTCAATCTAGTTGTTAGCC
3910	TAGTTCAATCTAGTTGTTAGCCA
3911	AGTTCAATCTAGTTGTTAGCCAA
3912	GTTCAATCTAGTTGTTAGCCAAG
3913	TTCAATCTAGTTGTTAGCCAAGG
3914	TCAATCTAGTTGTTAGCCAAGGA
3915	CAATCTAGTTGTTAGCCAAGGAC
3916	AATCTAGTTGTTAGCCAAGGACT
3917	ATCTAGTTGTTAGCCAAGGACTC
3918	TCTAGTTGTTAGCCAAGGACTCA
3919	CTAGTTGTTAGCCAAGGACTCAA
3920	TAGTTGTTAGCCAAGGACTCAAG
3921	AGTTGTTAGCCAAGGACTCAAGG
3922	GTTGTTAGCCAAGGACTCAAGGA
3923	TTGTTAGCCAAGGACTCAAGGAC
3924	TGTTAGCCAAGGACTCAAGGACT
3925	GTTAGCCAAGGACTCAAGGACTG
3926	TTAGCCAAGGACTCAAGGACTGA
3927	TAGCCAAGGACTCAAGGACTGAA
3928	AGCCAAGGACTCAAGGACTGAAT
3929	GCCAAGGACTCAAGGACTGAATT
3930	CCAAGGACTCAAGGACTGAATTG
3931	CAAGGACTCAAGGACTGAATTGT
3932	AAGGACTCAAGGACTGAATTGTT
3933	AGGACTCAAGGACTGAATTGTTT
3934	GGACTCAAGGACTGAATTGTTTT
3935	GACTCAAGGACTGAATTGTTTTA
3936	ACTCAAGGACTGAATTGTTTTAA

Fig. 29 cont'd (Sheet 82 of 170)

ID	SEQUENCE
3937	CTCAAGGACTGAATTGTTTTAAC
3938	TCAAGGACTGAATTGTTTTAACA
3939	CAAGGACTGAATTGTTTTAACAT
3940	AAGGACTGAATTGTTTTAACATA
3941	AGGACTGAATTGTTTTAACATAA
3942	GGACTGAATTGTTTTAACATAAG
3943	GACTGAATTGTTTTAACATAAGG
3944	ACTGAATTGTTTTAACATAAGGC
3945	CTGAATTGTTTTAACATAAGGCT
3946	TGAATTGTTTTAACATAAGGCTT
3947	GAATTGTTTTAACATAAGGCTTT
3948	AATTGTTTTAACATAAGGCTTTT
3949	ATTGTTTTAACATAAGGCTTTTC
3950	TTGTTTTAACATAAGGCTTTTCC
3951	TGTTTTAACATAAGGCTTTTCCT
3952	GTTTTAACATAAGGCTTTTCCTG
3953	TTTTAACATAAGGCTTTTCCTGT
3954	TTTAACATAAGGCTTTTCCTGTT
3955	TTAACATAAGGCTTTTCCTGTTC
3956	TAACATAAGGCTTTTCCTGTTCT
3957	AACATAAGGCTTTTCCTGTTCTG
3958	ACATAAGGCTTTTCCTGTTCTGG
3959	CATAAGGCTTTTCCTGTTCTGGG
3960	ATAAGGCTTTTCCTGTTCTGGGA
3961	TAAGGCTTTTCCTGTTCTGGGAG
3962	AAGGCTTTTCCTGTTCTGGGAGC
3963	AGGCTTTTCCTGTTCTGGGAGCC
3964	GGCTTTTCCTGTTCTGGGAGCCG
3965	GCTTTTCCTGTTCTGGGAGCCGC
3966	CTTTTCCTGTTCTGGGAGCCGCA
3967	TTTTCCTGTTCTGGGAGCCGCAC
3968	TTTCCTGTTCTGGGAGCCGCACT
3969	TTCCTGTTCTGGGAGCCGCACTT
3970	TCCTGTTCTGGGAGCCGCACTTC
3971	CCTGTTCTGGGAGCCGCACTTCA
3972	CTGTTCTGGGAGCCGCACTTCAT
3973	TGTTCTGGGAGCCGCACTTCATT
3974	GTTCTGGGAGCCGCACTTCATTA
3975	TTCTGGGAGCCGCACTTCATTAA
3976	TCTGGGAGCCGCACTTCATTAAA
3977	CTGGGAGCCGCACTTCATTAAAA
3978	TGGGAGCCGCACTTCATTAAAAT
3979	GGGAGCCGCACTTCATTAAAATT
3980	GGAGCCGCACTTCATTAAAATTC
3981	GAGCCGCACTTCATTAAAATTCT
3982	AGCCGCACTTCATTAAAATTCTT
3983	GCCGCACTTCATTAAAATTCTTC
3984	CCGCACTTCATTAAAATTCTTCT

Fig. 29 cont'd (Sheet 83 of 170)

ID	SEQUENCE
3985	CGCACTTCATTAAAATTCTTCTA
3986	GCACTTCATTAAAATTCTTCTAA
3987	CACTTCATTAAAATTCTTCTAAA
3988	ACTTCATTAAAATTCTTCTAAAA
3989	CTTCATTAAAATTCTTCTAAAAC
3990	TTCATTAAAATTCTTCTAAAACT
3991	TCATTAAAATTCTTCTAAAACTT
3992	CATTAAAATTCTTCTAAAACTTG
3993	ATTAAAATTCTTCTAAAACTTGT
3994	TTAAAATTCTTCTAAAACTTGTA
3995	TAAAATTCTTCTAAAACTTGTAT
3996	AAAATTCTTCTAAAACTTGTATG
3997	AAATTCTTCTAAAACTTGTATGT
3998	AATTCTTCTAAAACTTGTATGTT
3999	ATTCTTCTAAAACTTGTATGTTT
4000	TTCTTCTAAAACTTGTATGTTTA
4001	TCTTCTAAAACTTGTATGTTTAG
4002	CTTCTAAAACTTGTATGTTTAGA
4003	TTCTAAAACTTGTATGTTTAGAG
4004	TCTAAAACTTGTATGTTTAGAGT
4005	CTAAAACTTGTATGTTTAGAGTT
4006	TAAAACTTGTATGTTTAGAGTTA
4007	AAAACTTGTATGTTTAGAGTTAA
4008	AAACTTGTATGTTTAGAGTTAAG
4009	AACTTGTATGTTTAGAGTTAAGC
4010	ACTTGTATGTTTAGAGTTAAGCA
4011	CTTGTATGTTTAGAGTTAAGCAA
4012	TTGTATGTTTAGAGTTAAGCAAG
4013	TGTATGTTTAGAGTTAAGCAAGA
4014	GTATGTTTAGAGTTAAGCAAGAC
4015	TATGTTTAGAGTTAAGCAAGACT
4016	ATGTTTAGAGTTAAGCAAGACTT
4017	TGTTTAGAGTTAAGCAAGACTTT
4018	GTTTAGAGTTAAGCAAGACTTTT
4019	TTTAGAGTTAAGCAAGACTTTTT
4020	TTAGAGTTAAGCAAGACTTTTTT
4021	TAGAGTTAAGCAAGACTTTTTTT
4022	AGAGTTAAGCAAGACTTTTTTTC
4023	GAGTTAAGCAAGACTTTTTTTCT
4024	AGTTAAGCAAGACTTTTTTTCTT
4025	GTTAAGCAAGACTTTTTTTCTTC
4026	TTAAGCAAGACTTTTTTTCTTCC
4027	TAAGCAAGACTTTTTTTCTTCCT
4028	AAGCAAGACTTTTTTTCTTCCTC
4029	AGCAAGACTTTTTTTCTTCCTCT
4030	GCAAGACTTTTTTTCTTCCTCTC
4031	CAAGACTTTTTTTCTTCCTCTCC
4032	AAGACTTTTTTTCTTCCTCTCCA

Fig. 29 cont'd (Sheet 84 of 170)

ID	SEQUENCE
4033	AGACTTTTTTTCTTCCTCTCCAT
4034	GACTTTTTTTCTTCCTCTCCATG
4035	ACTTTTTTTCTTCCTCTCCATGA
4036	CTTTTTTTCTTCCTCTCCATGAG
4037	TTTTTTTCTTCCTCTCCATGAGT
4038	TTTTTTCTTCCTCTCCATGAGTT
4039	TTTTTCTTCCTCTCCATGAGTTG
4040	TTTTCTTCCTCTCCATGAGTTGT
4041	TTTCTTCCTCTCCATGAGTTGTG
4042	TTCTTCCTCTCCATGAGTTGTGA
4043	TCTTCCTCTCCATGAGTTGTGAA
4044	CTTCCTCTCCATGAGTTGTGAAA
4045	TTCCTCTCCATGAGTTGTGAAAT
4046	TCCTCTCCATGAGTTGTGAAATT
4047	CCTCTCCATGAGTTGTGAAATTT
4048	CTCTCCATGAGTTGTGAAATTTA
4049	TCTCCATGAGTTGTGAAATTTAA
4050	CTCCATGAGTTGTGAAATTTAAT
4051	TCCATGAGTTGTGAAATTTAATG
4052	CCATGAGTTGTGAAATTTAATGC
4053	CATGAGTTGTGAAATTTAATGCA
4054	ATGAGTTGTGAAATTTAATGCAC
4055	TGAGTTGTGAAATTTAATGCACA
4056	GAGTTGTGAAATTTAATGCACAA
4057	AGTTGTGAAATTTAATGCACAAC
4058	GTTGTGAAATTTAATGCACAACG
4059	TTGTGAAATTTAATGCACAACGC
4060	TGTGAAATTTAATGCACAACGCT
4061	GTGAAATTTAATGCACAACGCTG
4062	TGAAATTTAATGCACAACGCTGA
4063	GAAATTTAATGCACAACGCTGAT
4064	AAATTTAATGCACAACGCTGATG
4065	AATTTAATGCACAACGCTGATGT
4066	ATTTAATGCACAACGCTGATGTG
4067	TTTAATGCACAACGCTGATGTGG
4068	TTAATGCACAACGCTGATGTGGC
4069	TAATGCACAACGCTGATGTGGCT
4070	AATGCACAACGCTGATGTGGCTA
4071	ATGCACAACGCTGATGTGGCTAA
4072	TGCACAACGCTGATGTGGCTAAC
4073	GCACAACGCTGATGTGGCTAACA
4074	CACAACGCTGATGTGGCTAACAA
4075	ACAACGCTGATGTGGCTAACAAG
4076	CAACGCTGATGTGGCTAACAAGT
4077	AACGCTGATGTGGCTAACAAGTT
4078	ACGCTGATGTGGCTAACAAGTTT
4079	CGCTGATGTGGCTAACAAGTTTA
4080	GCTGATGTGGCTAACAAGTTTAT

Fig. 29 cont'd (Sheet 85 of 170)

ID	SEQUENCE
4081	CTGATGTGGCTAACAAGTTTATT
4082	TGATGTGGCTAACAAGTTTATTT
4083	GATGTGGCTAACAAGTTTATTTT
4084	ATGTGGCTAACAAGTTTATTTTA
4085	TGTGGCTAACAAGTTTATTTTAA
4086	GTGGCTAACAAGTTTATTTTAAG
4087	TGGCTAACAAGTTTATTTTAAGA
4088	GGCTAACAAGTTTATTTTAAGAA
4089	GCTAACAAGTTTATTTTAAGAAT
4090	CTAACAAGTTTATTTTAAGAATT
4091	TAACAAGTTTATTTTAAGAATTG
4092	AACAAGTTTATTTTAAGAATTGT
4093	ACAAGTTTATTTTAAGAATTGTT
4094	CAAGTTTATTTTAAGAATTGTTT
4095	AAGTTTATTTTAAGAATTGTTTA
4096	AGTTTATTTTAAGAATTGTTTAG
4097	GTTTATTTTAAGAATTGTTTAGA
4098	TTTATTTTAAGAATTGTTTAGAA
4099	TTATTTTAAGAATTGTTTAGAAA
4100	TATTTTAAGAATTGTTTAGAAAT
4101	ATTTTAAGAATTGTTTAGAAATG
4102	TTTTAAGAATTGTTTAGAAATGC
4103	TTTAAGAATTGTTTAGAAATGCT
4104	TTAAGAATTGTTTAGAAATGCTG
4105	TAAGAATTGTTTAGAAATGCTGT
4106	AAGAATTGTTTAGAAATGCTGTT
4107	AGAATTGTTTAGAAATGCTGTTG
4108	GAATTGTTTAGAAATGCTGTTGC
4109	AATTGTTTAGAAATGCTGTTGCT
4110	ATTGTTTAGAAATGCTGTTGCTT
4111	TTGTTTAGAAATGCTGTTGCTTC
4112	TGTTTAGAAATGCTGTTGCTTCA
4113	GTTTAGAAATGCTGTTGCTTCAG
4114	TTTAGAAATGCTGTTGCTTCAGG
4115	TTAGAAATGCTGTTGCTTCAGGT
4116	TAGAAATGCTGTTGCTTCAGGTT
4117	AGAAATGCTGTTGCTTCAGGTTC
4118	GAAATGCTGTTGCTTCAGGTTCT
4119	AAATGCTGTTGCTTCAGGTTCTT
4120	AATGCTGTTGCTTCAGGTTCTTA
4121	ATGCTGTTGCTTCAGGTTCTTAA
4122	TGCTGTTGCTTCAGGTTCTTAAA
4123	GCTGTTGCTTCAGGTTCTTAAAA
4124	CTGTTGCTTCAGGTTCTTAAAAT
4125	TGTTGCTTCAGGTTCTTAAAATC
4126	GTTGCTTCAGGTTCTTAAAATCA
4127	TTGCTTCAGGTTCTTAAAATCAC
4128	TGCTTCAGGTTCTTAAAATCACT

Fig. 29 cont'd (Sheet 86 of 170)

ID	SEQUENCE
4129	GCTTCAGGTTCTTAAAATCACTC
4130	CTTCAGGTTCTTAAAATCACTCA
4131	TTCAGGTTCTTAAAATCACTCAG
4132	TCAGGTTCTTAAAATCACTCAGC
4133	CAGGTTCTTAAAATCACTCAGCA
4134	AGGTTCTTAAAATCACTCAGCAC
4135	GGTTCTTAAAATCACTCAGCACT
4136	GTTCTTAAAATCACTCAGCACTC
4137	TTCTTAAAATCACTCAGCACTCC
4138	TCTTAAAATCACTCAGCACTCCA
4139	CTTAAAATCACTCAGCACTCCAA
4140	TTAAAATCACTCAGCACTCCAAC
4141	TAAAATCACTCAGCACTCCAACT
4142	AAAATCACTCAGCACTCCAACTT
4143	AAATCACTCAGCACTCCAACTTC
4144	AATCACTCAGCACTCCAACTTCT
4145	ATCACTCAGCACTCCAACTTCTA
4146	TCACTCAGCACTCCAACTTCTAA
4147	CACTCAGCACTCCAACTTCTAAT
4148	ACTCAGCACTCCAACTTCTAATC
4149	CTCAGCACTCCAACTTCTAATCA
4150	TCAGCACTCCAACTTCTAATCAA
4151	CAGCACTCCAACTTCTAATCAAA
4152	AGCACTCCAACTTCTAATCAAAT
4153	GCACTCCAACTTCTAATCAAATT
4154	CACTCCAACTTCTAATCAAATTT
4155	ACTCCAACTTCTAATCAAATTTT
4156	CTCCAACTTCTAATCAAATTTTT
4157	TCCAACTTCTAATCAAATTTTTG
4158	CCAACTTCTAATCAAATTTTTGG
4159	CAACTTCTAATCAAATTTTTGGA
4160	AACTTCTAATCAAATTTTTGGAG
4161	ACTTCTAATCAAATTTTTGGAGA
4162	CTTCTAATCAAATTTTTGGAGAC
4163	TTCTAATCAAATTTTTGGAGACT
4164	TCTAATCAAATTTTTGGAGACTT
4165	CTAATCAAATTTTTGGAGACTTA
4166	TAATCAAATTTTTGGAGACTTAA
4167	AATCAAATTTTTGGAGACTTAAC
4168	ATCAAATTTTTGGAGACTTAACA
4169	TCAAATTTTTGGAGACTTAACAG
4170	CAAATTTTTGGAGACTTAACAGC
4171	AAATTTTTGGAGACTTAACAGCA
4172	AATTTTTGGAGACTTAACAGCAT
4173	ATTTTTGGAGACTTAACAGCATT
4174	TTTTTGGAGACTTAACAGCATTT
4175	TTTTGGAGACTTAACAGCATTTG
4176	TTTGGAGACTTAACAGCATTTGT

Fig. 29 cont'd (Sheet 87 of 170)

ID	SEQUENCE
4177	TTGGAGACTTAACAGCATTTGTC
4178	TGGAGACTTAACAGCATTTGTCT
4179	GGAGACTTAACAGCATTTGTCTG
4180	GAGACTTAACAGCATTTGTCTGT
4181	AGACTTAACAGCATTTGTCTGTG
4182	GACTTAACAGCATTTGTCTGTGT
4183	ACTTAACAGCATTTGTCTGTGTT
4184	CTTAACAGCATTTGTCTGTGTTT
4185	TTAACAGCATTTGTCTGTGTTTG
4186	TAACAGCATTTGTCTGTGTTTGA
4187	AACAGCATTTGTCTGTGTTTGAA
4188	ACAGCATTTGTCTGTGTTTGAAC
4189	CAGCATTTGTCTGTGTTTGAACT
4190	AGCATTTGTCTGTGTTTGAACTA
4191	GCATTTGTCTGTGTTTGAACTAT
4192	CATTTGTCTGTGTTTGAACTATA
4193	ATTTGTCTGTGTTTGAACTATAA
4194	TTTGTCTGTGTTTGAACTATAAA
4195	TTGTCTGTGTTTGAACTATAAAA
4196	TGTCTGTGTTTGAACTATAAAAA
4197	GTCTGTGTTTGAACTATAAAAAG
4198	TCTGTGTTTGAACTATAAAAAGC
4199	CTGTGTTTGAACTATAAAAAGCA
4200	TGTGTTTGAACTATAAAAAGCAC
4201	GTGTTTGAACTATAAAAAGCACC
4202	TGTTTGAACTATAAAAAGCACCG
4203	GTTTGAACTATAAAAAGCACCGG
4204	TTTGAACTATAAAAAGCACCGGA
4205	TTGAACTATAAAAAGCACCGGAT
4206	TGAACTATAAAAAGCACCGGATC
4207	GAACTATAAAAAGCACCGGATCT
4208	AACTATAAAAAGCACCGGATCTT
4209	ACTATAAAAAGCACCGGATCTTT
4210	CTATAAAAAGCACCGGATCTTTT
4211	TATAAAAAGCACCGGATCTTTTC
4212	ATAAAAAGCACCGGATCTTTTCC
4213	TAAAAAGCACCGGATCTTTTCCA
4214	AAAAAGCACCGGATCTTTTCCAT
4215	AAAAGCACCGGATCTTTTCCATC
4216	AAAGCACCGGATCTTTTCCATCT
4217	AAGCACCGGATCTTTTCCATCTA
4218	AGCACCGGATCTTTTCCATCTAA
4219	GCACCGGATCTTTTCCATCTAAT
4220	CACCGGATCTTTTCCATCTAATT
4221	ACCGGATCTTTTCCATCTAATTC
4222	CCGGATCTTTTCCATCTAATTCC
4223	CGGATCTTTTCCATCTAATTCCG
4224	GGATCTTTTCCATCTAATTCCGC

Fig. 29 cont'd (Sheet 88 of 170)

ID	SEQUENCE
4225	GATCTTTTCCATCTAATTCCGCA
4226	ATCTTTTCCATCTAATTCCGCAA
4227	TCTTTTCCATCTAATTCCGCAAA
4228	CTTTTCCATCTAATTCCGCAAAA
4229	TTTTCCATCTAATTCCGCAAAAA
4230	TTTCCATCTAATTCCGCAAAAAT
4231	TTCCATCTAATTCCGCAAAAATT
4232	TCCATCTAATTCCGCAAAAATTG
4233	CCATCTAATTCCGCAAAAATTGA
4234	CATCTAATTCCGCAAAAATTGAT
4235	ATCTAATTCCGCAAAAATTGATC
4236	TCTAATTCCGCAAAAATTGATCA
4237	CTAATTCCGCAAAAATTGATCAT
4238	TAATTCCGCAAAAATTGATCATT
4239	AATTCCGCAAAAATTGATCATTT
4240	ATTCCGCAAAAATTGATCATTTG
4241	TTCCGCAAAAATTGATCATTTGC
4242	TCCGCAAAAATTGATCATTTGCA
4243	CCGCAAAAATTGATCATTTGCAA
4244	CGCAAAAATTGATCATTTGCAAA
4245	GCAAAAATTGATCATTTGCAAAG
4246	CAAAAATTGATCATTTGCAAAGT
4247	AAAAATTGATCATTTGCAAAGTC
4248	AAAATTGATCATTTGCAAAGTCA
4249	AAATTGATCATTTGCAAAGTCAA
4250	AATTGATCATTTGCAAAGTCAAA
4251	ATTGATCATTTGCAAAGTCAAAA
4252	TTGATCATTTGCAAAGTCAAAAC
4253	TGATCATTTGCAAAGTCAAAACT
4254	GATCATTTGCAAAGTCAAAACTA
4255	ATCATTTGCAAAGTCAAAACTAT
4256	TCATTTGCAAAGTCAAAACTATA
4257	CATTTGCAAAGTCAAAACTATAG
4258	ATTTGCAAAGTCAAAACTATAGC
4259	TTTGCAAAGTCAAAACTATAGCC
4260	TTGCAAAGTCAAAACTATAGCCA
4261	TGCAAAGTCAAAACTATAGCCAT
4262	GCAAAGTCAAAACTATAGCCATA
4263	CAAAGTCAAAACTATAGCCATAT
4264	AAAGTCAAAACTATAGCCATATC
4265	AAGTCAAAACTATAGCCATATCC
4266	AGTCAAAACTATAGCCATATCCA
4267	GTCAAAACTATAGCCATATCCAA
4268	TCAAAACTATAGCCATATCCAAA
4269	CAAAACTATAGCCATATCCAAAT
4270	AAAACTATAGCCATATCCAAATC
4271	AAACTATAGCCATATCCAAATCT
4272	AACTATAGCCATATCCAAATCTT

Fig. 29 cont'd (Sheet 89 of 170)

ID	SEQUENCE
4273	ACTATAGCCATATCCAAATCTTT
4274	CTATAGCCATATCCAAATCTTTT
4275	TATAGCCATATCCAAATCTTTTC
4276	ATAGCCATATCCAAATCTTTTCC
4277	TAGCCATATCCAAATCTTTTCCC
4278	AGCCATATCCAAATCTTTTCCCC
4279	GCCATATCCAAATCTTTTCCCCC
4280	CCATATCCAAATCTTTTCCCCCT
4281	CATATCCAAATCTTTTCCCCCTC
4282	ATATCCAAATCTTTTCCCCCTCC
4283	TATCCAAATCTTTTCCCCCTCCC
4284	ATCCAAATCTTTTCCCCCTCCCA
4285	TCCAAATCTTTTCCCCCTCCCAA
4286	CCAAATCTTTTCCCCCTCCCAAG
4287	CAAATCTTTTCCCCCTCCCAAGA
4288	AAATCTTTTCCCCCTCCCAAGAG
4289	AATCTTTTCCCCCTCCCAAGAGT
4290	ATCTTTTCCCCCTCCCAAGAGTT
4291	TCTTTTCCCCCTCCCAAGAGTTC
4292	CTTTTCCCCCTCCCAAGAGTTCT
4293	TTTTCCCCCTCCCAAGAGTTCTC
4294	TTTCCCCCTCCCAAGAGTTCTCA
4295	TTCCCCCTCCCAAGAGTTCTCAG
4296	TCCCCCTCCCAAGAGTTCTCAGT
4297	CCCCCTCCCAAGAGTTCTCAGTG
4298	CCCCTCCCAAGAGTTCTCAGTGT
4299	CCCTCCCAAGAGTTCTCAGTGTC
4300	CCTCCCAAGAGTTCTCAGTGTCT
4301	CTCCCAAGAGTTCTCAGTGTCTA
4302	TCCCAAGAGTTCTCAGTGTCTAC
4303	CCCAAGAGTTCTCAGTGTCTACA
4304	CCAAGAGTTCTCAGTGTCTACAT
4305	CAAGAGTTCTCAGTGTCTACATG
4306	AAGAGTTCTCAGTGTCTACATGT
4307	AGAGTTCTCAGTGTCTACATGTA
4308	GAGTTCTCAGTGTCTACATGTAG
4309	AGTTCTCAGTGTCTACATGTAGA
4310	GTTCTCAGTGTCTACATGTAGAC
4311	TTCTCAGTGTCTACATGTAGACT
4312	TCTCAGTGTCTACATGTAGACTA
4313	CTCAGTGTCTACATGTAGACTAT
4314	TCAGTGTCTACATGTAGACTATT
4315	CAGTGTCTACATGTAGACTATTC
4316	AGTGTCTACATGTAGACTATTCC
4317	GTGTCTACATGTAGACTATTCCT
4318	TGTCTACATGTAGACTATTCCTT
4319	GTCTACATGTAGACTATTCCTTT
4320	TCTACATGTAGACTATTCCTTTT

Fig. 29 cont'd (Sheet 90 of 170)

ID	SEQUENCE
4321	CTACATGTAGACTATTCCTTTTC
4322	TACATGTAGACTATTCCTTTTCT
4323	ACATGTAGACTATTCCTTTTCTG
4324	CATGTAGACTATTCCTTTTCTGT
4325	ATGTAGACTATTCCTTTTCTGTA
4326	TGTAGACTATTCCTTTTCTGTAT
4327	GTAGACTATTCCTTTTCTGTATA
4328	TAGACTATTCCTTTTCTGTATAA
4329	AGACTATTCCTTTTCTGTATAAA
4330	GACTATTCCTTTTCTGTATAAAG
4331	ACTATTCCTTTTCTGTATAAAGT
4332	CTATTCCTTTTCTGTATAAAGTT
4333	TATTCCTTTTCTGTATAAAGTTC
4334	ATTCCTTTTCTGTATAAAGTTCA
4335	TTCCTTTTCTGTATAAAGTTCAC
4336	TCCTTTTCTGTATAAAGTTCACT
4337	CCTTTTCTGTATAAAGTTCACTC
4338	CTTTTCTGTATAAAGTTCACTCT
4339	TTTTCTGTATAAAGTTCACTCTA
4340	TTTCTGTATAAAGTTCACTCTAG
4341	TTCTGTATAAAGTTCACTCTAGG
4342	TCTGTATAAAGTTCACTCTAGGA
4343	CTGTATAAAGTTCACTCTAGGAT
4344	TGTATAAAGTTCACTCTAGGATT
4345	GTATAAAGTTCACTCTAGGATTT
4346	TATAAAGTTCACTCTAGGATTTC
4347	ATAAAGTTCACTCTAGGATTTCA
4348	TAAAGTTCACTCTAGGATTTCAA
4349	AAAGTTCACTCTAGGATTTCAAG
4350	AAGTTCACTCTAGGATTTCAAGT
4351	AGTTCACTCTAGGATTTCAAGTC
4352	GTTCACTCTAGGATTTCAAGTCA
4353	TTCACTCTAGGATTTCAAGTCAC
4354	TCACTCTAGGATTTCAAGTCACC
4355	CACTCTAGGATTTCAAGTCACCA
4356	ACTCTAGGATTTCAAGTCACCAC
4357	CTCTAGGATTTCAAGTCACCACT
4358	TCTAGGATTTCAAGTCACCACTT
4359	CTAGGATTTCAAGTCACCACTTA
4360	TAGGATTTCAAGTCACCACTTAT
4361	AGGATTTCAAGTCACCACTTATT
4362	GGATTTCAAGTCACCACTTATTT
4363	GATTTCAAGTCACCACTTATTTT
4364	ATTTCAAGTCACCACTTATTTTA
4365	TTTCAAGTCACCACTTATTTTAC
4366	TTCAAGTCACCACTTATTTTACA
4367	TCAAGTCACCACTTATTTTACAT
4368	CAAGTCACCACTTATTTTACATT

Fig. 29 cont'd (Sheet 91 of 170)

ID	SEQUENCE
4369	AAGTCACCACTTATTTTACATTT
4370	AGTCACCACTTATTTTACATTTT
4371	GTCACCACTTATTTTACATTTTA
4372	TCACCACTTATTTTACATTTTAG
4373	CACCACTTATTTTACATTTTAGT
4374	ACCACTTATTTTACATTTTAGTC
4375	CCACTTATTTTACATTTTAGTCA
4376	CACTTATTTTACATTTTAGTCAT
4377	ACTTATTTTACATTTTAGTCATG
4378	CTTATTTTACATTTTAGTCATGC
4379	TTATTTTACATTTTAGTCATGCA
4380	TATTTTACATTTTAGTCATGCAA
4381	ATTTTACATTTTAGTCATGCAAA
4382	TTTTACATTTTAGTCATGCAAAG
4383	TTTACATTTTAGTCATGCAAAGA
4384	TTACATTTTAGTCATGCAAAGAT
4385	TACATTTTAGTCATGCAAAGATT
4386	ACATTTTAGTCATGCAAAGATTC
4387	CATTTTAGTCATGCAAAGATTCA
4388	ATTTTAGTCATGCAAAGATTCAA
4389	TTTTAGTCATGCAAAGATTCAAG
4390	TTTAGTCATGCAAAGATTCAAGT
4391	TTAGTCATGCAAAGATTCAAGTA
4392	TAGTCATGCAAAGATTCAAGTAG
4393	AGTCATGCAAAGATTCAAGTAGT
4394	GTCATGCAAAGATTCAAGTAGTT
4395	TCATGCAAAGATTCAAGTAGTTT
4396	CATGCAAAGATTCAAGTAGTTTT
4397	ATGCAAAGATTCAAGTAGTTTTG
4398	TGCAAAGATTCAAGTAGTTTTGC
4399	GCAAAGATTCAAGTAGTTTTGCA
4400	CAAAGATTCAAGTAGTTTTGCAA
4401	AAAGATTCAAGTAGTTTTGCAAT
4402	AAGATTCAAGTAGTTTTGCAATA
4403	AGATTCAAGTAGTTTTGCAATAA
4404	GATTCAAGTAGTTTTGCAATAAG
4405	ATTCAAGTAGTTTTGCAATAAGT
4406	TTCAAGTAGTTTTGCAATAAGTA
4407	TCAAGTAGTTTTGCAATAAGTAC
4408	CAAGTAGTTTTGCAATAAGTACT
4409	AAGTAGTTTTGCAATAAGTACTT
4410	AGTAGTTTTGCAATAAGTACTTA
4411	GTAGTTTTGCAATAAGTACTTAT
4412	TAGTTTTGCAATAAGTACTTATC
4413	AGTTTTGCAATAAGTACTTATCT
4414	GTTTTGCAATAAGTACTTATCTT
4415	TTTTGCAATAAGTACTTATCTTT
4416	TTTGCAATAAGTACTTATCTTTA

Fig. 29 cont'd (Sheet 92 of 170)

ID	SEQUENCE
4417	TTGCAATAAGTACTTATCTTTAT
4418	TGCAATAAGTACTTATCTTTATT
4419	GCAATAAGTACTTATCTTTATTT
4420	CAATAAGTACTTATCTTTATTTG
4421	AATAAGTACTTATCTTTATTTGT
4422	ATAAGTACTTATCTTTATTTGTA
4423	TAAGTACTTATCTTTATTTGTAA
4424	AAGTACTTATCTTTATTTGTAAT
4425	AGTACTTATCTTTATTTGTAATA
4426	GTACTTATCTTTATTTGTAATAA
4427	TACTTATCTTTATTTGTAATAAT
4428	ACTTATCTTTATTTGTAATAATT
4429	CTTATCTTTATTTGTAATAATTT
4430	TTATCTTTATTTGTAATAATTTA
4431	TATCTTTATTTGTAATAATTTAG
4432	ATCTTTATTTGTAATAATTTAGT
4433	TCTTTATTTGTAATAATTTAGTC
4434	CTTTATTTGTAATAATTTAGTCT
4435	TTTATTTGTAATAATTTAGTCTG
4436	TTATTTGTAATAATTTAGTCTGC
4437	TATTTGTAATAATTTAGTCTGCT
4438	ATTTGTAATAATTTAGTCTGCTG
4439	TTTGTAATAATTTAGTCTGCTGA
4440	TTGTAATAATTTAGTCTGCTGAT
4441	TGTAATAATTTAGTCTGCTGATC
4442	GTAATAATTTAGTCTGCTGATCA
4443	TAATAATTTAGTCTGCTGATCAA
4444	AATAATTTAGTCTGCTGATCAAA
4445	ATAATTTAGTCTGCTGATCAAAA
4446	TAATTTAGTCTGCTGATCAAAAG
4447	AATTTAGTCTGCTGATCAAAAGC
4448	ATTTAGTCTGCTGATCAAAAGCA
4449	TTTAGTCTGCTGATCAAAAGCAT
4450	TTAGTCTGCTGATCAAAAGCATT
4451	TAGTCTGCTGATCAAAAGCATTG
4452	AGTCTGCTGATCAAAAGCATTGT
4453	GTCTGCTGATCAAAAGCATTGTC
4454	TCTGCTGATCAAAAGCATTGTCT
4455	CTGCTGATCAAAAGCATTGTCTT
4456	TGCTGATCAAAAGCATTGTCTTA
4457	GCTGATCAAAAGCATTGTCTTAA
4458	CTGATCAAAAGCATTGTCTTAAT
4459	TGATCAAAAGCATTGTCTTAATT
4460	GATCAAAAGCATTGTCTTAATTT
4461	ATCAAAAGCATTGTCTTAATTTT
4462	TCAAAAGCATTGTCTTAATTTTT
4463	CAAAAGCATTGTCTTAATTTTTG
4464	AAAAGCATTGTCTTAATTTTTGA

Fig. 29 cont'd (Sheet 93 of 170)

ID	SEQUENCE
4465	AAAGCATTGTCTTAATTTTTGAG
4466	AAGCATTGTCTTAATTTTTGAGA
4467	AGCATTGTCTTAATTTTTGAGAA
4468	GCATTGTCTTAATTTTTGAGAAC
4469	CATTGTCTTAATTTTTGAGAACT
4470	ATTGTCTTAATTTTTGAGAACTG
4471	TTGTCTTAATTTTTGAGAACTGG
4472	TGTCTTAATTTTTGAGAACTGGT
4473	GTCTTAATTTTTGAGAACTGGTT
4474	TCTTAATTTTTGAGAACTGGTTT
4475	CTTAATTTTTGAGAACTGGTTTT
4476	TTAATTTTTGAGAACTGGTTTTA
4477	TAATTTTTGAGAACTGGTTTTAG
4478	AATTTTTGAGAACTGGTTTTAGC
4479	ATTTTTGAGAACTGGTTTTAGCA
4480	TTTTTGAGAACTGGTTTTAGCAT
4481	TTTTGAGAACTGGTTTTAGCATT
4482	TTTGAGAACTGGTTTTAGCATTT
4483	TTGAGAACTGGTTTTAGCATTTA
4484	TGAGAACTGGTTTTAGCATTTAC
4485	GAGAACTGGTTTTAGCATTTACA
4486	AGAACTGGTTTTAGCATTTACAA
4487	GAACTGGTTTTAGCATTTACAAA
4488	AACTGGTTTTAGCATTTACAAAC
4489	ACTGGTTTTAGCATTTACAAACT
4490	CTGGTTTTAGCATTTACAAACTA
4491	TGGTTTTAGCATTTACAAACTAA
4492	GGTTTTAGCATTTACAAACTAAA
4493	GTTTTAGCATTTACAAACTAAAT
4494	TTTTAGCATTTACAAACTAAATT
4495	TTTAGCATTTACAAACTAAATTC
4496	TTAGCATTTACAAACTAAATTCC
4497	TAGCATTTACAAACTAAATTCCA
4498	AGCATTTACAAACTAAATTCCAG
4499	GCATTTACAAACTAAATTCCAGT
4500	CATTTACAAACTAAATTCCAGTT
4501	ATTTACAAACTAAATTCCAGTTA
4502	TTTACAAACTAAATTCCAGTTAA
4503	TTACAAACTAAATTCCAGTTAAT
4504	TACAAACTAAATTCCAGTTAATT
4505	ACAAACTAAATTCCAGTTAATTA
4506	CAAACTAAATTCCAGTTAATTAA
4507	AAACTAAATTCCAGTTAATTAAT
4508	AACTAAATTCCAGTTAATTAATT
4509	ACTAAATTCCAGTTAATTAATTA
4510	CTAAATTCCAGTTAATTAATTAA
4511	TAAATTCCAGTTAATTAATTAAT
4512	AAATTCCAGTTAATTAATTAATA

Fig. 29 cont'd (Sheet 94 of 170)

ID	SEQUENCE
4513	AATTCCAGTTAATTAATTAATAG
4514	ATTCCAGTTAATTAATTAATAGC
4515	TTCCAGTTAATTAATTAATAGCT
4516	TCCAGTTAATTAATTAATAGCTT
4517	CCAGTTAATTAATTAATAGCTTT
4518	CAGTTAATTAATTAATAGCTTTA
4519	AGTTAATTAATTAATAGCTTTAT
4520	GTTAATTAATTAATAGCTTTATA
4521	TTAATTAATTAATAGCTTTATAT
4522	TAATTAATTAATAGCTTTATATT
4523	AATTAATTAATAGCTTTATATTG
4524	ATTAATTAATAGCTTTATATTGC
4525	TTAATTAATAGCTTTATATTGCC
4526	TAATTAATAGCTTTATATTGCCT
4527	AATTAATAGCTTTATATTGCCTT
4528	ATTAATAGCTTTATATTGCCTTT
4529	TTAATAGCTTTATATTGCCTTTC
4530	TAATAGCTTTATATTGCCTTTCC
4531	AATAGCTTTATATTGCCTTTCCT
4532	ATAGCTTTATATTGCCTTTCCTG
4533	TAGCTTTATATTGCCTTTCCTGC
4534	AGCTTTATATTGCCTTTCCTGCT
4535	GCTTTATATTGCCTTTCCTGCTA
4536	CTTTATATTGCCTTTCCTGCTAC
4537	TTTATATTGCCTTTCCTGCTACA
4538	TTATATTGCCTTTCCTGCTACAT
4539	TATATTGCCTTTCCTGCTACATT
4540	ATATTGCCTTTCCTGCTACATTT
4541	TATTGCCTTTCCTGCTACATTTG
4542	ATTGCCTTTCCTGCTACATTTGG
4543	TTGCCTTTCCTGCTACATTTGGT
4544	TGCCTTTCCTGCTACATTTGGTT
4545	GCCTTTCCTGCTACATTTGGTTT
4546	CCTTTCCTGCTACATTTGGTTTT
4547	CTTTCCTGCTACATTTGGTTTTT
4548	TTTCCTGCTACATTTGGTTTTTT
4549	TTCCTGCTACATTTGGTTTTTTC
4550	TCCTGCTACATTTGGTTTTTTCC
4551	CCTGCTACATTTGGTTTTTTCCC
4552	CTGCTACATTTGGTTTTTTCCCC
4553	TGCTACATTTGGTTTTTTCCCCT
4554	GCTACATTTGGTTTTTTCCCCTG
4555	CTACATTTGGTTTTTTCCCCTGT
4556	TACATTTGGTTTTTTCCCCTGTC
4557	ACATTTGGTTTTTTCCCCTGTCC
4558	CATTTGGTTTTTTCCCCTGTCCC
4559	ATTTGGTTTTTTCCCCTGTCCCT
4560	TTTGGTTTTTTCCCCTGTCCCTT

Fig. 29 cont'd (Sheet 95 of 170)

ID	SEQUENCE
4561	TTGGTTTTTTCCCCTGTCCCTTT
4562	TGGTTTTTTCCCCTGTCCCTTTG
4563	GGTTTTTTCCCCTGTCCCTTTGA
4564	GTTTTTTCCCCTGTCCCTTTGAT
4565	TTTTTTCCCCTGTCCCTTTGATT
4566	TTTTTCCCCTGTCCCTTTGATTA
4567	TTTTCCCCTGTCCCTTTGATTAC
4568	TTTCCCCTGTCCCTTTGATTACG
4569	TTCCCCTGTCCCTTTGATTACGG
4570	TCCCCTGTCCCTTTGATTACGGG
4571	CCCCTGTCCCTTTGATTACGGGC
4572	CCCTGTCCCTTTGATTACGGGCT
4573	CCTGTCCCTTTGATTACGGGCTA
4574	CTGTCCCTTTGATTACGGGCTAA
4575	TGTCCCTTTGATTACGGGCTAAG
4576	GTCCCTTTGATTACGGGCTAAGG
4577	TCCCTTTGATTACGGGCTAAGGT
4578	CCCTTTGATTACGGGCTAAGGTA
4579	CCTTTGATTACGGGCTAAGGTAG
4580	CTTTGATTACGGGCTAAGGTAGG
4581	TTTGATTACGGGCTAAGGTAGGG
4582	TTGATTACGGGCTAAGGTAGGGT
4583	TGATTACGGGCTAAGGTAGGGTA
4584	GATTACGGGCTAAGGTAGGGTAG
4585	ATTACGGGCTAAGGTAGGGTAGA
4586	TTACGGGCTAAGGTAGGGTAGAG
4587	TACGGGCTAAGGTAGGGTAGAGT
4588	ACGGGCTAAGGTAGGGTAGAGTG
4589	CGGGCTAAGGTAGGGTAGAGTGG
4590	GGGCTAAGGTAGGGTAGAGTGGG
4591	GGCTAAGGTAGGGTAGAGTGGGT
4592	GCTAAGGTAGGGTAGAGTGGGTG
4593	CTAAGGTAGGGTAGAGTGGGTGT
4594	TAAGGTAGGGTAGAGTGGGTGTA
4595	AAGGTAGGGTAGAGTGGGTGTAG
4596	AGGTAGGGTAGAGTGGGTGTAGT
4597	GGTAGGGTAGAGTGGGTGTAGTG
4598	GTAGGGTAGAGTGGGTGTAGTGA
4599	TAGGGTAGAGTGGGTGTAGTGAG
4600	AGGGTAGAGTGGGTGTAGTGAGT
4601	GGGTAGAGTGGGTGTAGTGAGTG
4602	GGTAGAGTGGGTGTAGTGAGTGT
4603	GTAGAGTGGGTGTAGTGAGTGTA
4604	TAGAGTGGGTGTAGTGAGTGTAT
4605	AGAGTGGGTGTAGTGAGTGTATA
4606	GAGTGGGTGTAGTGAGTGTATAT
4607	AGTGGGTGTAGTGAGTGTATATA
4608	GTGGGTGTAGTGAGTGTATATAA

Fig. 29 cont'd (Sheet 96 of 170)

ID	SEQUENCE
4609	TGGGTGTAGTGAGTGTATATAAT
4610	GGGTGTAGTGAGTGTATATAATG
4611	GGTGTAGTGAGTGTATATAATGT
4612	GTGTAGTGAGTGTATATAATGTG
4613	TGTAGTGAGTGTATATAATGTGA
4614	GTAGTGAGTGTATATAATGTGAT
4615	TAGTGAGTGTATATAATGTGATT
4616	AGTGAGTGTATATAATGTGATTT
4617	GTGAGTGTATATAATGTGATTTG
4618	TGAGTGTATATAATGTGATTTGG
4619	GAGTGTATATAATGTGATTTGGC
4620	AGTGTATATAATGTGATTTGGCC
4621	GTGTATATAATGTGATTTGGCCC
4622	TGTATATAATGTGATTTGGCCCT
4623	GTATATAATGTGATTTGGCCCTG
4624	TATATAATGTGATTTGGCCCTGT
4625	ATATAATGTGATTTGGCCCTGTG
4626	TATAATGTGATTTGGCCCTGTGT
4627	ATAATGTGATTTGGCCCTGTGTA
4628	TAATGTGATTTGGCCCTGTGTAT
4629	AATGTGATTTGGCCCTGTGTATT
4630	ATGTGATTTGGCCCTGTGTATTA
4631	TGTGATTTGGCCCTGTGTATTAT
4632	GTGATTTGGCCCTGTGTATTATG
4633	TGATTTGGCCCTGTGTATTATGA
4634	GATTTGGCCCTGTGTATTATGAT
4635	ATTTGGCCCTGTGTATTATGATA
4636	TTTGGCCCTGTGTATTATGATAT
4637	TTGGCCCTGTGTATTATGATATT
4638	TGGCCCTGTGTATTATGATATTT
4639	GGCCCTGTGTATTATGATATTTT
4640	GCCCTGTGTATTATGATATTTTG
4641	CCCTGTGTATTATGATATTTTGT
4642	CCTGTGTATTATGATATTTTGTT
4643	CTGTGTATTATGATATTTTGTTA
4644	TGTGTATTATGATATTTTGTTAT
4645	GTGTATTATGATATTTTGTTATT
4646	TGTATTATGATATTTTGTTATTT
4647	GTATTATGATATTTTGTTATTTT
4648	TATTATGATATTTTGTTATTTTT
4649	ATTATGATATTTTGTTATTTTTG
4650	TTATGATATTTTGTTATTTTTGT
4651	TATGATATTTTGTTATTTTTGTT
4652	ATGATATTTTGTTATTTTTGTTG
4653	TGATATTTTGTTATTTTTGTTGT
4654	GATATTTTGTTATTTTTGTTGTT
4655	ATATTTTGTTATTTTTGTTGTTA
4656	TATTTTGTTATTTTTGTTGTTAT

Fig. 29 cont'd (Sheet 97 of 170)

ID	SEQUENCE
4657	ATTTTGTTATTTTTGTTGTTATA
4658	TTTTGTTATTTTTGTTGTTATAT
4659	TTTGTTATTTTTGTTGTTATATT
4660	TTGTTATTTTTGTTGTTATATTA
4661	TGTTATTTTTGTTGTTATATTAT
4662	GTTATTTTTGTTGTTATATTATT
4663	TTATTTTTGTTGTTATATTATTT
4664	TATTTTTGTTGTTATATTATTTA
4665	ATTTTTGTTGTTATATTATTTAC
4666	TTTTTGTTGTTATATTATTTACA
4667	TTTTGTTGTTATATTATTTACAT
4668	TTTGTTGTTATATTATTTACATT
4669	TTGTTGTTATATTATTTACATTT
4670	TGTTGTTATATTATTTACATTTC
4671	GTTGTTATATTATTTACATTTCA
4672	TTGTTATATTATTTACATTTCAG
4673	TGTTATATTATTTACATTTCAGT
4674	GTTATATTATTTACATTTCAGTA
4675	TTATATTATTTACATTTCAGTAG
4676	TATATTATTTACATTTCAGTAGT
4677	ATATTATTTACATTTCAGTAGTT
4678	TATTATTTACATTTCAGTAGTTG
4679	ATTATTTACATTTCAGTAGTTGT
4680	TTATTTACATTTCAGTAGTTGTT
4681	TATTTACATTTCAGTAGTTGTTT
4682	ATTTACATTTCAGTAGTTGTTTT
4683	TTTACATTTCAGTAGTTGTTTTT
4684	TTACATTTCAGTAGTTGTTTTTT
4685	TACATTTCAGTAGTTGTTTTTTG
4686	ACATTTCAGTAGTTGTTTTTTGT
4687	CATTTCAGTAGTTGTTTTTTGTG
4688	ATTTCAGTAGTTGTTTTTTGTGT
4689	TTTCAGTAGTTGTTTTTTGTGTT
4690	TTCAGTAGTTGTTTTTTGTGTTT
4691	TCAGTAGTTGTTTTTTGTGTTTC
4692	CAGTAGTTGTTTTTTGTGTTTCC
4693	AGTAGTTGTTTTTTGTGTTTCCA
4694	GTAGTTGTTTTTTGTGTTTCCAT
4695	TAGTTGTTTTTTGTGTTTCCATT
4696	AGTTGTTTTTTGTGTTTCCATTT
4697	GTTGTTTTTTGTGTTTCCATTTT
4698	TTGTTTTTTGTGTTTCCATTTTA
4699	TGTTTTTTGTGTTTCCATTTTAG
4700	GTTTTTTGTGTTTCCATTTTAGT
4701	TTTTTTGTGTTTCCATTTTAGTG
4702	TTTTTGTGTTTCCATTTTAGTGG
4703	TTTTGTGTTTCCATTTTAGTGGA
4704	TTTGTGTTTCCATTTTAGTGGAT

Fig. 29 cont'd (Sheet 98 of 170)

ID	SEQUENCE
4705	TTGTGTTTCCATTTTAGTGGATA
4706	TGTGTTTCCATTTTAGTGGATAA
4707	GTGTTTCCATTTTAGTGGATAAA
4708	TGTTTCCATTTTAGTGGATAAAA
4709	GTTTCCATTTTAGTGGATAAAAT
4710	TTTCCATTTTAGTGGATAAAATT
4711	TTCCATTTTAGTGGATAAAATTT
4712	TCCATTTTAGTGGATAAAATTTG
4713	CCATTTTAGTGGATAAAATTTGT
4714	CATTTTAGTGGATAAAATTTGTA
4715	ATTTTAGTGGATAAAATTTGTAT
4716	TTTTAGTGGATAAAATTTGTATT
4717	TTTAGTGGATAAAATTTGTATTT
4718	TTAGTGGATAAAATTTGTATTTT
4719	TAGTGGATAAAATTTGTATTTTG
4720	AGTGGATAAAATTTGTATTTTGA
4721	GTGGATAAAATTTGTATTTTGAA
4722	TGGATAAAATTTGTATTTTGAAC
4723	GGATAAAATTTGTATTTTGAACT
4724	GATAAAATTTGTATTTTGAACTA
4725	ATAAAATTTGTATTTTGAACTAT
4726	TAAAATTTGTATTTTGAACTATG
4727	AAAATTTGTATTTTGAACTATGA
4728	AAATTTGTATTTTGAACTATGAA
4729	AATTTGTATTTTGAACTATGAAT
4730	ATTTGTATTTTGAACTATGAATG
4731	TTTGTATTTTGAACTATGAATGG
4732	TTGTATTTTGAACTATGAATGGA
4733	TGTATTTTGAACTATGAATGGAG
4734	GTATTTTGAACTATGAATGGAGA
4735	TATTTTGAACTATGAATGGAGAC
4736	ATTTTGAACTATGAATGGAGACT
4737	TTTTGAACTATGAATGGAGACTA
4738	TTTGAACTATGAATGGAGACTAC
4739	TTGAACTATGAATGGAGACTACC
4740	TGAACTATGAATGGAGACTACCG
4741	GAACTATGAATGGAGACTACCGC
4742	AACTATGAATGGAGACTACCGCC
4743	ACTATGAATGGAGACTACCGCCC
4744	CTATGAATGGAGACTACCGCCCC
4745	TATGAATGGAGACTACCGCCCCA
4746	ATGAATGGAGACTACCGCCCCAG
4747	TGAATGGAGACTACCGCCCCAGC
4748	GAATGGAGACTACCGCCCCAGCA
4749	AATGGAGACTACCGCCCCAGCAT
4750	ATGGAGACTACCGCCCCAGCATT
4751	TGGAGACTACCGCCCCAGCATTA
4752	GGAGACTACCGCCCCAGCATTAG

Fig. 29 cont'd (Sheet 99 of 170)

ID	SEQUENCE
4753	GAGACTACCGCCCCAGCATTAGT
4754	AGACTACCGCCCCAGCATTAGTT
4755	GACTACCGCCCCAGCATTAGTTT
4756	ACTACCGCCCCAGCATTAGTTTC
4757	CTACCGCCCCAGCATTAGTTTCA
4758	TACCGCCCCAGCATTAGTTTCAC
4759	ACCGCCCCAGCATTAGTTTCACA
4760	CCGCCCCAGCATTAGTTTCACAT
4761	CGCCCCAGCATTAGTTTCACATG
4762	GCCCCAGCATTAGTTTCACATGA
4763	CCCCAGCATTAGTTTCACATGAT
4764	CCCAGCATTAGTTTCACATGATA
4765	CCAGCATTAGTTTCACATGATAT
4766	CAGCATTAGTTTCACATGATATA
4767	AGCATTAGTTTCACATGATATAC
4768	GCATTAGTTTCACATGATATACC
4769	CATTAGTTTCACATGATATACCC
4770	ATTAGTTTCACATGATATACCCT
4771	TTAGTTTCACATGATATACCCTT
4772	TAGTTTCACATGATATACCCTTT
4773	AGTTTCACATGATATACCCTTTA
4774	GTTTCACATGATATACCCTTTAA
4775	TTTCACATGATATACCCTTTAAA
4776	TTCACATGATATACCCTTTAAAC
4777	TCACATGATATACCCTTTAAACC
4778	CACATGATATACCCTTTAAACCC
4779	ACATGATATACCCTTTAAACCCG
4780	CATGATATACCCTTTAAACCCGA
4781	ATGATATACCCTTTAAACCCGAA
4782	TGATATACCCTTTAAACCCGAAT
4783	GATATACCCTTTAAACCCGAATC
4784	ATATACCCTTTAAACCCGAATCA
4785	TATACCCTTTAAACCCGAATCAT
4786	ATACCCTTTAAACCCGAATCATT
4787	TACCCTTTAAACCCGAATCATTG
4788	ACCCTTTAAACCCGAATCATTGT
4789	CCCTTTAAACCCGAATCATTGTT
4790	CCTTTAAACCCGAATCATTGTTT
4791	CTTTAAACCCGAATCATTGTTTT
4792	TTTAAACCCGAATCATTGTTTTA
4793	TTAAACCCGAATCATTGTTTTAT
4794	TAAACCCGAATCATTGTTTTATT
4795	AAACCCGAATCATTGTTTTATTT
4796	AACCCGAATCATTGTTTTATTTC
4797	ACCCGAATCATTGTTTTATTTCC
4798	CCCGAATCATTGTTTTATTTCCT
4799	CCGAATCATTGTTTTATTTCCTG
4800	CGAATCATTGTTTTATTTCCTGA

Fig. 29 cont'd (Sheet 100 of 170)

ID	SEQUENCE
4801	GAATCATTGTTTTATTTCCTGAT
4802	AATCATTGTTTTATTTCCTGATT
4803	ATCATTGTTTTATTTCCTGATTA
4804	TCATTGTTTTATTTCCTGATTAC
4805	CATTGTTTTATTTCCTGATTACA
4806	ATTGTTTTATTTCCTGATTACAC
4807	TTGTTTTATTTCCTGATTACACA
4808	TGTTTTATTTCCTGATTACACAG
4809	GTTTTATTTCCTGATTACACAGG
4810	TTTTATTTCCTGATTACACAGGT
4811	TTTATTTCCTGATTACACAGGTG
4812	TTATTTCCTGATTACACAGGTGT
4813	TATTTCCTGATTACACAGGTGTT
4814	ATTTCCTGATTACACAGGTGTTG
4815	TTTCCTGATTACACAGGTGTTGA
4816	TTCCTGATTACACAGGTGTTGAA
4817	TCCTGATTACACAGGTGTTGAAT
4818	CCTGATTACACAGGTGTTGAATG
4819	CTGATTACACAGGTGTTGAATGG
4820	TGATTACACAGGTGTTGAATGGG
4821	GATTACACAGGTGTTGAATGGGG
4822	ATTACACAGGTGTTGAATGGGGA
4823	TTACACAGGTGTTGAATGGGGAA
4824	TACACAGGTGTTGAATGGGGAAA
4825	ACACAGGTGTTGAATGGGGAAAG
4826	CACAGGTGTTGAATGGGGAAAGG
4827	ACAGGTGTTGAATGGGGAAAGGG
4828	CAGGTGTTGAATGGGGAAAGGGG
4829	AGGTGTTGAATGGGGAAAGGGGC
4830	GGTGTTGAATGGGGAAAGGGGCT
4831	GTGTTGAATGGGGAAAGGGGCTA
4832	TGTTGAATGGGGAAAGGGGCTAG
4833	GTTGAATGGGGAAAGGGGCTAGT
4834	TTGAATGGGGAAAGGGGCTAGTA
4835	TGAATGGGGAAAGGGGCTAGTAT
4836	GAATGGGGAAAGGGGCTAGTATA
4837	AATGGGGAAAGGGGCTAGTATAT
4838	ATGGGGAAAGGGGCTAGTATATC
4839	TGGGGAAAGGGGCTAGTATATCA
4840	GGGGAAAGGGGCTAGTATATCAG
4841	GGGAAAGGGGCTAGTATATCAGT
4842	GGAAAGGGGCTAGTATATCAGTA
4843	GAAAGGGGCTAGTATATCAGTAG
4844	AAAGGGGCTAGTATATCAGTAGG
4845	AAGGGGCTAGTATATCAGTAGGA
4846	AGGGGCTAGTATATCAGTAGGAT
4847	GGGGCTAGTATATCAGTAGGATA
4848	GGGCTAGTATATCAGTAGGATAT

Fig. 29 cont'd (Sheet 101 of 170)

ID	SEQUENCE
4849	GGCTAGTATATCAGTAGGATATA
4850	GCTAGTATATCAGTAGGATATAC
4851	CTAGTATATCAGTAGGATATACT
4852	TAGTATATCAGTAGGATATACTA
4853	AGTATATCAGTAGGATATACTAT
4854	GTATATCAGTAGGATATACTATG
4855	TATATCAGTAGGATATACTATGG
4856	ATATCAGTAGGATATACTATGGG
4857	TATCAGTAGGATATACTATGGGA
4858	ATCAGTAGGATATACTATGGGAT
4859	TCAGTAGGATATACTATGGGATG
4860	CAGTAGGATATACTATGGGATGT
4861	AGTAGGATATACTATGGGATGTA
4862	GTAGGATATACTATGGGATGTAT
4863	TAGGATATACTATGGGATGTATA
4864	AGGATATACTATGGGATGTATAT
4865	GGATATACTATGGGATGTATATA
4866	GATATACTATGGGATGTATATAT
4867	ATATACTATGGGATGTATATATA
4868	TATACTATGGGATGTATATATAT
4869	ATACTATGGGATGTATATATATC
4870	TACTATGGGATGTATATATATCA
4871	ACTATGGGATGTATATATATCAT
4872	CTATGGGATGTATATATATCATT
4873	TATGGGATGTATATATATCATTG
4874	ATGGGATGTATATATATCATTGC
4875	TGGGATGTATATATATCATTGCT
4876	GGGATGTATATATATCATTGCTG
4877	GGATGTATATATATCATTGCTGT
4878	GATGTATATATATCATTGCTGTT
4879	ATGTATATATATCATTGCTGTTA
4880	TGTATATATATCATTGCTGTTAG
4881	GTATATATATCATTGCTGTTAGA
4882	TATATATATCATTGCTGTTAGAG
4883	ATATATATCATTGCTGTTAGAGA
4884	TATATATCATTGCTGTTAGAGAA
4885	ATATATCATTGCTGTTAGAGAAA
4886	TATATCATTGCTGTTAGAGAAAT
4887	ATATCATTGCTGTTAGAGAAATG
4888	TATCATTGCTGTTAGAGAAATGA
4889	ATCATTGCTGTTAGAGAAATGAA
4890	TCATTGCTGTTAGAGAAATGAAA
4891	CATTGCTGTTAGAGAAATGAAAT
4892	ATTGCTGTTAGAGAAATGAAATA
4893	TTGCTGTTAGAGAAATGAAATAA
4894	TGCTGTTAGAGAAATGAAATAAA
4895	GCTGTTAGAGAAATGAAATAAAA
4896	CTGTTAGAGAAATGAAATAAAAT

Fig. 29 cont'd (Sheet 102 of 170)

ID	SEQUENCE
4897	TGTTAGAGAAATGAAATAAAATG
4898	GTTAGAGAAATGAAATAAAATGG
4899	TTAGAGAAATGAAATAAAATGGG
4900	TAGAGAAATGAAATAAAATGGGG
4901	AGAGAAATGAAATAAAATGGGGC
4902	GAGAAATGAAATAAAATGGGGCT
4903	AGAAATGAAATAAAATGGGGCTG
4904	GAAATGAAATAAAATGGGGCTGG
4905	AAATGAAATAAAATGGGGCTGGG
4906	AATGAAATAAAATGGGGCTGGGC
4907	ATGAAATAAAATGGGGCTGGGCT
4908	TGAAATAAAATGGGGCTGGGCTC
4909	GAAATAAAATGGGGCTGGGCTCA
4910	AAATAAAATGGGGCTGGGCTCAG
4911	AATAAAATGGGGCTGGGCTCAGT
4912	ATAAAATGGGGCTGGGCTCAGTG
4913	TAAAATGGGGCTGGGCTCAGTGG
4914	AAAATGGGGCTGGGCTCAGTGGC
4915	AAATGGGGCTGGGCTCAGTGGCT
4916	AATGGGGCTGGGCTCAGTGGCTC
4917	ATGGGGCTGGGCTCAGTGGCTCA
4918	TGGGGCTGGGCTCAGTGGCTCAC
4919	GGGGCTGGGCTCAGTGGCTCACG
4920	GGGCTGGGCTCAGTGGCTCACGC
4921	GGCTGGGCTCAGTGGCTCACGCC
4922	GCTGGGCTCAGTGGCTCACGCCT
4923	CTGGGCTCAGTGGCTCACGCCTG
4924	TGGGCTCAGTGGCTCACGCCTGT
4925	GGGCTCAGTGGCTCACGCCTGTA
4926	GGCTCAGTGGCTCACGCCTGTAA
4927	GCTCAGTGGCTCACGCCTGTAAT
4928	CTCAGTGGCTCACGCCTGTAATC
4929	TCAGTGGCTCACGCCTGTAATCC
4930	CAGTGGCTCACGCCTGTAATCCC
4931	AGTGGCTCACGCCTGTAATCCCA
4932	GTGGCTCACGCCTGTAATCCCAG
4933	TGGCTCACGCCTGTAATCCCAGC
4934	GGCTCACGCCTGTAATCCCAGCA
4935	GCTCACGCCTGTAATCCCAGCAC
4936	CTCACGCCTGTAATCCCAGCACT
4937	TCACGCCTGTAATCCCAGCACTT
4938	CACGCCTGTAATCCCAGCACTTT
4939	ACGCCTGTAATCCCAGCACTTTG
4940	CGCCTGTAATCCCAGCACTTTGG
4941	GCCTGTAATCCCAGCACTTTGGG
4942	CCTGTAATCCCAGCACTTTGGGA
4943	CTGTAATCCCAGCACTTTGGGAG
4944	TGTAATCCCAGCACTTTGGGAGG

Fig. 29 cont'd (Sheet 103 of 170)

ID	SEQUENCE
4945	GTAATCCCAGCACTTTGGGAGGC
4946	TAATCCCAGCACTTTGGGAGGCT
4947	AATCCCAGCACTTTGGGAGGCTG
4948	ATCCCAGCACTTTGGGAGGCTGA
4949	TCCCAGCACTTTGGGAGGCTGAG
4950	CCCAGCACTTTGGGAGGCTGAGG
4951	CCAGCACTTTGGGAGGCTGAGGC
4952	CAGCACTTTGGGAGGCTGAGGCA
4953	AGCACTTTGGGAGGCTGAGGCAG
4954	GCACTTTGGGAGGCTGAGGCAGG
4955	CACTTTGGGAGGCTGAGGCAGGT
4956	ACTTTGGGAGGCTGAGGCAGGTG
4957	CTTTGGGAGGCTGAGGCAGGTGG
4958	TTTGGGAGGCTGAGGCAGGTGGA
4959	TTGGGAGGCTGAGGCAGGTGGAT
4960	TGGGAGGCTGAGGCAGGTGGATC
4961	GGGAGGCTGAGGCAGGTGGATCA
4962	GGAGGCTGAGGCAGGTGGATCAC
4963	GAGGCTGAGGCAGGTGGATCACG
4964	AGGCTGAGGCAGGTGGATCACGA
4965	GGCTGAGGCAGGTGGATCACGAG
4966	GCTGAGGCAGGTGGATCACGAGG
4967	CTGAGGCAGGTGGATCACGAGGT
4968	TGAGGCAGGTGGATCACGAGGTC
4969	GAGGCAGGTGGATCACGAGGTCA
4970	AGGCAGGTGGATCACGAGGTCAG
4971	GGCAGGTGGATCACGAGGTCAGG
4972	GCAGGTGGATCACGAGGTCAGGA
4973	CAGGTGGATCACGAGGTCAGGAG
4974	AGGTGGATCACGAGGTCAGGAGA
4975	GGTGGATCACGAGGTCAGGAGAT
4976	GTGGATCACGAGGTCAGGAGATC
4977	TGGATCACGAGGTCAGGAGATCG
4978	GGATCACGAGGTCAGGAGATCGA
4979	GATCACGAGGTCAGGAGATCGAG
4980	ATCACGAGGTCAGGAGATCGAGA
4981	TCACGAGGTCAGGAGATCGAGAC
4982	CACGAGGTCAGGAGATCGAGACC
4983	ACGAGGTCAGGAGATCGAGACCA
4984	CGAGGTCAGGAGATCGAGACCAT
4985	GAGGTCAGGAGATCGAGACCATC
4986	AGGTCAGGAGATCGAGACCATCC
4987	GGTCAGGAGATCGAGACCATCCT
4988	GTCAGGAGATCGAGACCATCCTG
4989	TCAGGAGATCGAGACCATCCTGG
4990	CAGGAGATCGAGACCATCCTGGC
4991	AGGAGATCGAGACCATCCTGGCT
4992	GGAGATCGAGACCATCCTGGCTA

Fig. 29 cont'd (Sheet 104 of 170)

ID	SEQUENCE
4993	GAGATCGAGACCATCCTGGCTAA
4994	AGATCGAGACCATCCTGGCTAAC
4995	GATCGAGACCATCCTGGCTAACA
4996	ATCGAGACCATCCTGGCTAACAC
4997	TCGAGACCATCCTGGCTAACACG
4998	CGAGACCATCCTGGCTAACACGG
4999	GAGACCATCCTGGCTAACACGGT
5000	AGACCATCCTGGCTAACACGGTG
5001	GACCATCCTGGCTAACACGGTGA
5002	ACCATCCTGGCTAACACGGTGAA
5003	CCATCCTGGCTAACACGGTGAAA
5004	CATCCTGGCTAACACGGTGAAAC
5005	ATCCTGGCTAACACGGTGAAACC
5006	TCCTGGCTAACACGGTGAAACCC
5007	CCTGGCTAACACGGTGAAACCCC
5008	CTGGCTAACACGGTGAAACCCCG
5009	TGGCTAACACGGTGAAACCCCGT
5010	GGCTAACACGGTGAAACCCCGTC
5011	GCTAACACGGTGAAACCCCGTCT
5012	CTAACACGGTGAAACCCCGTCTC
5013	TAACACGGTGAAACCCCGTCTCT
5014	AACACGGTGAAACCCCGTCTCTA
5015	ACACGGTGAAACCCCGTCTCTAC
5016	CACGGTGAAACCCCGTCTCTACT
5017	ACGGTGAAACCCCGTCTCTACTA
5018	CGGTGAAACCCCGTCTCTACTAA
5019	GGTGAAACCCCGTCTCTACTAAA
5020	GTGAAACCCCGTCTCTACTAAAA
5021	TGAAACCCCGTCTCTACTAAAAA
5022	GAAACCCCGTCTCTACTAAAAAA
5023	AAACCCCGTCTCTACTAAAAAAC
5024	AACCCCGTCTCTACTAAAAAACA
5025	ACCCCGTCTCTACTAAAAAACAG
5026	CCCCGTCTCTACTAAAAAACAGA
5027	CCCGTCTCTACTAAAAAACAGAA
5028	CCGTCTCTACTAAAAAACAGAAA
5029	CGTCTCTACTAAAAAACAGAAAA
5030	GTCTCTACTAAAAAACAGAAAAT
5031	TCTCTACTAAAAAACAGAAAATT
5032	CTCTACTAAAAAACAGAAAATTA
5033	TCTACTAAAAAACAGAAAATTAG
5034	CTACTAAAAAACAGAAAATTAGC
5035	TACTAAAAAACAGAAAATTAGCC
5036	ACTAAAAAACAGAAAATTAGCCG
5037	CTAAAAAACAGAAAATTAGCCGG
5038	TAAAAAACAGAAAATTAGCCGGG
5039	AAAAAACAGAAAATTAGCCGGGC
5040	AAAAACAGAAAATTAGCCGGGCG

Fig. 29 cont'd (Sheet 105 of 170)

ID	SEQUENCE
5041	AAAACAGAAAATTAGCCGGGCGT
5042	AAACAGAAAATTAGCCGGGCGTG
5043	AACAGAAAATTAGCCGGGCGTGG
5044	ACAGAAAATTAGCCGGGCGTGGT
5045	CAGAAAATTAGCCGGGCGTGGTG
5046	AGAAAATTAGCCGGGCGTGGTGG
5047	GAAAATTAGCCGGGCGTGGTGGC
5048	AAAATTAGCCGGGCGTGGTGGCG
5049	AAATTAGCCGGGCGTGGTGGCGG
5050	AATTAGCCGGGCGTGGTGGCGGG
5051	ATTAGCCGGGCGTGGTGGCGGGC
5052	TTAGCCGGGCGTGGTGGCGGGCG
5053	CGGGCGCCTGTAGTCCCAGCTAC
5054	GGGCGCCTGTAGTCCCAGCTACT
5055	GGCGCCTGTAGTCCCAGCTACTC
5056	GCGCCTGTAGTCCCAGCTACTCG
5057	CGCCTGTAGTCCCAGCTACTCGG
5058	GCCTGTAGTCCCAGCTACTCGGG
5059	CCTGTAGTCCCAGCTACTCGGGA
5060	CTGTAGTCCCAGCTACTCGGGAG
5061	TGTAGTCCCAGCTACTCGGGAGG
5062	GTAGTCCCAGCTACTCGGGAGGC
5063	TAGTCCCAGCTACTCGGGAGGCT
5064	AGTCCCAGCTACTCGGGAGGCTG
5065	GTCCCAGCTACTCGGGAGGCTGA
5066	TCCCAGCTACTCGGGAGGCTGAG
5067	CCCAGCTACTCGGGAGGCTGAGG
5068	CCAGCTACTCGGGAGGCTGAGGC
5069	CAGCTACTCGGGAGGCTGAGGCA
5070	AGCTACTCGGGAGGCTGAGGCAG
5071	GCTACTCGGGAGGCTGAGGCAGG
5072	CTACTCGGGAGGCTGAGGCAGGA
5073	TACTCGGGAGGCTGAGGCAGGAG
5074	ACTCGGGAGGCTGAGGCAGGAGA
5075	CTCGGGAGGCTGAGGCAGGAGAA
5076	TCGGGAGGCTGAGGCAGGAGAAT
5077	CGGGAGGCTGAGGCAGGAGAATG
5078	GGGAGGCTGAGGCAGGAGAATGG
5079	GGAGGCTGAGGCAGGAGAATGGT
5080	GAGGCTGAGGCAGGAGAATGGTG
5081	AGGCTGAGGCAGGAGAATGGTGT
5082	GGCTGAGGCAGGAGAATGGTGTG
5083	GCTGAGGCAGGAGAATGGTGTGA
5084	CTGAGGCAGGAGAATGGTGTGAA
5085	TGAGGCAGGAGAATGGTGTGAAC
5086	GAGGCAGGAGAATGGTGTGAACC
5087	AGGCAGGAGAATGGTGTGAACCC
5088	GGCAGGAGAATGGTGTGAACCCG

Fig. 29 cont'd (Sheet 106 of 170)

ID	SEQUENCE
5089	GCAGGAGAATGGTGTGAACCCGG
5090	CAGGAGAATGGTGTGAACCCGGG
5091	AGGAGAATGGTGTGAACCCGGGA
5092	GGAGAATGGTGTGAACCCGGGAG
5093	GAGAATGGTGTGAACCCGGGAGG
5094	AGAATGGTGTGAACCCGGGAGGC
5095	GAATGGTGTGAACCCGGGAGGCA
5096	AATGGTGTGAACCCGGGAGGCAG
5097	ATGGTGTGAACCCGGGAGGCAGA
5098	TGGTGTGAACCCGGGAGGCAGAG
5099	GGTGTGAACCCGGGAGGCAGAGC
5100	GTGTGAACCCGGGAGGCAGAGCT
5101	TGTGAACCCGGGAGGCAGAGCTT
5102	GTGAACCCGGGAGGCAGAGCTTG
5103	TGAACCCGGGAGGCAGAGCTTGC
5104	GAACCCGGGAGGCAGAGCTTGCA
5105	AACCCGGGAGGCAGAGCTTGCAG
5106	ACCCGGGAGGCAGAGCTTGCAGT
5107	CCCGGGAGGCAGAGCTTGCAGTG
5108	CCGGGAGGCAGAGCTTGCAGTGA
5109	CGGGAGGCAGAGCTTGCAGTGAG
5110	GGGAGGCAGAGCTTGCAGTGAGC
5111	GGAGGCAGAGCTTGCAGTGAGCC
5112	GAGGCAGAGCTTGCAGTGAGCCG
5113	AGGCAGAGCTTGCAGTGAGCCGA
5114	GGCAGAGCTTGCAGTGAGCCGAG
5115	GCAGAGCTTGCAGTGAGCCGAGA
5116	CAGAGCTTGCAGTGAGCCGAGAT
5117	AGAGCTTGCAGTGAGCCGAGATC
5118	GAGCTTGCAGTGAGCCGAGATCT
5119	AGCTTGCAGTGAGCCGAGATCTC
5120	GCTTGCAGTGAGCCGAGATCTCG
5121	CTTGCAGTGAGCCGAGATCTCGC
5122	TTGCAGTGAGCCGAGATCTCGCC
5123	TGCAGTGAGCCGAGATCTCGCCA
5124	GCAGTGAGCCGAGATCTCGCCAC
5125	CAGTGAGCCGAGATCTCGCCACT
5126	AGTGAGCCGAGATCTCGCCACTG
5127	GTGAGCCGAGATCTCGCCACTGC
5128	TGAGCCGAGATCTCGCCACTGCA
5129	GAGCCGAGATCTCGCCACTGCAC
5130	AGCCGAGATCTCGCCACTGCACT
5131	GCCGAGATCTCGCCACTGCACTC
5132	CCGAGATCTCGCCACTGCACTCC
5133	CGAGATCTCGCCACTGCACTCCA
5134	GAGATCTCGCCACTGCACTCCAG
5135	AGATCTCGCCACTGCACTCCAGC
5136	GATCTCGCCACTGCACTCCAGCC

Fig. 29 cont'd (Sheet 107 of 170)

ID	SEQUENCE
5137	ATCTCGCCACTGCACTCCAGCCT
5138	TCTCGCCACTGCACTCCAGCCTG
5139	CTCGCCACTGCACTCCAGCCTGG
5140	TCGCCACTGCACTCCAGCCTGGG
5141	CGCCACTGCACTCCAGCCTGGGC
5142	GCCACTGCACTCCAGCCTGGGCA
5143	CCACTGCACTCCAGCCTGGGCAA
5144	CACTGCACTCCAGCCTGGGCAAC
5145	ACTGCACTCCAGCCTGGGCAACA
5146	CTGCACTCCAGCCTGGGCAACAG
5147	TGCACTCCAGCCTGGGCAACAGA
5148	GCACTCCAGCCTGGGCAACAGAG
5149	CACTCCAGCCTGGGCAACAGAGC
5150	ACTCCAGCCTGGGCAACAGAGCA
5151	CTCCAGCCTGGGCAACAGAGCAA
5152	TCCAGCCTGGGCAACAGAGCAAG
5153	CCAGCCTGGGCAACAGAGCAAGA
5154	CAGCCTGGGCAACAGAGCAAGAC
5155	AGCCTGGGCAACAGAGCAAGACT
5156	GCCTGGGCAACAGAGCAAGACTC
5157	CCTGGGCAACAGAGCAAGACTCT
5158	CTGGGCAACAGAGCAAGACTCTG
5159	TGGGCAACAGAGCAAGACTCTGT
5160	GGGCAACAGAGCAAGACTCTGTC
5161	GGCAACAGAGCAAGACTCTGTCT
5162	GCAACAGAGCAAGACTCTGTCTC
5163	CAACAGAGCAAGACTCTGTCTCA
5164	AACAGAGCAAGACTCTGTCTCAA
5165	ACAGAGCAAGACTCTGTCTCAAA
5166	CAGAGCAAGACTCTGTCTCAAAA
5167	AGAGCAAGACTCTGTCTCAAAAA
5168	GAGCAAGACTCTGTCTCAAAAAA
5169	AGCAAGACTCTGTCTCAAAAAAA
5170	GCAAGACTCTGTCTCAAAAAAAA
5171	AAAAAAAAGAAATAAGAAAATGG
5172	AAAAAAAGAAATAAGAAAATGGG
5173	AAAAAAGAAATAAGAAAATGGGA
5174	AAAAAGAAATAAGAAAATGGGAA
5175	AAAAGAAATAAGAAAATGGGAAG
5176	AAAGAAATAAGAAAATGGGAAGC
5177	AAGAAATAAGAAAATGGGAAGCA
5178	AGAAATAAGAAAATGGGAAGCAA
5179	GAAATAAGAAAATGGGAAGCAAT
5180	AAATAAGAAAATGGGAAGCAATA
5181	AATAAGAAAATGGGAAGCAATAT
5182	ATAAGAAAATGGGAAGCAATATT
5183	TAAGAAAATGGGAAGCAATATTT
5184	AAGAAAATGGGAAGCAATATTTG

Fig. 29 cont'd (Sheet 108 of 170)

ID	SEQUENCE
5185	AGAAAATGGGAAGCAATATTTGA
5186	GAAAATGGGAAGCAATATTTGAC
5187	AAAATGGGAAGCAATATTTGACA
5188	AAATGGGAAGCAATATTTGACAT
5189	AATGGGAAGCAATATTTGACATA
5190	ATGGGAAGCAATATTTGACATAG
5191	TGGGAAGCAATATTTGACATAGT
5192	GGGAAGCAATATTTGACATAGTT
5193	GGAAGCAATATTTGACATAGTTC
5194	GAAGCAATATTTGACATAGTTCT
5195	AAGCAATATTTGACATAGTTCTT
5196	AGCAATATTTGACATAGTTCTTT
5197	GCAATATTTGACATAGTTCTTTT
5198	CAATATTTGACATAGTTCTTTTT
5199	AATATTTGACATAGTTCTTTTTA
5200	ATATTTGACATAGTTCTTTTTAG
5201	TATTTGACATAGTTCTTTTTAGT
5202	ATTTGACATAGTTCTTTTTAGTC
5203	TTTGACATAGTTCTTTTTAGTCA
5204	TTGACATAGTTCTTTTTAGTCAA
5205	TGACATAGTTCTTTTTAGTCAAA
5206	GACATAGTTCTTTTTAGTCAAAT
5207	ACATAGTTCTTTTTAGTCAAATC
5208	CATAGTTCTTTTTAGTCAAATCT
5209	ATAGTTCTTTTTAGTCAAATCTA
5210	TAGTTCTTTTTAGTCAAATCTAC
5211	AGTTCTTTTTAGTCAAATCTACT
5212	GTTCTTTTTAGTCAAATCTACTT
5213	TTCTTTTTAGTCAAATCTACTTG
5214	TCTTTTTAGTCAAATCTACTTGT
5215	CTTTTTAGTCAAATCTACTTGTT
5216	TTTTTAGTCAAATCTACTTGTTA
5217	TTTTAGTCAAATCTACTTGTTAA
5218	TTTAGTCAAATCTACTTGTTAAA
5219	TTAGTCAAATCTACTTGTTAAAA
5220	TAGTCAAATCTACTTGTTAAAAA
5221	AGTCAAATCTACTTGTTAAAAAA
5222	GTCAAATCTACTTGTTAAAAAAA
5223	TCAAATCTACTTGTTAAAAAAAG
5224	CAAATCTACTTGTTAAAAAAAGG
5225	AAATCTACTTGTTAAAAAAAGGG
5226	AATCTACTTGTTAAAAAAAGGGT
5227	ATCTACTTGTTAAAAAAAGGGTA
5228	TCTACTTGTTAAAAAAAGGGTAG
5229	CTACTTGTTAAAAAAAGGGTAGC
5230	TACTTGTTAAAAAAAGGGTAGCA
5231	ACTTGTTAAAAAAAGGGTAGCAG
5232	CTTGTTAAAAAAAGGGTAGCAGT

Fig. 29 cont'd (Sheet 109 of 170)

ID	SEQUENCE
5233	TTGTTAAAAAAAGGGTAGCAGTT
5234	TGTTAAAAAAAGGGTAGCAGTTT
5235	GTTAAAAAAAGGGTAGCAGTTTA
5236	TTAAAAAAAGGGTAGCAGTTTAT
5237	TAAAAAAAGGGTAGCAGTTTATT
5238	AAAAAAAGGGTAGCAGTTTATTC
5239	AAAAAAGGGTAGCAGTTTATTCA
5240	AAAAAGGGTAGCAGTTTATTCAT
5241	AAAAGGGTAGCAGTTTATTCATC
5242	AAAGGGTAGCAGTTTATTCATCT
5243	AAGGGTAGCAGTTTATTCATCTG
5244	AGGGTAGCAGTTTATTCATCTGT
5245	GGGTAGCAGTTTATTCATCTGTG
5246	GGTAGCAGTTTATTCATCTGTGA
5247	GTAGCAGTTTATTCATCTGTGAA
5248	TAGCAGTTTATTCATCTGTGAAA
5249	AGCAGTTTATTCATCTGTGAAAG
5250	GCAGTTTATTCATCTGTGAAAGG
5251	CAGTTTATTCATCTGTGAAAGGA
5252	AGTTTATTCATCTGTGAAAGGAA
5253	GTTTATTCATCTGTGAAAGGAAA
5254	TTTATTCATCTGTGAAAGGAAAA
5255	TTATTCATCTGTGAAAGGAAAAT
5256	TATTCATCTGTGAAAGGAAAATA
5257	ATTCATCTGTGAAAGGAAAATAA
5258	TTCATCTGTGAAAGGAAAATAAT
5259	TCATCTGTGAAAGGAAAATAATA
5260	CATCTGTGAAAGGAAAATAATAC
5261	ATCTGTGAAAGGAAAATAATACT
5262	TCTGTGAAAGGAAAATAATACTT
5263	CTGTGAAAGGAAAATAATACTTA
5264	TGTGAAAGGAAAATAATACTTAT
5265	GTGAAAGGAAAATAATACTTATC
5266	TGAAAGGAAAATAATACTTATCT
5267	GAAAGGAAAATAATACTTATCTT
5268	AAAGGAAAATAATACTTATCTTA
5269	AAGGAAAATAATACTTATCTTAC
5270	AGGAAAATAATACTTATCTTACA
5271	GGAAAATAATACTTATCTTACAA
5272	GAAAATAATACTTATCTTACAAG
5273	AAAATAATACTTATCTTACAAGG
5274	AAATAATACTTATCTTACAAGGT
5275	AATAATACTTATCTTACAAGGTT
5276	ATAATACTTATCTTACAAGGTTG
5277	TAATACTTATCTTACAAGGTTGC
5278	AATACTTATCTTACAAGGTTGCA
5279	ATACTTATCTTACAAGGTTGCAA
5280	TACTTATCTTACAAGGTTGCAAG

Fig. 29 cont'd (Sheet 110 of 170)

ID	SEQUENCE
5281	ACTTATCTTACAAGGTTGCAAGA
5282	CTTATCTTACAAGGTTGCAAGAG
5283	TTATCTTACAAGGTTGCAAGAGC
5284	TATCTTACAAGGTTGCAAGAGCT
5285	ATCTTACAAGGTTGCAAGAGCTC
5286	TCTTACAAGGTTGCAAGAGCTCA
5287	CTTACAAGGTTGCAAGAGCTCAA
5288	TTACAAGGTTGCAAGAGCTCAAG
5289	TACAAGGTTGCAAGAGCTCAAGG
5290	ACAAGGTTGCAAGAGCTCAAGGA
5291	CAAGGTTGCAAGAGCTCAAGGAG
5292	AAGGTTGCAAGAGCTCAAGGAGA
5293	AGGTTGCAAGAGCTCAAGGAGAC
5294	GGTTGCAAGAGCTCAAGGAGACC
5295	GTTGCAAGAGCTCAAGGAGACCA
5296	TTGCAAGAGCTCAAGGAGACCAT
5297	TGCAAGAGCTCAAGGAGACCATG
5298	GCAAGAGCTCAAGGAGACCATGT
5299	CAAGAGCTCAAGGAGACCATGTA
5300	AAGAGCTCAAGGAGACCATGTAT
5301	AGAGCTCAAGGAGACCATGTATG
5302	GAGCTCAAGGAGACCATGTATGT
5303	AGCTCAAGGAGACCATGTATGTA
5304	GCTCAAGGAGACCATGTATGTAA
5305	CTCAAGGAGACCATGTATGTAAA
5306	TCAAGGAGACCATGTATGTAAAG
5307	CAAGGAGACCATGTATGTAAAGT
5308	AAGGAGACCATGTATGTAAAGTT
5309	AGGAGACCATGTATGTAAAGTTC
5310	GGAGACCATGTATGTAAAGTTCC
5311	GAGACCATGTATGTAAAGTTCCT
5312	AGACCATGTATGTAAAGTTCCTG
5313	GACCATGTATGTAAAGTTCCTGC
5314	ACCATGTATGTAAAGTTCCTGCT
5315	CCATGTATGTAAAGTTCCTGCTG
5316	CATGTATGTAAAGTTCCTGCTGT
5317	ATGTATGTAAAGTTCCTGCTGTA
5318	TGTATGTAAAGTTCCTGCTGTAA
5319	GTATGTAAAGTTCCTGCTGTAAA
5320	TATGTAAAGTTCCTGCTGTAAAT
5321	ATGTAAAGTTCCTGCTGTAAATA
5322	TGTAAAGTTCCTGCTGTAAATAT
5323	GTAAAGTTCCTGCTGTAAATATG
5324	TAAAGTTCCTGCTGTAAATATGA
5325	AAAGTTCCTGCTGTAAATATGAA
5326	AAGTTCCTGCTGTAAATATGAAC
5327	AGTTCCTGCTGTAAATATGAACT
5328	GTTCCTGCTGTAAATATGAACTC

Fig. 29 cont'd (Sheet 111 of 170)

ID	SEQUENCE
5329	TTCCTGCTGTAAATATGAACTCC
5330	TCCTGCTGTAAATATGAACTCCC
5331	CCTGCTGTAAATATGAACTCCCA
5332	CTGCTGTAAATATGAACTCCCAT
5333	TGCTGTAAATATGAACTCCCATC
5334	GCTGTAAATATGAACTCCCATCC
5335	CTGTAAATATGAACTCCCATCCT
5336	TGTAAATATGAACTCCCATCCTA
5337	GTAAATATGAACTCCCATCCTAA
5338	TAAATATGAACTCCCATCCTAAT
5339	AAATATGAACTCCCATCCTAATA
5340	AATATGAACTCCCATCCTAATAC
5341	ATATGAACTCCCATCCTAATACC
5342	TATGAACTCCCATCCTAATACCC
5343	ATGAACTCCCATCCTAATACCCT
5344	TGAACTCCCATCCTAATACCCTT
5345	GAACTCCCATCCTAATACCCTTT
5346	AACTCCCATCCTAATACCCTTTT
5347	ACTCCCATCCTAATACCCTTTTA
5348	CTCCCATCCTAATACCCTTTTAC
5349	TCCCATCCTAATACCCTTTTACC
5350	CCCATCCTAATACCCTTTTACCT
5351	CCATCCTAATACCCTTTTACCTC
5352	CATCCTAATACCCTTTTACCTCT
5353	ATCCTAATACCCTTTTACCTCTC
5354	TCCTAATACCCTTTTACCTCTCT
5355	CCTAATACCCTTTTACCTCTCTG
5356	CTAATACCCTTTTACCTCTCTGT
5357	TAATACCCTTTTACCTCTCTGTG
5358	AATACCCTTTTACCTCTCTGTGG
5359	ATACCCTTTTACCTCTCTGTGGG
5360	TACCCTTTTACCTCTCTGTGGGT
5361	ACCCTTTTACCTCTCTGTGGGTT
5362	CCCTTTTACCTCTCTGTGGGTTT
5363	CCTTTTACCTCTCTGTGGGTTTG
5364	CTTTTACCTCTCTGTGGGTTTGT
5365	TTTTACCTCTCTGTGGGTTTGTC
5366	TTTACCTCTCTGTGGGTTTGTCT
5367	TTACCTCTCTGTGGGTTTGTCTT
5368	TACCTCTCTGTGGGTTTGTCTTG
5369	ACCTCTCTGTGGGTTTGTCTTGA
5370	CCTCTCTGTGGGTTTGTCTTGAC
5371	CTCTCTGTGGGTTTGTCTTGACC
5372	TCTCTGTGGGTTTGTCTTGACCT
5373	CTCTGTGGGTTTGTCTTGACCTG
5374	TCTGTGGGTTTGTCTTGACCTGG
5375	CTGTGGGTTTGTCTTGACCTGGA
5376	TGTGGGTTTGTCTTGACCTGGAA

Fig. 29 cont'd (Sheet 112 of 170)

ID	SEQUENCE
5377	GTGGGTTTGTCTTGACCTGGAAA
5378	TGGGTTTGTCTTGACCTGGAAAT
5379	GGGTTTGTCTTGACCTGGAAATT
5380	GGTTTGTCTTGACCTGGAAATTT
5381	GTTTGTCTTGACCTGGAAATTTG
5382	TTTGTCTTGACCTGGAAATTTGG
5383	TTGTCTTGACCTGGAAATTTGGG
5384	TGTCTTGACCTGGAAATTTGGGC
5385	GTCTTGACCTGGAAATTTGGGCT
5386	TCTTGACCTGGAAATTTGGGCTA
5387	CTTGACCTGGAAATTTGGGCTAA
5388	TTGACCTGGAAATTTGGGCTAAA
5389	TGACCTGGAAATTTGGGCTAAAA
5390	GACCTGGAAATTTGGGCTAAAAC
5391	ACCTGGAAATTTGGGCTAAAACT
5392	CCTGGAAATTTGGGCTAAAACTT
5393	CTGGAAATTTGGGCTAAAACTTA
5394	TGGAAATTTGGGCTAAAACTTAG
5395	GGAAATTTGGGCTAAAACTTAGA
5396	GAAATTTGGGCTAAAACTTAGAA
5397	AAATTTGGGCTAAAACTTAGAAA
5398	AATTTGGGCTAAAACTTAGAAAA
5399	ATTTGGGCTAAAACTTAGAAAAA
5400	TTTGGGCTAAAACTTAGAAAAAA
5401	TTGGGCTAAAACTTAGAAAAAAT
5402	TGGGCTAAAACTTAGAAAAAATT
5403	GGGCTAAAACTTAGAAAAAATTC
5404	GGCTAAAACTTAGAAAAAATTCT
5405	GCTAAAACTTAGAAAAAATTCTT
5406	CTAAAACTTAGAAAAAATTCTTA
5407	TAAAACTTAGAAAAAATTCTTAC
5408	AAAACTTAGAAAAAATTCTTACA
5409	AAACTTAGAAAAAATTCTTACAT
5410	AACTTAGAAAAAATTCTTACATG
5411	ACTTAGAAAAAATTCTTACATGA
5412	CTTAGAAAAAATTCTTACATGAT
5413	TTAGAAAAAATTCTTACATGATA
5414	TAGAAAAAATTCTTACATGATAA
5415	AGAAAAAATTCTTACATGATAAC
5416	GAAAAAATTCTTACATGATAACT
5417	AAAAAATTCTTACATGATAACTC
5418	AAAAATTCTTACATGATAACTCA
5419	AAAATTCTTACATGATAACTCAG
5420	AAATTCTTACATGATAACTCAGT
5421	AATTCTTACATGATAACTCAGTG
5422	ATTCTTACATGATAACTCAGTGA
5423	TTCTTACATGATAACTCAGTGAT
5424	TCTTACATGATAACTCAGTGATG

Fig. 29 cont'd (Sheet 113 of 170)

ID	SEQUENCE
5425	CTTACATGATAACTCAGTGATGC
5426	TTACATGATAACTCAGTGATGCT
5427	TACATGATAACTCAGTGATGCTT
5428	ACATGATAACTCAGTGATGCTTA
5429	CATGATAACTCAGTGATGCTTAC
5430	ATGATAACTCAGTGATGCTTACT
5431	TGATAACTCAGTGATGCTTACTC
5432	GATAACTCAGTGATGCTTACTCA
5433	ATAACTCAGTGATGCTTACTCAT
5434	TAACTCAGTGATGCTTACTCATA
5435	AACTCAGTGATGCTTACTCATAG
5436	ACTCAGTGATGCTTACTCATAGT
5437	CTCAGTGATGCTTACTCATAGTT
5438	TCAGTGATGCTTACTCATAGTTT
5439	CAGTGATGCTTACTCATAGTTTT
5440	AGTGATGCTTACTCATAGTTTTT
5441	GTGATGCTTACTCATAGTTTTTG
5442	TGATGCTTACTCATAGTTTTTGG
5443	GATGCTTACTCATAGTTTTTGGT
5444	ATGCTTACTCATAGTTTTTGGTG
5445	TGCTTACTCATAGTTTTTGGTGT
5446	GCTTACTCATAGTTTTTGGTGTT
5447	CTTACTCATAGTTTTTGGTGTTT
5448	TTACTCATAGTTTTTGGTGTTTC
5449	TACTCATAGTTTTTGGTGTTTCT
5450	ACTCATAGTTTTTGGTGTTTCTC
5451	CTCATAGTTTTTGGTGTTTCTCA
5452	TCATAGTTTTTGGTGTTTCTCAT
5453	CATAGTTTTTGGTGTTTCTCATA
5454	ATAGTTTTTGGTGTTTCTCATAG
5455	TAGTTTTTGGTGTTTCTCATAGA
5456	AGTTTTTGGTGTTTCTCATAGAT
5457	GTTTTTGGTGTTTCTCATAGATA
5458	TTTTTGGTGTTTCTCATAGATAA
5459	TTTTGGTGTTTCTCATAGATAAG
5460	TTTGGTGTTTCTCATAGATAAGA
5461	TTGGTGTTTCTCATAGATAAGAT
5462	TGGTGTTTCTCATAGATAAGATA
5463	GGTGTTTCTCATAGATAAGATAT
5464	GTGTTTCTCATAGATAAGATATA
5465	TGTTTCTCATAGATAAGATATAA
5466	GTTTCTCATAGATAAGATATAAA
5467	TTTCTCATAGATAAGATATAAAT
5468	TTCTCATAGATAAGATATAAATC
5469	TCTCATAGATAAGATATAAATCA
5470	CTCATAGATAAGATATAAATCAG
5471	TCATAGATAAGATATAAATCAGC
5472	CATAGATAAGATATAAATCAGCT

Fig. 29 cont'd (Sheet 114 of 170)

ID	SEQUENCE
5473	ATAGATAAGATATAAATCAGCTG
5474	TAGATAAGATATAAATCAGCTGG
5475	AGATAAGATATAAATCAGCTGGG
5476	GATAAGATATAAATCAGCTGGGC
5477	ATAAGATATAAATCAGCTGGGCG
5478	TAAGATATAAATCAGCTGGGCGC
5479	AAGATATAAATCAGCTGGGCGCG
5480	AGATATAAATCAGCTGGGCGCGG
5481	GATATAAATCAGCTGGGCGCGGT
5482	ATATAAATCAGCTGGGCGCGGTG
5483	TATAAATCAGCTGGGCGCGGTGG
5484	ATAAATCAGCTGGGCGCGGTGGC
5485	TAAATCAGCTGGGCGCGGTGGCT
5486	AAATCAGCTGGGCGCGGTGGCTC
5487	AATCAGCTGGGCGCGGTGGCTCA
5488	ATCAGCTGGGCGCGGTGGCTCAT
5489	TCAGCTGGGCGCGGTGGCTCATG
5490	CAGCTGGGCGCGGTGGCTCATGC
5491	AGCTGGGCGCGGTGGCTCATGCC
5492	GCTGGGCGCGGTGGCTCATGCCT
5493	CTGGGCGCGGTGGCTCATGCCTG
5494	TGGGCGCGGTGGCTCATGCCTGT
5495	GGGCGCGGTGGCTCATGCCTGTA
5496	GGCGCGGTGGCTCATGCCTGTAA
5497	GCGCGGTGGCTCATGCCTGTAAT
5498	CGCGGTGGCTCATGCCTGTAATC
5499	GCGGTGGCTCATGCCTGTAATCC
5500	CGGTGGCTCATGCCTGTAATCCC
5501	GGTGGCTCATGCCTGTAATCCCA
5502	GTGGCTCATGCCTGTAATCCCAG
5503	TGGCTCATGCCTGTAATCCCAGC
5504	GGCTCATGCCTGTAATCCCAGCA
5505	GCTCATGCCTGTAATCCCAGCAC
5506	CTCATGCCTGTAATCCCAGCACT
5507	TCATGCCTGTAATCCCAGCACTT
5508	CATGCCTGTAATCCCAGCACTTT
5509	ATGCCTGTAATCCCAGCACTTTG
5510	TGCCTGTAATCCCAGCACTTTGG
5511	GCCTGTAATCCCAGCACTTTGGG
5512	CCTGTAATCCCAGCACTTTGGGA
5513	CTGTAATCCCAGCACTTTGGGAG
5514	TGTAATCCCAGCACTTTGGGAGG
5515	GTAATCCCAGCACTTTGGGAGGC
5516	TAATCCCAGCACTTTGGGAGGCC
5517	AATCCCAGCACTTTGGGAGGCCG
5518	ATCCCAGCACTTTGGGAGGCCGA
5519	TCCCAGCACTTTGGGAGGCCGAG
5520	CCCAGCACTTTGGGAGGCCGAGG

Fig. 29 cont'd (Sheet 115 of 170)

ID	SEQUENCE
5521	CCAGCACTTTGGGAGGCCGAGGC
5522	CAGCACTTTGGGAGGCCGAGGCG
5523	AGCACTTTGGGAGGCCGAGGCGG
5524	GCACTTTGGGAGGCCGAGGCGGG
5525	CACTTTGGGAGGCCGAGGCGGGC
5526	ACTTTGGGAGGCCGAGGCGGGCA
5527	CTTTGGGAGGCCGAGGCGGGCAG
5528	TTTGGGAGGCCGAGGCGGGCAGA
5529	TTGGGAGGCCGAGGCGGGCAGAT
5530	TGGGAGGCCGAGGCGGGCAGATC
5531	GGGAGGCCGAGGCGGGCAGATCA
5532	GGAGGCCGAGGCGGGCAGATCAC
5533	GAGGCCGAGGCGGGCAGATCACC
5534	AGGCCGAGGCGGGCAGATCACCT
5535	GGCCGAGGCGGGCAGATCACCTG
5536	GCCGAGGCGGGCAGATCACCTGA
5537	CCGAGGCGGGCAGATCACCTGAG
5538	CGAGGCGGGCAGATCACCTGAGG
5539	GAGGCGGGCAGATCACCTGAGGT
5540	AGGCGGGCAGATCACCTGAGGTC
5541	GGCGGGCAGATCACCTGAGGTCG
5542	GCGGGCAGATCACCTGAGGTCGG
5543	CGGGCAGATCACCTGAGGTCGGG
5544	GGGCAGATCACCTGAGGTCGGGA
5545	GGCAGATCACCTGAGGTCGGGAG
5546	GCAGATCACCTGAGGTCGGGAGG
5547	CAGATCACCTGAGGTCGGGAGGT
5548	AGATCACCTGAGGTCGGGAGGTC
5549	GATCACCTGAGGTCGGGAGGTCG
5550	ATCACCTGAGGTCGGGAGGTCGA
5551	TCACCTGAGGTCGGGAGGTCGAG
5552	CACCTGAGGTCGGGAGGTCGAGA
5553	ACCTGAGGTCGGGAGGTCGAGAC
5554	CCTGAGGTCGGGAGGTCGAGACC
5555	CTGAGGTCGGGAGGTCGAGACCA
5556	TGAGGTCGGGAGGTCGAGACCAG
5557	GAGGTCGGGAGGTCGAGACCAGC
5558	AGGTCGGGAGGTCGAGACCAGCC
5559	GGTCGGGAGGTCGAGACCAGCCT
5560	GTCGGGAGGTCGAGACCAGCCTG
5561	TCGGGAGGTCGAGACCAGCCTGA
5562	CGGGAGGTCGAGACCAGCCTGAC
5563	GGGAGGTCGAGACCAGCCTGACC
5564	GGAGGTCGAGACCAGCCTGACCA
5565	GAGGTCGAGACCAGCCTGACCAA
5566	AGGTCGAGACCAGCCTGACCAAC
5567	GGTCGAGACCAGCCTGACCAACA
5568	GTCGAGACCAGCCTGACCAACAT

Fig. 29 cont'd (Sheet 116 of 170)

ID	SEQUENCE
5569	TCGAGACCAGCCTGACCAACATG
5570	CGAGACCAGCCTGACCAACATGG
5571	GAGACCAGCCTGACCAACATGGA
5572	AGACCAGCCTGACCAACATGGAG
5573	GACCAGCCTGACCAACATGGAGA
5574	ACCAGCCTGACCAACATGGAGAA
5575	CCAGCCTGACCAACATGGAGAAA
5576	CAGCCTGACCAACATGGAGAAAC
5577	AGCCTGACCAACATGGAGAAACC
5578	GCCTGACCAACATGGAGAAACCC
5579	CCTGACCAACATGGAGAAACCCC
5580	CTGACCAACATGGAGAAACCCCG
5581	TGACCAACATGGAGAAACCCCGT
5582	GACCAACATGGAGAAACCCCGTC
5583	ACCAACATGGAGAAACCCCGTCT
5584	CCAACATGGAGAAACCCCGTCTC
5585	CAACATGGAGAAACCCCGTCTCT
5586	AACATGGAGAAACCCCGTCTCTA
5587	ACATGGAGAAACCCCGTCTCTAC
5588	CATGGAGAAACCCCGTCTCTACT
5589	ATGGAGAAACCCCGTCTCTACTA
5590	TGGAGAAACCCCGTCTCTACTAA
5591	GGAGAAACCCCGTCTCTACTAAA
5592	GAGAAACCCCGTCTCTACTAAAA
5593	AGAAACCCCGTCTCTACTAAAAA
5594	GAAACCCCGTCTCTACTAAAAAT
5595	AAACCCCGTCTCTACTAAAAATA
5596	AACCCCGTCTCTACTAAAAATAC
5597	ACCCCGTCTCTACTAAAAATACA
5598	CCCCGTCTCTACTAAAAATACAA
5599	CCCGTCTCTACTAAAAATACAAA
5600	CCGTCTCTACTAAAAATACAAAA
5601	CGTCTCTACTAAAAATACAAAAT
5602	GTCTCTACTAAAAATACAAAATT
5603	TCTCTACTAAAAATACAAAATTA
5604	CTCTACTAAAAATACAAAATTAG
5605	TCTACTAAAAATACAAAATTAGC
5606	CTACTAAAAATACAAAATTAGCT
5607	TACTAAAAATACAAAATTAGCTG
5608	ACTAAAAATACAAAATTAGCTGG
5609	CTAAAAATACAAAATTAGCTGGG
5610	TAAAAATACAAAATTAGCTGGGC
5611	AAAAATACAAAATTAGCTGGGCG
5612	AAAATACAAAATTAGCTGGGCGT
5613	AAATACAAAATTAGCTGGGCGTG
5614	AATACAAAATTAGCTGGGCGTGG
5615	ATACAAAATTAGCTGGGCGTGGT
5616	TACAAAATTAGCTGGGCGTGGTG

Fig. 29 cont'd (Sheet 117 of 170)

ID	SEQUENCE
5617	ACAAAATTAGCTGGGCGTGGTGG
5618	CAAAATTAGCTGGGCGTGGTGGC
5619	AAAATTAGCTGGGCGTGGTGGCT
5620	AAATTAGCTGGGCGTGGTGGCTC
5621	AATTAGCTGGGCGTGGTGGCTCA
5622	ATTAGCTGGGCGTGGTGGCTCAT
5623	TTAGCTGGGCGTGGTGGCTCATG
5624	TAGCTGGGCGTGGTGGCTCATGC
5625	AGCTGGGCGTGGTGGCTCATGCC
5626	GCTGGGCGTGGTGGCTCATGCCT
5627	CTGGGCGTGGTGGCTCATGCCTG
5628	TGGGCGTGGTGGCTCATGCCTGT
5629	GGGCGTGGTGGCTCATGCCTGTA
5630	GGCGTGGTGGCTCATGCCTGTAA
5631	GCGTGGTGGCTCATGCCTGTAAT
5632	CGTGGTGGCTCATGCCTGTAATC
5633	GTGGTGGCTCATGCCTGTAATCC
5634	TGGTGGCTCATGCCTGTAATCCC
5635	GGTGGCTCATGCCTGTAATCCCA
5636	GTGGCTCATGCCTGTAATCCCAG
5637	TGGCTCATGCCTGTAATCCCAGC
5638	GGCTCATGCCTGTAATCCCAGCT
5639	GCTCATGCCTGTAATCCCAGCTA
5640	CTCATGCCTGTAATCCCAGCTAC
5641	TCATGCCTGTAATCCCAGCTACT
5642	CATGCCTGTAATCCCAGCTACTT
5643	ATGCCTGTAATCCCAGCTACTTG
5644	TGCCTGTAATCCCAGCTACTTGG
5645	GCCTGTAATCCCAGCTACTTGGG
5646	CCTGTAATCCCAGCTACTTGGGA
5647	CTGTAATCCCAGCTACTTGGGAG
5648	TGTAATCCCAGCTACTTGGGAGG
5649	GTAATCCCAGCTACTTGGGAGGC
5650	TAATCCCAGCTACTTGGGAGGCT
5651	AATCCCAGCTACTTGGGAGGCTG
5652	ATCCCAGCTACTTGGGAGGCTGA
5653	TCCCAGCTACTTGGGAGGCTGAG
5654	CCCAGCTACTTGGGAGGCTGAGG
5655	CCAGCTACTTGGGAGGCTGAGGC
5656	CAGCTACTTGGGAGGCTGAGGCA
5657	AGCTACTTGGGAGGCTGAGGCAG
5658	GCTACTTGGGAGGCTGAGGCAGG
5659	CTACTTGGGAGGCTGAGGCAGGA
5660	TACTTGGGAGGCTGAGGCAGGAG
5661	ACTTGGGAGGCTGAGGCAGGAGA
5662	CTTGGGAGGCTGAGGCAGGAGAA
5663	TTGGGAGGCTGAGGCAGGAGAAT
5664	TGGGAGGCTGAGGCAGGAGAATC

Fig. 29 cont'd (Sheet 118 of 170)

ID	SEQUENCE
5665	GGGAGGCTGAGGCAGGAGAATCG
5666	GGAGGCTGAGGCAGGAGAATCGC
5667	GAGGCTGAGGCAGGAGAATCGCT
5668	AGGCTGAGGCAGGAGAATCGCTT
5669	GGCTGAGGCAGGAGAATCGCTTG
5670	GCTGAGGCAGGAGAATCGCTTGA
5671	CTGAGGCAGGAGAATCGCTTGAA
5672	TGAGGCAGGAGAATCGCTTGAAC
5673	GAGGCAGGAGAATCGCTTGAACC
5674	AGGCAGGAGAATCGCTTGAACCC
5675	GGCAGGAGAATCGCTTGAACCCA
5676	GCAGGAGAATCGCTTGAACCCAG
5677	CAGGAGAATCGCTTGAACCCAGG
5678	AGGAGAATCGCTTGAACCCAGGA
5679	GGAGAATCGCTTGAACCCAGGAG
5680	GAGAATCGCTTGAACCCAGGAGG
5681	AGAATCGCTTGAACCCAGGAGGC
5682	GAATCGCTTGAACCCAGGAGGCG
5683	AATCGCTTGAACCCAGGAGGCGG
5684	ATCGCTTGAACCCAGGAGGCGGA
5685	TCGCTTGAACCCAGGAGGCGGAG
5686	CGCTTGAACCCAGGAGGCGGAGG
5687	GCTTGAACCCAGGAGGCGGAGGT
5688	CTTGAACCCAGGAGGCGGAGGTT
5689	TTGAACCCAGGAGGCGGAGGTTG
5690	TGAACCCAGGAGGCGGAGGTTGT
5691	GAACCCAGGAGGCGGAGGTTGTG
5692	AACCCAGGAGGCGGAGGTTGTGG
5693	ACCCAGGAGGCGGAGGTTGTGGT
5694	CCCAGGAGGCGGAGGTTGTGGTG
5695	CCAGGAGGCGGAGGTTGTGGTGA
5696	CAGGAGGCGGAGGTTGTGGTGAG
5697	AGGAGGCGGAGGTTGTGGTGAGC
5698	GGAGGCGGAGGTTGTGGTGAGCG
5699	GAGGCGGAGGTTGTGGTGAGCGA
5700	AGGCGGAGGTTGTGGTGAGCGAA
5701	GGCGGAGGTTGTGGTGAGCGAAG
5702	GCGGAGGTTGTGGTGAGCGAAGA
5703	CGGAGGTTGTGGTGAGCGAAGAT
5704	GGAGGTTGTGGTGAGCGAAGATC
5705	GAGGTTGTGGTGAGCGAAGATCG
5706	AGGTTGTGGTGAGCGAAGATCGT
5707	GGTTGTGGTGAGCGAAGATCGTG
5708	GTTGTGGTGAGCGAAGATCGTGC
5709	TTGTGGTGAGCGAAGATCGTGCC
5710	TGTGGTGAGCGAAGATCGTGCCA
5711	GTGGTGAGCGAAGATCGTGCCAT
5712	TGGTGAGCGAAGATCGTGCCATT

Fig. 29 cont'd (Sheet 119 of 170)

ID	SEQUENCE
5713	GGTGAGCGAAGATCGTGCCATTG
5714	GTGAGCGAAGATCGTGCCATTGC
5715	TGAGCGAAGATCGTGCCATTGCA
5716	GAGCGAAGATCGTGCCATTGCAC
5717	AGCGAAGATCGTGCCATTGCACT
5718	GCGAAGATCGTGCCATTGCACTC
5719	CGAAGATCGTGCCATTGCACTCC
5720	GAAGATCGTGCCATTGCACTCCA
5721	AAGATCGTGCCATTGCACTCCAG
5722	AGATCGTGCCATTGCACTCCAGC
5723	GATCGTGCCATTGCACTCCAGCC
5724	ATCGTGCCATTGCACTCCAGCCT
5725	TCGTGCCATTGCACTCCAGCCTG
5726	CGTGCCATTGCACTCCAGCCTGG
5727	GTGCCATTGCACTCCAGCCTGGG
5728	TGCCATTGCACTCCAGCCTGGGC
5729	GCCATTGCACTCCAGCCTGGGCA
5730	CCATTGCACTCCAGCCTGGGCAA
5731	CATTGCACTCCAGCCTGGGCAAC
5732	ATTGCACTCCAGCCTGGGCAACA
5733	TTGCACTCCAGCCTGGGCAACAA
5734	TGCACTCCAGCCTGGGCAACAAG
5735	GCACTCCAGCCTGGGCAACAAGA
5736	CACTCCAGCCTGGGCAACAAGAG
5737	ACTCCAGCCTGGGCAACAAGAGC
5738	CTCCAGCCTGGGCAACAAGAGCA
5739	TCCAGCCTGGGCAACAAGAGCAA
5740	CCAGCCTGGGCAACAAGAGCAAA
5741	CAGCCTGGGCAACAAGAGCAAAA
5742	AGCCTGGGCAACAAGAGCAAAAC
5743	GCCTGGGCAACAAGAGCAAAACT
5744	CCTGGGCAACAAGAGCAAAACTC
5745	CTGGGCAACAAGAGCAAAACTCT
5746	TGGGCAACAAGAGCAAAACTCTG
5747	GGGCAACAAGAGCAAAACTCTGT
5748	GGCAACAAGAGCAAAACTCTGTC
5749	GCAACAAGAGCAAAACTCTGTCT
5750	CAACAAGAGCAAAACTCTGTCTC
5751	AACAAGAGCAAAACTCTGTCTCA
5752	ACAAGAGCAAAACTCTGTCTCAA
5753	CAAGAGCAAAACTCTGTCTCAAA
5754	AAGAGCAAAACTCTGTCTCAAAA
5755	AGAGCAAAACTCTGTCTCAAAAA
5756	GAGCAAAACTCTGTCTCAAAAAA
5757	AGCAAAACTCTGTCTCAAAAAAA
5758	GCAAAACTCTGTCTCAAAAAAAA
5759	AAAAAAAAGATATAAATCACAAT
5760	AAAAAAAGATATAAATCACAATA

Fig. 29 cont'd (Sheet 120 of 170)

ID	SEQUENCE
5761	AAAAAAGATATAAATCACAATAA
5762	AAAAAGATATAAATCACAATAAA
5763	AAAAGATATAAATCACAATAAAT
5764	AAAGATATAAATCACAATAAATA
5765	AAGATATAAATCACAATAAATAA
5766	AGATATAAATCACAATAAATAAA
5767	GATATAAATCACAATAAATAAAT
5768	ATATAAATCACAATAAATAAATA
5769	TATAAATCACAATAAATAAATAG
5770	ATAAATCACAATAAATAAATAGG
5771	TAAATCACAATAAATAAATAGGT
5772	AAATCACAATAAATAAATAGGTC
5773	AATCACAATAAATAAATAGGTCA
5774	ATCACAATAAATAAATAGGTCAA
5775	TCACAATAAATAAATAGGTCAAT
5776	CACAATAAATAAATAGGTCAATA
5777	ACAATAAATAAATAGGTCAATAC
5778	CAATAAATAAATAGGTCAATACA
5779	AATAAATAAATAGGTCAATACAA
5780	ATAAATAAATAGGTCAATACAAA
5781	TAAATAAATAGGTCAATACAAAT
5782	AAATAAATAGGTCAATACAAATG
5783	AATAAATAGGTCAATACAAATGT
5784	ATAAATAGGTCAATACAAATGTT
5785	TAAATAGGTCAATACAAATGTTA
5786	AAATAGGTCAATACAAATGTTAG
5787	AATAGGTCAATACAAATGTTAGC
5788	ATAGGTCAATACAAATGTTAGCC
5789	TAGGTCAATACAAATGTTAGCCA
5790	AGGTCAATACAAATGTTAGCCAG
5791	GGTCAATACAAATGTTAGCCAGG
5792	GTCAATACAAATGTTAGCCAGGC
5793	TCAATACAAATGTTAGCCAGGCG
5794	CAATACAAATGTTAGCCAGGCGT
5795	AATACAAATGTTAGCCAGGCGTG
5796	ATACAAATGTTAGCCAGGCGTGG
5797	TACAAATGTTAGCCAGGCGTGGT
5798	ACAAATGTTAGCCAGGCGTGGTG
5799	CAAATGTTAGCCAGGCGTGGTGG
5800	AAATGTTAGCCAGGCGTGGTGGC
5801	AATGTTAGCCAGGCGTGGTGGCA
5802	ATGTTAGCCAGGCGTGGTGGCAC
5803	TGTTAGCCAGGCGTGGTGGCACA
5804	GTTAGCCAGGCGTGGTGGCACAT
5805	TTAGCCAGGCGTGGTGGCACATG
5806	TAGCCAGGCGTGGTGGCACATGC
5807	AGCCAGGCGTGGTGGCACATGCC
5808	GCCAGGCGTGGTGGCACATGCCC

Fig. 29 cont'd (Sheet 121 of 170)

ID	SEQUENCE
5809	CCAGGCGTGGTGGCACATGCCCA
5810	CAGGCGTGGTGGCACATGCCCAT
5811	AGGCGTGGTGGCACATGCCCATA
5812	GGCGTGGTGGCACATGCCCATAG
5813	GCGTGGTGGCACATGCCCATAGT
5814	CGTGGTGGCACATGCCCATAGTC
5815	GTGGTGGCACATGCCCATAGTCG
5816	TGGTGGCACATGCCCATAGTCGC
5817	GGTGGCACATGCCCATAGTCGCA
5818	GTGGCACATGCCCATAGTCGCAG
5819	TGGCACATGCCCATAGTCGCAGC
5820	GGCACATGCCCATAGTCGCAGCT
5821	GCACATGCCCATAGTCGCAGCTA
5822	CACATGCCCATAGTCGCAGCTAC
5823	ACATGCCCATAGTCGCAGCTACT
5824	CATGCCCATAGTCGCAGCTACTC
5825	ATGCCCATAGTCGCAGCTACTCT
5826	TGCCCATAGTCGCAGCTACTCTG
5827	GCCCATAGTCGCAGCTACTCTGG
5828	CCCATAGTCGCAGCTACTCTGGA
5829	CCATAGTCGCAGCTACTCTGGAG
5830	CATAGTCGCAGCTACTCTGGAGG
5831	ATAGTCGCAGCTACTCTGGAGGC
5832	TAGTCGCAGCTACTCTGGAGGCA
5833	AGTCGCAGCTACTCTGGAGGCAG
5834	GTCGCAGCTACTCTGGAGGCAGA
5835	TCGCAGCTACTCTGGAGGCAGAG
5836	CGCAGCTACTCTGGAGGCAGAGG
5837	GCAGCTACTCTGGAGGCAGAGGC
5838	CAGCTACTCTGGAGGCAGAGGCA
5839	AGCTACTCTGGAGGCAGAGGCAG
5840	GCTACTCTGGAGGCAGAGGCAGG
5841	CTACTCTGGAGGCAGAGGCAGGA
5842	TACTCTGGAGGCAGAGGCAGGAG
5843	ACTCTGGAGGCAGAGGCAGGAGG
5844	CTCTGGAGGCAGAGGCAGGAGGA
5845	TCTGGAGGCAGAGGCAGGAGGAT
5846	CTGGAGGCAGAGGCAGGAGGATC
5847	TGGAGGCAGAGGCAGGAGGATCA
5848	GGAGGCAGAGGCAGGAGGATCAC
5849	GAGGCAGAGGCAGGAGGATCACT
5850	AGGCAGAGGCAGGAGGATCACTT
5851	GGCAGAGGCAGGAGGATCACTTG
5852	GCAGAGGCAGGAGGATCACTTGA
5853	CAGAGGCAGGAGGATCACTTGAG
5854	AGAGGCAGGAGGATCACTTGAGC
5855	GAGGCAGGAGGATCACTTGAGCC
5856	AGGCAGGAGGATCACTTGAGCCC

Fig. 29 cont'd (Sheet 122 of 170)

ID	SEQUENCE
5857	GGCAGGAGGATCACTTGAGCCCA
5858	GCAGGAGGATCACTTGAGCCCAT
5859	CAGGAGGATCACTTGAGCCCATG
5860	AGGAGGATCACTTGAGCCCATGA
5861	GGAGGATCACTTGAGCCCATGAA
5862	GAGGATCACTTGAGCCCATGAAT
5863	AGGATCACTTGAGCCCATGAATT
5864	GGATCACTTGAGCCCATGAATTT
5865	GATCACTTGAGCCCATGAATTTG
5866	ATCACTTGAGCCCATGAATTTGA
5867	TCACTTGAGCCCATGAATTTGAG
5868	CACTTGAGCCCATGAATTTGAGG
5869	ACTTGAGCCCATGAATTTGAGGC
5870	CTTGAGCCCATGAATTTGAGGCA
5871	TTGAGCCCATGAATTTGAGGCAG
5872	TGAGCCCATGAATTTGAGGCAGC
5873	GAGCCCATGAATTTGAGGCAGCA
5874	AGCCCATGAATTTGAGGCAGCAG
5875	GCCCATGAATTTGAGGCAGCAGT
5876	CCCATGAATTTGAGGCAGCAGTG
5877	CCATGAATTTGAGGCAGCAGTGA
5878	CATGAATTTGAGGCAGCAGTGAG
5879	ATGAATTTGAGGCAGCAGTGAGC
5880	TGAATTTGAGGCAGCAGTGAGCT
5881	GAATTTGAGGCAGCAGTGAGCTA
5882	AATTTGAGGCAGCAGTGAGCTAT
5883	ATTTGAGGCAGCAGTGAGCTATG
5884	TTTGAGGCAGCAGTGAGCTATGA
5885	TTGAGGCAGCAGTGAGCTATGAT
5886	TGAGGCAGCAGTGAGCTATGATT
5887	GAGGCAGCAGTGAGCTATGATTG
5888	AGGCAGCAGTGAGCTATGATTGT
5889	GGCAGCAGTGAGCTATGATTGTG
5890	GCAGCAGTGAGCTATGATTGTGC
5891	CAGCAGTGAGCTATGATTGTGCC
5892	AGCAGTGAGCTATGATTGTGCCA
5893	GCAGTGAGCTATGATTGTGCCAC
5894	CAGTGAGCTATGATTGTGCCACT
5895	AGTGAGCTATGATTGTGCCACTG
5896	GTGAGCTATGATTGTGCCACTGT
5897	TGAGCTATGATTGTGCCACTGTA
5898	GAGCTATGATTGTGCCACTGTAC
5899	AGCTATGATTGTGCCACTGTACT
5900	GCTATGATTGTGCCACTGTACTC
5901	CTATGATTGTGCCACTGTACTCC
5902	TATGATTGTGCCACTGTACTCCA
5903	ATGATTGTGCCACTGTACTCCAG
5904	TGATTGTGCCACTGTACTCCAGT

Fig. 29 cont'd (Sheet 123 of 170)

ID	SEQUENCE
5905	GATTGTGCCACTGTACTCCAGTC
5906	ATTGTGCCACTGTACTCCAGTCT
5907	TTGTGCCACTGTACTCCAGTCTG
5908	TGTGCCACTGTACTCCAGTCTGG
5909	GTGCCACTGTACTCCAGTCTGGG
5910	TGCCACTGTACTCCAGTCTGGGT
5911	GCCACTGTACTCCAGTCTGGGTG
5912	CCACTGTACTCCAGTCTGGGTGA
5913	CACTGTACTCCAGTCTGGGTGAC
5914	ACTGTACTCCAGTCTGGGTGACA
5915	CTGTACTCCAGTCTGGGTGACAG
5916	TGTACTCCAGTCTGGGTGACAGA
5917	GTACTCCAGTCTGGGTGACAGAG
5918	TACTCCAGTCTGGGTGACAGAGT
5919	ACTCCAGTCTGGGTGACAGAGTG
5920	CTCCAGTCTGGGTGACAGAGTGA
5921	TCCAGTCTGGGTGACAGAGTGAG
5922	CCAGTCTGGGTGACAGAGTGAGA
5923	CAGTCTGGGTGACAGAGTGAGAC
5924	AGTCTGGGTGACAGAGTGAGACC
5925	GTCTGGGTGACAGAGTGAGACCC
5926	TCTGGGTGACAGAGTGAGACCCC
5927	CTGGGTGACAGAGTGAGACCCCA
5928	TGGGTGACAGAGTGAGACCCCAT
5929	GGGTGACAGAGTGAGACCCCATC
5930	GGTGACAGAGTGAGACCCCATCT
5931	GTGACAGAGTGAGACCCCATCTC
5932	TGACAGAGTGAGACCCCATCTCT
5933	GACAGAGTGAGACCCCATCTCTA
5934	ACAGAGTGAGACCCCATCTCTAA
5935	CAGAGTGAGACCCCATCTCTAAA
5936	AGAGTGAGACCCCATCTCTAAAT
5937	GAGTGAGACCCCATCTCTAAATA
5938	AGTGAGACCCCATCTCTAAATAA
5939	GTGAGACCCCATCTCTAAATAAA
5940	TGAGACCCCATCTCTAAATAAAT
5941	GAGACCCCATCTCTAAATAAATA
5942	AGACCCCATCTCTAAATAAATAG
5943	GACCCCATCTCTAAATAAATAGG
5944	ACCCCATCTCTAAATAAATAGGT
5945	CCCCATCTCTAAATAAATAGGTC
5946	CCCATCTCTAAATAAATAGGTCA
5947	CCATCTCTAAATAAATAGGTCAA
5948	CATCTCTAAATAAATAGGTCAAA
5949	ATCTCTAAATAAATAGGTCAAAC
5950	TCTCTAAATAAATAGGTCAAACC
5951	CTCTAAATAAATAGGTCAAACCC
5952	TCTAAATAAATAGGTCAAACCCT

Fig. 29 cont'd (Sheet 124 of 170)

ID	SEQUENCE
5953	CTAAATAAATAGGTCAAACCCTT
5954	TAAATAAATAGGTCAAACCCTTA
5955	AAATAAATAGGTCAAACCCTTAA
5956	AATAAATAGGTCAAACCCTTAAA
5957	ATAAATAGGTCAAACCCTTAAAA
5958	TAAATAGGTCAAACCCTTAAAAA
5959	AAATAGGTCAAACCCTTAAAAAT
5960	AATAGGTCAAACCCTTAAAAATA
5961	ATAGGTCAAACCCTTAAAAATAT
5962	TAGGTCAAACCCTTAAAAATATT
5963	AGGTCAAACCCTTAAAAATATTT
5964	GGTCAAACCCTTAAAAATATTTA
5965	GTCAAACCCTTAAAAATATTTAA
5966	TCAAACCCTTAAAAATATTTAAA
5967	CAAACCCTTAAAAATATTTAAAT
5968	AAACCCTTAAAAATATTTAAATT
5969	AACCCTTAAAAATATTTAAATTC
5970	ACCCTTAAAAATATTTAAATTCT
5971	CCCTTAAAAATATTTAAATTCTT
5972	CCTTAAAAATATTTAAATTCTTA
5973	CTTAAAAATATTTAAATTCTTAA
5974	TTAAAAATATTTAAATTCTTAAA
5975	TAAAAATATTTAAATTCTTAAAA
5976	AAAAATATTTAAATTCTTAAAAA
5977	AAAATATTTAAATTCTTAAAAAA
5978	AAATATTTAAATTCTTAAAAAAT
5979	AATATTTAAATTCTTAAAAAATT
5980	ATATTTAAATTCTTAAAAAATTG
5981	TATTTAAATTCTTAAAAAATTGA
5982	ATTTAAATTCTTAAAAAATTGAA
5983	TTTAAATTCTTAAAAAATTGAAA
5984	TTAAATTCTTAAAAAATTGAAAA
5985	TAAATTCTTAAAAAATTGAAAAG
5986	AAATTCTTAAAAAATTGAAAAGA
5987	AATTCTTAAAAAATTGAAAAGAT
5988	ATTCTTAAAAAATTGAAAAGATT
5989	TTCTTAAAAAATTGAAAAGATTA
5990	TCTTAAAAAATTGAAAAGATTAT
5991	CTTAAAAAATTGAAAAGATTATT
5992	TTAAAAAATTGAAAAGATTATTC
5993	TAAAAAATTGAAAAGATTATTCT
5994	AAAAAATTGAAAAGATTATTCTT
5995	AAAAATTGAAAAGATTATTCTTC
5996	AAAATTGAAAAGATTATTCTTCT
5997	AAATTGAAAAGATTATTCTTCTC
5998	AATTGAAAAGATTATTCTTCTCA
5999	ATTGAAAAGATTATTCTTCTCAA
6000	TTGAAAAGATTATTCTTCTCAAA

Fig. 29 cont'd (Sheet 125 of 170)

ID	SEQUENCE
6001	TGAAAAGATTATTCTTCTCAAAT
6002	GAAAAGATTATTCTTCTCAAATT
6003	AAAAGATTATTCTTCTCAAATTT
6004	AAAGATTATTCTTCTCAAATTTA
6005	AAGATTATTCTTCTCAAATTTAG
6006	AGATTATTCTTCTCAAATTTAGT
6007	GATTATTCTTCTCAAATTTAGTT
6008	ATTATTCTTCTCAAATTTAGTTG
6009	TTATTCTTCTCAAATTTAGTTGA
6010	TATTCTTCTCAAATTTAGTTGAG
6011	ATTCTTCTCAAATTTAGTTGAGC
6012	TTCTTCTCAAATTTAGTTGAGCT
6013	TCTTCTCAAATTTAGTTGAGCTT
6014	CTTCTCAAATTTAGTTGAGCTTT
6015	TTCTCAAATTTAGTTGAGCTTTC
6016	TCTCAAATTTAGTTGAGCTTTCT
6017	CTCAAATTTAGTTGAGCTTTCTA
6018	TCAAATTTAGTTGAGCTTTCTAA
6019	CAAATTTAGTTGAGCTTTCTAAG
6020	AAATTTAGTTGAGCTTTCTAAGA
6021	AATTTAGTTGAGCTTTCTAAGAG
6022	ATTTAGTTGAGCTTTCTAAGAGA
6023	TTTAGTTGAGCTTTCTAAGAGAA
6024	TTAGTTGAGCTTTCTAAGAGAAG
6025	TAGTTGAGCTTTCTAAGAGAAGC
6026	AGTTGAGCTTTCTAAGAGAAGCA
6027	GTTGAGCTTTCTAAGAGAAGCAA
6028	TTGAGCTTTCTAAGAGAAGCAAT
6029	TGAGCTTTCTAAGAGAAGCAATT
6030	GAGCTTTCTAAGAGAAGCAATTG
6031	AGCTTTCTAAGAGAAGCAATTGG
6032	GCTTTCTAAGAGAAGCAATTGGC
6033	CTTTCTAAGAGAAGCAATTGGCT
6034	TTTCTAAGAGAAGCAATTGGCTT
6035	TTCTAAGAGAAGCAATTGGCTTT
6036	TCTAAGAGAAGCAATTGGCTTTT
6037	CTAAGAGAAGCAATTGGCTTTTT
6038	TAAGAGAAGCAATTGGCTTTTTC
6039	AAGAGAAGCAATTGGCTTTTTCC
6040	AGAGAAGCAATTGGCTTTTTCCC
6041	GAGAAGCAATTGGCTTTTTCCCA
6042	AGAAGCAATTGGCTTTTTCCCAC
6043	GAAGCAATTGGCTTTTTCCCACT
6044	AAGCAATTGGCTTTTTCCCACTT
6045	AGCAATTGGCTTTTTCCCACTTC
6046	GCAATTGGCTTTTTCCCACTTCA
6047	CAATTGGCTTTTTCCCACTTCAA
6048	AATTGGCTTTTTCCCACTTCAAT

Fig. 29 cont'd (Sheet 126 of 170)

ID	SEQUENCE
6049	ATTGGCTTTTTCCCACTTCAATA
6050	TTGGCTTTTTCCCACTTCAATAA
6051	TGGCTTTTTCCCACTTCAATAAT
6052	GGCTTTTTCCCACTTCAATAATC
6053	GCTTTTTCCCACTTCAATAATCA
6054	CTTTTTCCCACTTCAATAATCAT
6055	TTTTTCCCACTTCAATAATCATT
6056	TTTTCCCACTTCAATAATCATTT
6057	TTTCCCACTTCAATAATCATTTT
6058	TTCCCACTTCAATAATCATTTTC
6059	TCCCACTTCAATAATCATTTTCA
6060	CCCACTTCAATAATCATTTTCAG
6061	CCACTTCAATAATCATTTTCAGT
6062	CACTTCAATAATCATTTTCAGTT
6063	ACTTCAATAATCATTTTCAGTTT
6064	CTTCAATAATCATTTTCAGTTTG
6065	TTCAATAATCATTTTCAGTTTGA
6066	TCAATAATCATTTTCAGTTTGAC
6067	CAATAATCATTTTCAGTTTGACT
6068	AATAATCATTTTCAGTTTGACTC
6069	ATAATCATTTTCAGTTTGACTCA
6070	TAATCATTTTCAGTTTGACTCAT
6071	AATCATTTTCAGTTTGACTCATA
6072	ATCATTTTCAGTTTGACTCATAC
6073	TCATTTTCAGTTTGACTCATACA
6074	CATTTTCAGTTTGACTCATACAG
6075	ATTTTCAGTTTGACTCATACAGT
6076	TTTTCAGTTTGACTCATACAGTT
6077	TTTCAGTTTGACTCATACAGTTA
6078	TTCAGTTTGACTCATACAGTTAA
6079	TCAGTTTGACTCATACAGTTAAC
6080	CAGTTTGACTCATACAGTTAACA
6081	AGTTTGACTCATACAGTTAACAC
6082	GTTTGACTCATACAGTTAACACA
6083	TTTGACTCATACAGTTAACACAA
6084	TTGACTCATACAGTTAACACAAT
6085	TGACTCATACAGTTAACACAATG
6086	GACTCATACAGTTAACACAATGT
6087	ACTCATACAGTTAACACAATGTG
6088	CTCATACAGTTAACACAATGTGA
6089	TCATACAGTTAACACAATGTGAA
6090	CATACAGTTAACACAATGTGAAT
6091	ATACAGTTAACACAATGTGAATT
6092	TACAGTTAACACAATGTGAATTT
6093	ACAGTTAACACAATGTGAATTTC
6094	CAGTTAACACAATGTGAATTTCT
6095	AGTTAACACAATGTGAATTTCTT
6096	GTTAACACAATGTGAATTTCTTC

Fig. 29 cont'd (Sheet 127 of 170)

ID	SEQUENCE
6097	TTAACACAATGTGAATTTCTTCC
6098	TAACACAATGTGAATTTCTTCCT
6099	AACACAATGTGAATTTCTTCCTC
6100	ACACAATGTGAATTTCTTCCTCA
6101	CACAATGTGAATTTCTTCCTCAG
6102	ACAATGTGAATTTCTTCCTCAGC
6103	CAATGTGAATTTCTTCCTCAGCA
6104	AATGTGAATTTCTTCCTCAGCAT
6105	ATGTGAATTTCTTCCTCAGCATA
6106	TGTGAATTTCTTCCTCAGCATAA
6107	GTGAATTTCTTCCTCAGCATAAC
6108	TGAATTTCTTCCTCAGCATAACA
6109	GAATTTCTTCCTCAGCATAACAG
6110	AATTTCTTCCTCAGCATAACAGA
6111	ATTTCTTCCTCAGCATAACAGAG
6112	TTTCTTCCTCAGCATAACAGAGT
6113	TTCTTCCTCAGCATAACAGAGTT
6114	TCTTCCTCAGCATAACAGAGTTA
6115	CTTCCTCAGCATAACAGAGTTAT
6116	TTCCTCAGCATAACAGAGTTATA
6117	TCCTCAGCATAACAGAGTTATAG
6118	CCTCAGCATAACAGAGTTATAGA
6119	CTCAGCATAACAGAGTTATAGAA
6120	TCAGCATAACAGAGTTATAGAAT
6121	CAGCATAACAGAGTTATAGAATG
6122	AGCATAACAGAGTTATAGAATGA
6123	GCATAACAGAGTTATAGAATGAC
6124	CATAACAGAGTTATAGAATGACA
6125	ATAACAGAGTTATAGAATGACAG
6126	TAACAGAGTTATAGAATGACAGG
6127	AACAGAGTTATAGAATGACAGGG
6128	ACAGAGTTATAGAATGACAGGGC
6129	CAGAGTTATAGAATGACAGGGCT
6130	AGAGTTATAGAATGACAGGGCTG
6131	GAGTTATAGAATGACAGGGCTGG
6132	AGTTATAGAATGACAGGGCTGGA
6133	GTTATAGAATGACAGGGCTGGAA
6134	TTATAGAATGACAGGGCTGGAAG
6135	TATAGAATGACAGGGCTGGAAGT
6136	ATAGAATGACAGGGCTGGAAGTG
6137	TAGAATGACAGGGCTGGAAGTGA
6138	AGAATGACAGGGCTGGAAGTGAC
6139	GAATGACAGGGCTGGAAGTGACC
6140	AATGACAGGGCTGGAAGTGACCT
6141	ATGACAGGGCTGGAAGTGACCTT
6142	TGACAGGGCTGGAAGTGACCTTA
6143	GACAGGGCTGGAAGTGACCTTAG
6144	ACAGGGCTGGAAGTGACCTTAGA

Fig. 29 cont'd (Sheet 128 of 170)

ID	SEQUENCE
6145	CAGGGCTGGAAGTGACCTTAGAG
6146	AGGGCTGGAAGTGACCTTAGAGA
6147	GGGCTGGAAGTGACCTTAGAGAG
6148	GGCTGGAAGTGACCTTAGAGAGT
6149	GCTGGAAGTGACCTTAGAGAGTA
6150	CTGGAAGTGACCTTAGAGAGTAT
6151	TGGAAGTGACCTTAGAGAGTATC
6152	GGAAGTGACCTTAGAGAGTATCC
6153	GAAGTGACCTTAGAGAGTATCCA
6154	AAGTGACCTTAGAGAGTATCCAG
6155	AGTGACCTTAGAGAGTATCCAGT
6156	GTGACCTTAGAGAGTATCCAGTT
6157	TGACCTTAGAGAGTATCCAGTTC
6158	GACCTTAGAGAGTATCCAGTTCT
6159	ACCTTAGAGAGTATCCAGTTCTT
6160	CCTTAGAGAGTATCCAGTTCTTT
6161	CTTAGAGAGTATCCAGTTCTTTC
6162	TTAGAGAGTATCCAGTTCTTTCA
6163	TAGAGAGTATCCAGTTCTTTCAT
6164	AGAGAGTATCCAGTTCTTTCATT
6165	GAGAGTATCCAGTTCTTTCATTT
6166	AGAGTATCCAGTTCTTTCATTTT
6167	GAGTATCCAGTTCTTTCATTTTA
6168	AGTATCCAGTTCTTTCATTTTAC
6169	GTATCCAGTTCTTTCATTTTACA
6170	TATCCAGTTCTTTCATTTTACAG
6171	ATCCAGTTCTTTCATTTTACAGG
6172	TCCAGTTCTTTCATTTTACAGGT
6173	CCAGTTCTTTCATTTTACAGGTG
6174	CAGTTCTTTCATTTTACAGGTGA
6175	AGTTCTTTCATTTTACAGGTGAG
6176	GTTCTTTCATTTTACAGGTGAGG
6177	TTCTTTCATTTTACAGGTGAGGC
6178	TCTTTCATTTTACAGGTGAGGCA
6179	CTTTCATTTTACAGGTGAGGCAA
6180	TTTCATTTTACAGGTGAGGCAAC
6181	TTCATTTTACAGGTGAGGCAACT
6182	TCATTTTACAGGTGAGGCAACTG
6183	CATTTTACAGGTGAGGCAACTGA
6184	ATTTTACAGGTGAGGCAACTGAG
6185	TTTTACAGGTGAGGCAACTGAGA
6186	TTTACAGGTGAGGCAACTGAGAC
6187	TTACAGGTGAGGCAACTGAGACT
6188	TACAGGTGAGGCAACTGAGACTC
6189	ACAGGTGAGGCAACTGAGACTCA
6190	CAGGTGAGGCAACTGAGACTCAA
6191	AGGTGAGGCAACTGAGACTCAAA
6192	GGTGAGGCAACTGAGACTCAAAG

Fig. 29 cont'd (Sheet 129 of 170)

ID	SEQUENCE
6193	GTGAGGCAACTGAGACTCAAAGG
6194	TGAGGCAACTGAGACTCAAAGGT
6195	GAGGCAACTGAGACTCAAAGGTG
6196	AGGCAACTGAGACTCAAAGGTGA
6197	GGCAACTGAGACTCAAAGGTGAT
6198	GCAACTGAGACTCAAAGGTGATG
6199	CAACTGAGACTCAAAGGTGATGT
6200	AACTGAGACTCAAAGGTGATGTA
6201	ACTGAGACTCAAAGGTGATGTAA
6202	CTGAGACTCAAAGGTGATGTAAT
6203	TGAGACTCAAAGGTGATGTAATT
6204	GAGACTCAAAGGTGATGTAATTT
6205	AGACTCAAAGGTGATGTAATTTG
6206	GACTCAAAGGTGATGTAATTTGT
6207	ACTCAAAGGTGATGTAATTTGTG
6208	CTCAAAGGTGATGTAATTTGTGC
6209	TCAAAGGTGATGTAATTTGTGCA
6210	CAAAGGTGATGTAATTTGTGCAA
6211	AAAGGTGATGTAATTTGTGCAAA
6212	AAGGTGATGTAATTTGTGCAAAG
6213	AGGTGATGTAATTTGTGCAAAGA
6214	GGTGATGTAATTTGTGCAAAGAT
6215	GTGATGTAATTTGTGCAAAGATT
6216	TGATGTAATTTGTGCAAAGATTA
6217	GATGTAATTTGTGCAAAGATTAT
6218	ATGTAATTTGTGCAAAGATTATA
6219	TGTAATTTGTGCAAAGATTATAG
6220	GTAATTTGTGCAAAGATTATAGC
6221	TAATTTGTGCAAAGATTATAGCT
6222	AATTTGTGCAAAGATTATAGCTA
6223	ATTTGTGCAAAGATTATAGCTAA
6224	TTTGTGCAAAGATTATAGCTAAT
6225	TTGTGCAAAGATTATAGCTAATT
6226	TGTGCAAAGATTATAGCTAATTA
6227	GTGCAAAGATTATAGCTAATTAG
6228	TGCAAAGATTATAGCTAATTAGT
6229	GCAAAGATTATAGCTAATTAGTA
6230	CAAAGATTATAGCTAATTAGTAG
6231	AAAGATTATAGCTAATTAGTAGC
6232	AAGATTATAGCTAATTAGTAGCA
6233	AGATTATAGCTAATTAGTAGCAG
6234	GATTATAGCTAATTAGTAGCAGA
6235	ATTATAGCTAATTAGTAGCAGAG
6236	TTATAGCTAATTAGTAGCAGAGC
6237	TATAGCTAATTAGTAGCAGAGCC
6238	ATAGCTAATTAGTAGCAGAGCCC
6239	TAGCTAATTAGTAGCAGAGCCCT
6240	AGCTAATTAGTAGCAGAGCCCTG

Fig. 29 cont'd (Sheet 130 of 170)

ID	SEQUENCE
6241	GCTAATTAGTAGCAGAGCCCTGA
6242	CTAATTAGTAGCAGAGCCCTGAC
6243	TAATTAGTAGCAGAGCCCTGACT
6244	AATTAGTAGCAGAGCCCTGACTG
6245	ATTAGTAGCAGAGCCCTGACTGG
6246	TTAGTAGCAGAGCCCTGACTGGG
6247	TAGTAGCAGAGCCCTGACTGGGA
6248	AGTAGCAGAGCCCTGACTGGGAC
6249	GTAGCAGAGCCCTGACTGGGACA
6250	TAGCAGAGCCCTGACTGGGACAT
6251	AGCAGAGCCCTGACTGGGACATA
6252	GCAGAGCCCTGACTGGGACATAG
6253	CAGAGCCCTGACTGGGACATAGT
6254	AGAGCCCTGACTGGGACATAGTT
6255	GAGCCCTGACTGGGACATAGTTT
6256	AGCCCTGACTGGGACATAGTTTG
6257	GCCCTGACTGGGACATAGTTTGA
6258	CCCTGACTGGGACATAGTTTGAA
6259	CCTGACTGGGACATAGTTTGAAG
6260	CTGACTGGGACATAGTTTGAAGG
6261	TGACTGGGACATAGTTTGAAGGT
6262	GACTGGGACATAGTTTGAAGGTG
6263	ACTGGGACATAGTTTGAAGGTGA
6264	CTGGGACATAGTTTGAAGGTGAA
6265	TGGGACATAGTTTGAAGGTGAAA
6266	GGGACATAGTTTGAAGGTGAAAA
6267	GGACATAGTTTGAAGGTGAAAAA
6268	GACATAGTTTGAAGGTGAAAAAC
6269	ACATAGTTTGAAGGTGAAAAACT
6270	CATAGTTTGAAGGTGAAAAACTT
6271	ATAGTTTGAAGGTGAAAAACTTC
6272	TAGTTTGAAGGTGAAAAACTTCA
6273	AGTTTGAAGGTGAAAAACTTCAC
6274	GTTTGAAGGTGAAAAACTTCACC
6275	TTTGAAGGTGAAAAACTTCACCA
6276	TTGAAGGTGAAAAACTTCACCAA
6277	TGAAGGTGAAAAACTTCACCAAG
6278	GAAGGTGAAAAACTTCACCAAGC
6279	AAGGTGAAAAACTTCACCAAGCT
6280	AGGTGAAAAACTTCACCAAGCTA
6281	GGTGAAAAACTTCACCAAGCTAC
6282	GTGAAAAACTTCACCAAGCTACC
6283	TGAAAAACTTCACCAAGCTACCT
6284	GAAAAACTTCACCAAGCTACCTT
6285	AAAAACTTCACCAAGCTACCTTT
6286	AAAACTTCACCAAGCTACCTTTC
6287	AAACTTCACCAAGCTACCTTTCT
6288	AACTTCACCAAGCTACCTTTCTT

Fig. 29 cont'd (Sheet 131 of 170)

ID	SEQUENCE
6289	ACTTCACCAAGCTACCTTTCTTG
6290	CTTCACCAAGCTACCTTTCTTGA
6291	TTCACCAAGCTACCTTTCTTGAA
6292	TCACCAAGCTACCTTTCTTGAAA
6293	CACCAAGCTACCTTTCTTGAAAG
6294	ACCAAGCTACCTTTCTTGAAAGG
6295	CCAAGCTACCTTTCTTGAAAGGT
6296	CAAGCTACCTTTCTTGAAAGGTC
6297	AAGCTACCTTTCTTGAAAGGTCC
6298	AGCTACCTTTCTTGAAAGGTCCA
6299	GCTACCTTTCTTGAAAGGTCCAA
6300	CTACCTTTCTTGAAAGGTCCAAA
6301	TACCTTTCTTGAAAGGTCCAAAT
6302	ACCTTTCTTGAAAGGTCCAAATG
6303	CCTTTCTTGAAAGGTCCAAATGT
6304	CTTTCTTGAAAGGTCCAAATGTT
6305	TTTCTTGAAAGGTCCAAATGTTT
6306	TTCTTGAAAGGTCCAAATGTTTA
6307	TCTTGAAAGGTCCAAATGTTTAT
6308	CTTGAAAGGTCCAAATGTTTATG
6309	TTGAAAGGTCCAAATGTTTATGT
6310	TGAAAGGTCCAAATGTTTATGTT
6311	GAAAGGTCCAAATGTTTATGTTT
6312	AAAGGTCCAAATGTTTATGTTTT
6313	AAGGTCCAAATGTTTATGTTTTC
6314	AGGTCCAAATGTTTATGTTTTCA
6315	GGTCCAAATGTTTATGTTTTCAA
6316	GTCCAAATGTTTATGTTTTCAAC
6317	TCCAAATGTTTATGTTTTCAACT
6318	CCAAATGTTTATGTTTTCAACTA
6319	CAAATGTTTATGTTTTCAACTAC
6320	AAATGTTTATGTTTTCAACTACT
6321	AATGTTTATGTTTTCAACTACTC
6322	ATGTTTATGTTTTCAACTACTCT
6323	TGTTTATGTTTTCAACTACTCTT
6324	GTTTATGTTTTCAACTACTCTTT
6325	TTTATGTTTTCAACTACTCTTTC
6326	TTATGTTTTCAACTACTCTTTCC
6327	TATGTTTTCAACTACTCTTTCCA
6328	ATGTTTTCAACTACTCTTTCCAC
6329	TGTTTTCAACTACTCTTTCCACT
6330	GTTTTCAACTACTCTTTCCACTG
6331	TTTTCAACTACTCTTTCCACTGT
6332	TTTCAACTACTCTTTCCACTGTA
6333	TTCAACTACTCTTTCCACTGTAC
6334	TCAACTACTCTTTCCACTGTACC
6335	CAACTACTCTTTCCACTGTACCA
6336	AACTACTCTTTCCACTGTACCAT

Fig. 29 cont'd (Sheet 132 of 170)

ID	SEQUENCE
6337	ACTACTCTTTCCACTGTACCATA
6338	CTACTCTTTCCACTGTACCATAA
6339	TACTCTTTCCACTGTACCATAAC
6340	ACTCTTTCCACTGTACCATAACT
6341	CTCTTTCCACTGTACCATAACTT
6342	TCTTTCCACTGTACCATAACTTT
6343	CTTTCCACTGTACCATAACTTTC
6344	TTTCCACTGTACCATAACTTTCA
6345	TTCCACTGTACCATAACTTTCAC
6346	TCCACTGTACCATAACTTTCACT
6347	CCACTGTACCATAACTTTCACTA
6348	CACTGTACCATAACTTTCACTAC
6349	ACTGTACCATAACTTTCACTACA
6350	CTGTACCATAACTTTCACTACAT
6351	TGTACCATAACTTTCACTACATA
6352	GTACCATAACTTTCACTACATAT
6353	TACCATAACTTTCACTACATATT
6354	ACCATAACTTTCACTACATATTA
6355	CCATAACTTTCACTACATATTAA
6356	CATAACTTTCACTACATATTAAA
6357	ATAACTTTCACTACATATTAAAT
6358	TAACTTTCACTACATATTAAATG
6359	AACTTTCACTACATATTAAATGA
6360	ACTTTCACTACATATTAAATGAC
6361	CTTTCACTACATATTAAATGACA
6362	TTTCACTACATATTAAATGACAC
6363	TTCACTACATATTAAATGACACT
6364	TCACTACATATTAAATGACACTT
6365	CACTACATATTAAATGACACTTT
6366	ACTACATATTAAATGACACTTTA
6367	CTACATATTAAATGACACTTTAT
6368	TACATATTAAATGACACTTTATA
6369	ACATATTAAATGACACTTTATAA
6370	CATATTAAATGACACTTTATAAC
6371	ATATTAAATGACACTTTATAACT
6372	TATTAAATGACACTTTATAACTA
6373	ATTAAATGACACTTTATAACTAA
6374	TTAAATGACACTTTATAACTAAT
6375	TAAATGACACTTTATAACTAATA
6376	AAATGACACTTTATAACTAATAT
6377	AATGACACTTTATAACTAATATA
6378	ATGACACTTTATAACTAATATAA
6379	TGACACTTTATAACTAATATAAT
6380	GACACTTTATAACTAATATAATA
6381	ACACTTTATAACTAATATAATAG
6382	CACTTTATAACTAATATAATAGG
6383	ACTTTATAACTAATATAATAGGA
6384	CTTTATAACTAATATAATAGGAC

Fig. 29 cont'd (Sheet 133 of 170)

ID	SEQUENCE
6385	TTTATAACTAATATAATAGGACA
6386	TTATAACTAATATAATAGGACAA
6387	TATAACTAATATAATAGGACAAT
6388	ATAACTAATATAATAGGACAATC
6389	TAACTAATATAATAGGACAATCA
6390	AACTAATATAATAGGACAATCAT
6391	ACTAATATAATAGGACAATCATC
6392	CTAATATAATAGGACAATCATCA
6393	TAATATAATAGGACAATCATCAA
6394	AATATAATAGGACAATCATCAAT
6395	ATATAATAGGACAATCATCAATG
6396	TATAATAGGACAATCATCAATGC
6397	ATAATAGGACAATCATCAATGCA
6398	TAATAGGACAATCATCAATGCAT
6399	AATAGGACAATCATCAATGCATA
6400	ATAGGACAATCATCAATGCATAT
6401	TAGGACAATCATCAATGCATATA
6402	AGGACAATCATCAATGCATATAT
6403	GGACAATCATCAATGCATATATA
6404	GACAATCATCAATGCATATATAG
6405	ACAATCATCAATGCATATATAGC
6406	CAATCATCAATGCATATATAGCC
6407	AATCATCAATGCATATATAGCCA
6408	ATCATCAATGCATATATAGCCAG
6409	TCATCAATGCATATATAGCCAGC
6410	CATCAATGCATATATAGCCAGCC
6411	ATCAATGCATATATAGCCAGCCC
6412	TCAATGCATATATAGCCAGCCCT
6413	CAATGCATATATAGCCAGCCCTT
6414	AATGCATATATAGCCAGCCCTTC
6415	ATGCATATATAGCCAGCCCTTCA
6416	TGCATATATAGCCAGCCCTTCAT
6417	GCATATATAGCCAGCCCTTCATA
6418	CATATATAGCCAGCCCTTCATAT
6419	ATATATAGCCAGCCCTTCATATC
6420	TATATAGCCAGCCCTTCATATCT
6421	ATATAGCCAGCCCTTCATATCTG
6422	TATAGCCAGCCCTTCATATCTGT
6423	ATAGCCAGCCCTTCATATCTGTG
6424	TAGCCAGCCCTTCATATCTGTGG
6425	AGCCAGCCCTTCATATCTGTGGG
6426	GCCAGCCCTTCATATCTGTGGGT
6427	CCAGCCCTTCATATCTGTGGGTT
6428	CAGCCCTTCATATCTGTGGGTTT
6429	AGCCCTTCATATCTGTGGGTTTT
6430	GCCCTTCATATCTGTGGGTTTTG
6431	CCCTTCATATCTGTGGGTTTTGC
6432	CCTTCATATCTGTGGGTTTTGCA

Fig. 29 cont'd (Sheet 134 of 170)

ID	SEQUENCE
6433	CTTCATATCTGTGGGTTTTGCAT
6434	TTCATATCTGTGGGTTTTGCATC
6435	TCATATCTGTGGGTTTTGCATCC
6436	CATATCTGTGGGTTTTGCATCCA
6437	ATATCTGTGGGTTTTGCATCCAT
6438	TATCTGTGGGTTTTGCATCCATG
6439	ATCTGTGGGTTTTGCATCCATGG
6440	TCTGTGGGTTTTGCATCCATGGA
6441	CTGTGGGTTTTGCATCCATGGAT
6442	TGTGGGTTTTGCATCCATGGATT
6443	GTGGGTTTTGCATCCATGGATTC
6444	TGGGTTTTGCATCCATGGATTCA
6445	GGGTTTTGCATCCATGGATTCAA
6446	GGTTTTGCATCCATGGATTCAAC
6447	GTTTTGCATCCATGGATTCAACC
6448	TTTTGCATCCATGGATTCAACCA
6449	TTTGCATCCATGGATTCAACCAA
6450	TTGCATCCATGGATTCAACCAAG
6451	TGCATCCATGGATTCAACCAAGG
6452	GCATCCATGGATTCAACCAAGGA
6453	CATCCATGGATTCAACCAAGGAG
6454	ATCCATGGATTCAACCAAGGAGG
6455	TCCATGGATTCAACCAAGGAGGA
6456	CCATGGATTCAACCAAGGAGGAA
6457	CATGGATTCAACCAAGGAGGAAT
6458	ATGGATTCAACCAAGGAGGAATT
6459	TGGATTCAACCAAGGAGGAATTG
6460	GGATTCAACCAAGGAGGAATTGA
6461	GATTCAACCAAGGAGGAATTGAA
6462	ATTCAACCAAGGAGGAATTGAAA
6463	TTCAACCAAGGAGGAATTGAAAA
6464	TCAACCAAGGAGGAATTGAAAAC
6465	CAACCAAGGAGGAATTGAAAACA
6466	AACCAAGGAGGAATTGAAAACAC
6467	ACCAAGGAGGAATTGAAAACACT
6468	CCAAGGAGGAATTGAAAACACTG
6469	CAAGGAGGAATTGAAAACACTGA
6470	AAGGAGGAATTGAAAACACTGAG
6471	AGGAGGAATTGAAAACACTGAGA
6472	GGAGGAATTGAAAACACTGAGAA
6473	GAGGAATTGAAAACACTGAGAAA
6474	AGGAATTGAAAACACTGAGAAAA
6475	GGAATTGAAAACACTGAGAAAAA
6476	GAATTGAAAACACTGAGAAAAAA
6477	AATTGAAAACACTGAGAAAAAAA
6478	ATTGAAAACACTGAGAAAAAAAA
6479	AAAAAAAAGACCACACAATAAAA
6480	AAAAAAAGACCACACAATAAAAA

Fig. 29 cont'd (Sheet 135 of 170)

ID	SEQUENCE
6481	AAAAAAGACCACACAATAAAAAA
6482	AAAAAGACCACACAATAAAAAAA
6483	AAAAGACCACACAATAAAAAAAA
6484	AAAAAAAATACAAAATAATACAA
6485	AAAAAAATACAAAATAATACAAA
6486	AAAAAATACAAAATAATACAAAG
6487	AAAAATACAAAATAATACAAAGA
6488	AAAATACAAAATAATACAAAGAA
6489	AAATACAAAATAATACAAAGAAA
6490	AATACAAAATAATACAAAGAAAA
6491	ATACAAAATAATACAAAGAAAAA
6492	TACAAAATAATACAAAGAAAAAG
6493	ACAAAATAATACAAAGAAAAAGC
6494	CAAAATAATACAAAGAAAAAGCC
6495	AAAATAATACAAAGAAAAAGCCA
6496	AAATAATACAAAGAAAAAGCCAA
6497	AATAATACAAAGAAAAAGCCAAA
6498	ATAATACAAAGAAAAAGCCAAAA
6499	TAATACAAAGAAAAAGCCAAAAT
6500	AATACAAAGAAAAAGCCAAAATT
6501	ATACAAAGAAAAAGCCAAAATTG
6502	TACAAAGAAAAAGCCAAAATTGT
6503	ACAAAGAAAAAGCCAAAATTGTC
6504	CAAAGAAAAAGCCAAAATTGTCA
6505	AAAGAAAAAGCCAAAATTGTCAT
6506	AAGAAAAAGCCAAAATTGTCATA
6507	AGAAAAAGCCAAAATTGTCATAC
6508	GAAAAAGCCAAAATTGTCATACT
6509	AAAAAGCCAAAATTGTCATACTG
6510	AAAAGCCAAAATTGTCATACTGT
6511	AAAGCCAAAATTGTCATACTGTT
6512	AAGCCAAAATTGTCATACTGTTG
6513	AGCCAAAATTGTCATACTGTTGT
6514	GCCAAAATTGTCATACTGTTGTT
6515	CCAAAATTGTCATACTGTTGTTA
6516	CAAAATTGTCATACTGTTGTTAA
6517	AAAATTGTCATACTGTTGTTAAG
6518	AAATTGTCATACTGTTGTTAAGC
6519	AATTGTCATACTGTTGTTAAGCA
6520	ATTGTCATACTGTTGTTAAGCAA
6521	TTGTCATACTGTTGTTAAGCAAC
6522	TGTCATACTGTTGTTAAGCAACA
6523	GTCATACTGTTGTTAAGCAACAG
6524	TCATACTGTTGTTAAGCAACAGT
6525	CATACTGTTGTTAAGCAACAGTA
6526	ATACTGTTGTTAAGCAACAGTAT
6527	TACTGTTGTTAAGCAACAGTATA
6528	ACTGTTGTTAAGCAACAGTATAA

Fig. 29 cont'd (Sheet 136 of 170)

ID	SEQUENCE
6529	CTGTTGTTAAGCAACAGTATAAC
6530	TGTTGTTAAGCAACAGTATAACA
6531	GTTGTTAAGCAACAGTATAACAA
6532	TTGTTAAGCAACAGTATAACAAC
6533	TGTTAAGCAACAGTATAACAACT
6534	GTTAAGCAACAGTATAACAACTA
6535	TTAAGCAACAGTATAACAACTAT
6536	TAAGCAACAGTATAACAACTATT
6537	AAGCAACAGTATAACAACTATTT
6538	AGCAACAGTATAACAACTATTTA
6539	GCAACAGTATAACAACTATTTAC
6540	CAACAGTATAACAACTATTTACA
6541	AACAGTATAACAACTATTTACAT
6542	ACAGTATAACAACTATTTACATA
6543	CAGTATAACAACTATTTACATAG
6544	AGTATAACAACTATTTACATAGC
6545	GTATAACAACTATTTACATAGCA
6546	TATAACAACTATTTACATAGCAT
6547	ATAACAACTATTTACATAGCATT
6548	TAACAACTATTTACATAGCATTA
6549	AACAACTATTTACATAGCATTAA
6550	ACAACTATTTACATAGCATTAAG
6551	CAACTATTTACATAGCATTAAGG
6552	AACTATTTACATAGCATTAAGGT
6553	ACTATTTACATAGCATTAAGGTT
6554	CTATTTACATAGCATTAAGGTTG
6555	TATTTACATAGCATTAAGGTTGG
6556	ATTTACATAGCATTAAGGTTGGT
6557	TTTACATAGCATTAAGGTTGGTG
6558	TTACATAGCATTAAGGTTGGTGC
6559	TACATAGCATTAAGGTTGGTGCA
6560	ACATAGCATTAAGGTTGGTGCAA
6561	CATAGCATTAAGGTTGGTGCAAA
6562	ATAGCATTAAGGTTGGTGCAAAA
6563	TAGCATTAAGGTTGGTGCAAAAA
6564	AGCATTAAGGTTGGTGCAAAAAT
6565	GCATTAAGGTTGGTGCAAAAATG
6566	CATTAAGGTTGGTGCAAAAATGC
6567	ATTAAGGTTGGTGCAAAAATGCA
6568	TTAAGGTTGGTGCAAAAATGCAA
6569	TAAGGTTGGTGCAAAAATGCAAA
6570	AAGGTTGGTGCAAAAATGCAAAA
6571	AGGTTGGTGCAAAAATGCAAAAA
6572	GGTTGGTGCAAAAATGCAAAAAA
6573	GTTGGTGCAAAAATGCAAAAAAA
6574	TTGGTGCAAAAATGCAAAAAAAA
6575	AAAAAAAAGCAATTATTTTTAAA
6576	AAAAAAAGCAATTATTTTTAAAC

Fig. 29 cont'd (Sheet 137 of 170)

ID	SEQUENCE
6577	AAAAAAGCAATTATTTTTAAACC
6578	AAAAAGCAATTATTTTTAAACCA
6579	AAAAGCAATTATTTTTAAACCAA
6580	AAAGCAATTATTTTTAAACCAAC
6581	AAGCAATTATTTTTAAACCAACC
6582	AGCAATTATTTTTAAACCAACCT
6583	GCAATTATTTTTAAACCAACCTA
6584	CAATTATTTTTAAACCAACCTAA
6585	AATTATTTTTAAACCAACCTAAT
6586	ATTATTTTTAAACCAACCTAATA
6587	TTATTTTTAAACCAACCTAATAT
6588	TATTTTTAAACCAACCTAATATA
6589	ATTTTTAAACCAACCTAATATAT
6590	TTTTTAAACCAACCTAATATATT
6591	TTTTAAACCAACCTAATATATTG
6592	TTTAAACCAACCTAATATATTGT
6593	TTAAACCAACCTAATATATTGTA
6594	TAAACCAACCTAATATATTGTAT
6595	AAACCAACCTAATATATTGTATT
6596	AACCAACCTAATATATTGTATTA
6597	ACCAACCTAATATATTGTATTAG
6598	CCAACCTAATATATTGTATTAGG
6599	CAACCTAATATATTGTATTAGGT
6600	AACCTAATATATTGTATTAGGTA
6601	ACCTAATATATTGTATTAGGTAT
6602	CCTAATATATTGTATTAGGTATT
6603	CTAATATATTGTATTAGGTATTA
6604	TAATATATTGTATTAGGTATTAA
6605	AATATATTGTATTAGGTATTAAA
6606	ATATATTGTATTAGGTATTAAAG
6607	TATATTGTATTAGGTATTAAAGT
6608	ATATTGTATTAGGTATTAAAGTC
6609	TATTGTATTAGGTATTAAAGTCA
6610	ATTGTATTAGGTATTAAAGTCAT
6611	TTGTATTAGGTATTAAAGTCATC
6612	TGTATTAGGTATTAAAGTCATCT
6613	GTATTAGGTATTAAAGTCATCTG
6614	TATTAGGTATTAAAGTCATCTGG
6615	ATTAGGTATTAAAGTCATCTGGA
6616	TTAGGTATTAAAGTCATCTGGAC
6617	TAGGTATTAAAGTCATCTGGACA
6618	AGGTATTAAAGTCATCTGGACAT
6619	GGTATTAAAGTCATCTGGACATG
6620	GTATTAAAGTCATCTGGACATGA
6621	TATTAAAGTCATCTGGACATGAA
6622	ATTAAAGTCATCTGGACATGAAT
6623	TTAAAGTCATCTGGACATGAATT
6624	TAAAGTCATCTGGACATGAATTA

Fig. 29 cont'd (Sheet 138 of 170)

ID	SEQUENCE
6625	AAAGTCATCTGGACATGAATTAA
6626	AAGTCATCTGGACATGAATTAAA
6627	AGTCATCTGGACATGAATTAAAG
6628	GTCATCTGGACATGAATTAAAGT
6629	TCATCTGGACATGAATTAAAGTA
6630	CATCTGGACATGAATTAAAGTAT
6631	ATCTGGACATGAATTAAAGTATA
6632	TCTGGACATGAATTAAAGTATAT
6633	CTGGACATGAATTAAAGTATATG
6634	TGGACATGAATTAAAGTATATGA
6635	GGACATGAATTAAAGTATATGAT
6636	GACATGAATTAAAGTATATGATG
6637	ACATGAATTAAAGTATATGATGC
6638	CATGAATTAAAGTATATGATGCC
6639	ATGAATTAAAGTATATGATGCCA
6640	TGAATTAAAGTATATGATGCCAG
6641	GAATTAAAGTATATGATGCCAGC
6642	AATTAAAGTATATGATGCCAGCC
6643	ATTAAAGTATATGATGCCAGCCT
6644	TTAAAGTATATGATGCCAGCCTG
6645	TAAAGTATATGATGCCAGCCTGG
6646	AAAGTATATGATGCCAGCCTGGA
6647	AAGTATATGATGCCAGCCTGGAC
6648	AGTATATGATGCCAGCCTGGACA
6649	GTATATGATGCCAGCCTGGACAA
6650	TATATGATGCCAGCCTGGACAAA
6651	ATATGATGCCAGCCTGGACAAAA
6652	TATGATGCCAGCCTGGACAAAAG
6653	ATGATGCCAGCCTGGACAAAAGG
6654	TGATGCCAGCCTGGACAAAAGGC
6655	GATGCCAGCCTGGACAAAAGGCA
6656	ATGCCAGCCTGGACAAAAGGCAA
6657	TGCCAGCCTGGACAAAAGGCAAA
6658	GCCAGCCTGGACAAAAGGCAAAA
6659	CCAGCCTGGACAAAAGGCAAAAC
6660	CAGCCTGGACAAAAGGCAAAACC
6661	AGCCTGGACAAAAGGCAAAACCC
6662	GCCTGGACAAAAGGCAAAACCCT
6663	CCTGGACAAAAGGCAAAACCCTG
6664	CTGGACAAAAGGCAAAACCCTGT
6665	TGGACAAAAGGCAAAACCCTGTC
6666	GGACAAAAGGCAAAACCCTGTCT
6667	GACAAAAGGCAAAACCCTGTCTC
6668	ACAAAAGGCAAAACCCTGTCTCT
6669	CAAAAGGCAAAACCCTGTCTCTA
6670	AAAAGGCAAAACCCTGTCTCTAC
6671	AAAGGCAAAACCCTGTCTCTACA
6672	AAGGCAAAACCCTGTCTCTACAA

Fig. 29 cont'd (Sheet 139 of 170)

ID	SEQUENCE
6673	AGGCAAAACCCTGTCTCTACAAA
6674	GGCAAAACCCTGTCTCTACAAAA
6675	GCAAAACCCTGTCTCTACAAAAA
6676	CAAAACCCTGTCTCTACAAAAAA
6677	AAAACCCTGTCTCTACAAAAAAT
6678	AAACCCTGTCTCTACAAAAAATA
6679	AACCCTGTCTCTACAAAAAATAC
6680	ACCCTGTCTCTACAAAAAATACA
6681	CCCTGTCTCTACAAAAAATACAA
6682	CCTGTCTCTACAAAAAATACAAA
6683	CTGTCTCTACAAAAAATACAAAA
6684	TGTCTCTACAAAAAATACAAAAA
6685	GTCTCTACAAAAAATACAAAAAT
6686	TCTCTACAAAAAATACAAAAATT
6687	CTCTACAAAAAATACAAAAATTA
6688	TCTACAAAAAATACAAAAATTAG
6689	CTACAAAAAATACAAAAATTAGC
6690	TACAAAAAATACAAAAATTAGCT
6691	ACAAAAAATACAAAAATTAGCTG
6692	CAAAAAATACAAAAATTAGCTGG
6693	AAAAAATACAAAAATTAGCTGGG
6694	AAAAATACAAAAATTAGCTGGGC
6695	AAAATACAAAAATTAGCTGGGCA
6696	AAATACAAAAATTAGCTGGGCAT
6697	AATACAAAAATTAGCTGGGCATG
6698	ATACAAAAATTAGCTGGGCATGG
6699	TACAAAAATTAGCTGGGCATGGT
6700	ACAAAAATTAGCTGGGCATGGTG
6701	CAAAAATTAGCTGGGCATGGTGG
6702	AAAAATTAGCTGGGCATGGTGGT
6703	AAAATTAGCTGGGCATGGTGGTG
6704	AAATTAGCTGGGCATGGTGGTGT
6705	AATTAGCTGGGCATGGTGGTGTG
6706	ATTAGCTGGGCATGGTGGTGTGT
6707	TTAGCTGGGCATGGTGGTGTGTG
6708	TAGCTGGGCATGGTGGTGTGTGC
6709	AGCTGGGCATGGTGGTGTGTGCC
6710	GCTGGGCATGGTGGTGTGTGCCT
6711	CTGGGCATGGTGGTGTGTGCCTG
6712	TGGGCATGGTGGTGTGTGCCTGT
6713	GGGCATGGTGGTGTGTGCCTGTA
6714	GGCATGGTGGTGTGTGCCTGTAG
6715	GCATGGTGGTGTGTGCCTGTAGT
6716	CATGGTGGTGTGTGCCTGTAGTC
6717	ATGGTGGTGTGTGCCTGTAGTCC
6718	TGGTGGTGTGTGCCTGTAGTCCT
6719	GGTGGTGTGTGCCTGTAGTCCTG
6720	GTGGTGTGTGCCTGTAGTCCTGG

Fig. 29 cont'd (Sheet 140 of 170)

ID	SEQUENCE
6721	TGGTGTGTGCCTGTAGTCCTGGC
6722	GGTGTGTGCCTGTAGTCCTGGCT
6723	GTGTGTGCCTGTAGTCCTGGCTA
6724	TGTGTGCCTGTAGTCCTGGCTAC
6725	GTGTGCCTGTAGTCCTGGCTACT
6726	TGTGCCTGTAGTCCTGGCTACTC
6727	GTGCCTGTAGTCCTGGCTACTCC
6728	TGCCTGTAGTCCTGGCTACTCCG
6729	GCCTGTAGTCCTGGCTACTCCGG
6730	CCTGTAGTCCTGGCTACTCCGGA
6731	CTGTAGTCCTGGCTACTCCGGAG
6732	TGTAGTCCTGGCTACTCCGGAGC
6733	GTAGTCCTGGCTACTCCGGAGCC
6734	TAGTCCTGGCTACTCCGGAGCCT
6735	AGTCCTGGCTACTCCGGAGCCTG
6736	GTCCTGGCTACTCCGGAGCCTGA
6737	TCCTGGCTACTCCGGAGCCTGAG
6738	CCTGGCTACTCCGGAGCCTGAGG
6739	CTGGCTACTCCGGAGCCTGAGGT
6740	TGGCTACTCCGGAGCCTGAGGTG
6741	GGCTACTCCGGAGCCTGAGGTGG
6742	GCTACTCCGGAGCCTGAGGTGGG
6743	CTACTCCGGAGCCTGAGGTGGGA
6744	TACTCCGGAGCCTGAGGTGGGAG
6745	ACTCCGGAGCCTGAGGTGGGAGG
6746	CTCCGGAGCCTGAGGTGGGAGGA
6747	TCCGGAGCCTGAGGTGGGAGGAT
6748	CCGGAGCCTGAGGTGGGAGGATC
6749	CGGAGCCTGAGGTGGGAGGATCG
6750	GGAGCCTGAGGTGGGAGGATCGC
6751	GAGCCTGAGGTGGGAGGATCGCT
6752	AGCCTGAGGTGGGAGGATCGCTT
6753	GCCTGAGGTGGGAGGATCGCTTG
6754	CCTGAGGTGGGAGGATCGCTTGA
6755	CTGAGGTGGGAGGATCGCTTGAG
6756	TGAGGTGGGAGGATCGCTTGAGT
6757	GAGGTGGGAGGATCGCTTGAGTC
6758	AGGTGGGAGGATCGCTTGAGTCT
6759	GGTGGGAGGATCGCTTGAGTCTG
6760	GTGGGAGGATCGCTTGAGTCTGG
6761	TGGGAGGATCGCTTGAGTCTGGG
6762	GGGAGGATCGCTTGAGTCTGGGA
6763	GGAGGATCGCTTGAGTCTGGGAG
6764	GAGGATCGCTTGAGTCTGGGAGG
6765	AGGATCGCTTGAGTCTGGGAGGC
6766	GGATCGCTTGAGTCTGGGAGGCA
6767	GATCGCTTGAGTCTGGGAGGCAG
6768	ATCGCTTGAGTCTGGGAGGCAGA

Fig. 29 cont'd (Sheet 141 of 170)

ID	SEQUENCE
6769	TCGCTTGAGTCTGGGAGGCAGAG
6770	CGCTTGAGTCTGGGAGGCAGAGG
6771	GCTTGAGTCTGGGAGGCAGAGGC
6772	CTTGAGTCTGGGAGGCAGAGGCT
6773	TTGAGTCTGGGAGGCAGAGGCTG
6774	TGAGTCTGGGAGGCAGAGGCTGC
6775	GAGTCTGGGAGGCAGAGGCTGCA
6776	AGTCTGGGAGGCAGAGGCTGCAT
6777	GTCTGGGAGGCAGAGGCTGCATT
6778	TCTGGGAGGCAGAGGCTGCATTG
6779	CTGGGAGGCAGAGGCTGCATTGA
6780	TGGGAGGCAGAGGCTGCATTGAG
6781	GGGAGGCAGAGGCTGCATTGAGC
6782	GGAGGCAGAGGCTGCATTGAGCT
6783	GAGGCAGAGGCTGCATTGAGCTA
6784	AGGCAGAGGCTGCATTGAGCTAT
6785	GGCAGAGGCTGCATTGAGCTATG
6786	GCAGAGGCTGCATTGAGCTATGA
6787	CAGAGGCTGCATTGAGCTATGAT
6788	AGAGGCTGCATTGAGCTATGATC
6789	GAGGCTGCATTGAGCTATGATCA
6790	AGGCTGCATTGAGCTATGATCAT
6791	GGCTGCATTGAGCTATGATCATG
6792	GCTGCATTGAGCTATGATCATGG
6793	CTGCATTGAGCTATGATCATGGC
6794	TGCATTGAGCTATGATCATGGCA
6795	GCATTGAGCTATGATCATGGCAC
6796	CATTGAGCTATGATCATGGCACT
6797	ATTGAGCTATGATCATGGCACTG
6798	TTGAGCTATGATCATGGCACTGC
6799	TGAGCTATGATCATGGCACTGCA
6800	GAGCTATGATCATGGCACTGCAT
6801	AGCTATGATCATGGCACTGCATT
6802	GCTATGATCATGGCACTGCATTC
6803	CTATGATCATGGCACTGCATTCC
6804	TATGATCATGGCACTGCATTCCA
6805	ATGATCATGGCACTGCATTCCAG
6806	TGATCATGGCACTGCATTCCAGC
6807	GATCATGGCACTGCATTCCAGCC
6808	ATCATGGCACTGCATTCCAGCCT
6809	TCATGGCACTGCATTCCAGCCTG
6810	CATGGCACTGCATTCCAGCCTGG
6811	ATGGCACTGCATTCCAGCCTGGG
6812	TGGCACTGCATTCCAGCCTGGGT
6813	GGCACTGCATTCCAGCCTGGGTG
6814	GCACTGCATTCCAGCCTGGGTGA
6815	CACTGCATTCCAGCCTGGGTGAC
6816	ACTGCATTCCAGCCTGGGTGACA

Fig. 29 cont'd (Sheet 142 of 170)

ID	SEQUENCE
6817	CTGCATTCCAGCCTGGGTGACAG
6818	TGCATTCCAGCCTGGGTGACAGT
6819	GCATTCCAGCCTGGGTGACAGTG
6820	CATTCCAGCCTGGGTGACAGTGC
6821	ATTCCAGCCTGGGTGACAGTGCA
6822	TTCCAGCCTGGGTGACAGTGCAA
6823	TCCAGCCTGGGTGACAGTGCAAG
6824	CCAGCCTGGGTGACAGTGCAAGA
6825	CAGCCTGGGTGACAGTGCAAGAC
6826	AGCCTGGGTGACAGTGCAAGACC
6827	GCCTGGGTGACAGTGCAAGACCT
6828	CCTGGGTGACAGTGCAAGACCTT
6829	CTGGGTGACAGTGCAAGACCTTG
6830	TGGGTGACAGTGCAAGACCTTGT
6831	GGGTGACAGTGCAAGACCTTGTC
6832	GGTGACAGTGCAAGACCTTGTCT
6833	GTGACAGTGCAAGACCTTGTCTC
6834	TGACAGTGCAAGACCTTGTCTCA
6835	GACAGTGCAAGACCTTGTCTCAG
6836	ACAGTGCAAGACCTTGTCTCAGA
6837	CAGTGCAAGACCTTGTCTCAGAA
6838	AGTGCAAGACCTTGTCTCAGAAT
6839	GTGCAAGACCTTGTCTCAGAATA
6840	TGCAAGACCTTGTCTCAGAATAA
6841	GCAAGACCTTGTCTCAGAATAAA
6842	CAAGACCTTGTCTCAGAATAAAT
6843	AAGACCTTGTCTCAGAATAAATA
6844	AGACCTTGTCTCAGAATAAATAA
6845	GACCTTGTCTCAGAATAAATAAA
6846	ACCTTGTCTCAGAATAAATAAAG
6847	CCTTGTCTCAGAATAAATAAAGT
6848	CTTGTCTCAGAATAAATAAAGTA
6849	TTGTCTCAGAATAAATAAAGTAT
6850	TGTCTCAGAATAAATAAAGTATG
6851	GTCTCAGAATAAATAAAGTATGT
6852	TCTCAGAATAAATAAAGTATGTG
6853	CTCAGAATAAATAAAGTATGTGA
6854	TCAGAATAAATAAAGTATGTGAT
6855	CAGAATAAATAAAGTATGTGATG
6856	AGAATAAATAAAGTATGTGATGA
6857	GAATAAATAAAGTATGTGATGAA
6858	AATAAATAAAGTATGTGATGAAG
6859	ATAAATAAAGTATGTGATGAAGA
6860	TAAATAAAGTATGTGATGAAGAT
6861	AAATAAAGTATGTGATGAAGATG
6862	AATAAAGTATGTGATGAAGATGT
6863	ATAAAGTATGTGATGAAGATGTG
6864	TAAAGTATGTGATGAAGATGTGC

Fig. 29 cont'd (Sheet 143 of 170)

ID	SEQUENCE
6865	AAAGTATGTGATGAAGATGTGCA
6866	AAGTATGTGATGAAGATGTGCAT
6867	AGTATGTGATGAAGATGTGCATA
6868	GTATGTGATGAAGATGTGCATAC
6869	TATGTGATGAAGATGTGCATACA
6870	ATGTGATGAAGATGTGCATACAT
6871	TGTGATGAAGATGTGCATACATT
6872	GTGATGAAGATGTGCATACATTA
6873	TGATGAAGATGTGCATACATTAT
6874	GATGAAGATGTGCATACATTATA
6875	ATGAAGATGTGCATACATTATAT
6876	TGAAGATGTGCATACATTATATG
6877	GAAGATGTGCATACATTATATGC
6878	AAGATGTGCATACATTATATGCA
6879	AGATGTGCATACATTATATGCAA
6880	GATGTGCATACATTATATGCAAA
6881	ATGTGCATACATTATATGCAAAT
6882	TGTGCATACATTATATGCAAATA
6883	GTGCATACATTATATGCAAATAC
6884	TGCATACATTATATGCAAATACT
6885	GCATACATTATATGCAAATACTG
6886	CATACATTATATGCAAATACTGT
6887	ATACATTATATGCAAATACTGTT
6888	TACATTATATGCAAATACTGTTT
6889	ACATTATATGCAAATACTGTTTT
6890	CATTATATGCAAATACTGTTTTT
6891	ATTATATGCAAATACTGTTTTTT
6892	TTATATGCAAATACTGTTTTTTT
6893	TATATGCAAATACTGTTTTTTTT
6894	TTTTTTTTAATTTAAACAGTCTC
6895	TTTTTTTAATTTAAACAGTCTCA
6896	TTTTTTAATTTAAACAGTCTCAC
6897	TTTTTAATTTAAACAGTCTCACT
6898	TTTTAATTTAAACAGTCTCACTG
6899	TTTAATTTAAACAGTCTCACTGT
6900	TTAATTTAAACAGTCTCACTGTG
6901	TAATTTAAACAGTCTCACTGTGT
6902	AATTTAAACAGTCTCACTGTGTT
6903	ATTTAAACAGTCTCACTGTGTTG
6904	TTTAAACAGTCTCACTGTGTTGC
6905	TTAAACAGTCTCACTGTGTTGCC
6906	TAAACAGTCTCACTGTGTTGCCC
6907	AAACAGTCTCACTGTGTTGCCCA
6908	AACAGTCTCACTGTGTTGCCCAG
6909	ACAGTCTCACTGTGTTGCCCAGG
6910	CAGTCTCACTGTGTTGCCCAGGA
6911	AGTCTCACTGTGTTGCCCAGGAT
6912	GTCTCACTGTGTTGCCCAGGATG

Fig. 29 cont'd (Sheet 144 of 170)

ID	SEQUENCE
6913	TCTCACTGTGTTGCCCAGGATGG
6914	CTCACTGTGTTGCCCAGGATGGA
6915	TCACTGTGTTGCCCAGGATGGAG
6916	CACTGTGTTGCCCAGGATGGAGT
6917	ACTGTGTTGCCCAGGATGGAGTG
6918	CTGTGTTGCCCAGGATGGAGTGC
6919	TGTGTTGCCCAGGATGGAGTGCA
6920	GTGTTGCCCAGGATGGAGTGCAA
6921	TGTTGCCCAGGATGGAGTGCAAT
6922	GTTGCCCAGGATGGAGTGCAATG
6923	TTGCCCAGGATGGAGTGCAATGG
6924	TGCCCAGGATGGAGTGCAATGGC
6925	GCCCAGGATGGAGTGCAATGGCA
6926	CCCAGGATGGAGTGCAATGGCAC
6927	CCAGGATGGAGTGCAATGGCACA
6928	CAGGATGGAGTGCAATGGCACAA
6929	AGGATGGAGTGCAATGGCACAAT
6930	GGATGGAGTGCAATGGCACAATC
6931	GATGGAGTGCAATGGCACAATCT
6932	ATGGAGTGCAATGGCACAATCTT
6933	TGGAGTGCAATGGCACAATCTTG
6934	GGAGTGCAATGGCACAATCTTGG
6935	GAGTGCAATGGCACAATCTTGGC
6936	AGTGCAATGGCACAATCTTGGCT
6937	GTGCAATGGCACAATCTTGGCTC
6938	TGCAATGGCACAATCTTGGCTCA
6939	GCAATGGCACAATCTTGGCTCAT
6940	CAATGGCACAATCTTGGCTCATG
6941	AATGGCACAATCTTGGCTCATGG
6942	ATGGCACAATCTTGGCTCATGGC
6943	TGGCACAATCTTGGCTCATGGCA
6944	GGCACAATCTTGGCTCATGGCAA
6945	GCACAATCTTGGCTCATGGCAAA
6946	CACAATCTTGGCTCATGGCAAAC
6947	ACAATCTTGGCTCATGGCAAACT
6948	CAATCTTGGCTCATGGCAAACTC
6949	AATCTTGGCTCATGGCAAACTCT
6950	ATCTTGGCTCATGGCAAACTCTG
6951	TCTTGGCTCATGGCAAACTCTGC
6952	CTTGGCTCATGGCAAACTCTGCC
6953	TTGGCTCATGGCAAACTCTGCCT
6954	TGGCTCATGGCAAACTCTGCCTC
6955	GGCTCATGGCAAACTCTGCCTCG
6956	GCTCATGGCAAACTCTGCCTCGC
6957	CTCATGGCAAACTCTGCCTCGCA
6958	TCATGGCAAACTCTGCCTCGCAA
6959	CATGGCAAACTCTGCCTCGCAAG
6960	ATGGCAAACTCTGCCTCGCAAGC

Fig. 29 cont'd (Sheet 145 of 170)

ID	SEQUENCE
6961	TGGCAAACTCTGCCTCGCAAGCA
6962	GGCAAACTCTGCCTCGCAAGCAG
6963	GCAAACTCTGCCTCGCAAGCAGC
6964	CAAACTCTGCCTCGCAAGCAGCT
6965	AAACTCTGCCTCGCAAGCAGCTG
6966	AACTCTGCCTCGCAAGCAGCTGG
6967	ACTCTGCCTCGCAAGCAGCTGGG
6968	CTCTGCCTCGCAAGCAGCTGGGA
6969	TCTGCCTCGCAAGCAGCTGGGAC
6970	CTGCCTCGCAAGCAGCTGGGACT
6971	TGCCTCGCAAGCAGCTGGGACTA
6972	GCCTCGCAAGCAGCTGGGACTAC
6973	CCTCGCAAGCAGCTGGGACTACA
6974	CTCGCAAGCAGCTGGGACTACAG
6975	TCGCAAGCAGCTGGGACTACAGG
6976	CGCAAGCAGCTGGGACTACAGGC
6977	GCAAGCAGCTGGGACTACAGGCA
6978	CAAGCAGCTGGGACTACAGGCAT
6979	AAGCAGCTGGGACTACAGGCATG
6980	AGCAGCTGGGACTACAGGCATGC
6981	GCAGCTGGGACTACAGGCATGCT
6982	CAGCTGGGACTACAGGCATGCTC
6983	AGCTGGGACTACAGGCATGCTCC
6984	GCTGGGACTACAGGCATGCTCCA
6985	CTGGGACTACAGGCATGCTCCAC
6986	TGGGACTACAGGCATGCTCCACG
6987	GGGACTACAGGCATGCTCCACGG
6988	GGACTACAGGCATGCTCCACGGT
6989	GACTACAGGCATGCTCCACGGTG
6990	ACTACAGGCATGCTCCACGGTGC
6991	CTACAGGCATGCTCCACGGTGCC
6992	TACAGGCATGCTCCACGGTGCCC
6993	ACAGGCATGCTCCACGGTGCCCA
6994	CAGGCATGCTCCACGGTGCCCAG
6995	AGGCATGCTCCACGGTGCCCAGT
6996	GGCATGCTCCACGGTGCCCAGTT
6997	GCATGCTCCACGGTGCCCAGTTA
6998	CATGCTCCACGGTGCCCAGTTAA
6999	ATGCTCCACGGTGCCCAGTTAAT
7000	TGCTCCACGGTGCCCAGTTAATT
7001	GCTCCACGGTGCCCAGTTAATTT
7002	CTCCACGGTGCCCAGTTAATTTT
7003	TCCACGGTGCCCAGTTAATTTTT
7004	CCACGGTGCCCAGTTAATTTTTT
7005	CACGGTGCCCAGTTAATTTTTTT
7006	ACGGTGCCCAGTTAATTTTTTTT
7007	CGGTGCCCAGTTAATTTTTTTTG
7008	GGTGCCCAGTTAATTTTTTTTGT

Fig. 29 cont'd (Sheet 146 of 170)

ID	SEQUENCE
7009	GTGCCCAGTTAATTTTTTTTGTA
7010	TGCCCAGTTAATTTTTTTTGTAT
7011	GCCCAGTTAATTTTTTTTGTATT
7012	CCCAGTTAATTTTTTTTGTATTC
7013	CCAGTTAATTTTTTTTGTATTCT
7014	CAGTTAATTTTTTTTGTATTCTT
7015	AGTTAATTTTTTTTGTATTCTTA
7016	GTTAATTTTTTTTGTATTCTTAG
7017	TTAATTTTTTTTGTATTCTTAGT
7018	TAATTTTTTTTGTATTCTTAGTA
7019	AATTTTTTTTGTATTCTTAGTAG
7020	ATTTTTTTTGTATTCTTAGTAGA
7021	TTTTTTTTGTATTCTTAGTAGAG
7022	TTTTTTTGTATTCTTAGTAGAGA
7023	TTTTTTGTATTCTTAGTAGAGAC
7024	TTTTTGTATTCTTAGTAGAGACA
7025	TTTTGTATTCTTAGTAGAGACAG
7026	TTTGTATTCTTAGTAGAGACAGG
7027	TTGTATTCTTAGTAGAGACAGGG
7028	TGTATTCTTAGTAGAGACAGGGT
7029	GTATTCTTAGTAGAGACAGGGTT
7030	TATTCTTAGTAGAGACAGGGTTT
7031	ATTCTTAGTAGAGACAGGGTTTC
7032	TTCTTAGTAGAGACAGGGTTTCA
7033	TCTTAGTAGAGACAGGGTTTCAC
7034	CTTAGTAGAGACAGGGTTTCACC
7035	TTAGTAGAGACAGGGTTTCACCA
7036	TAGTAGAGACAGGGTTTCACCAT
7037	AGTAGAGACAGGGTTTCACCATG
7038	GTAGAGACAGGGTTTCACCATGT
7039	TAGAGACAGGGTTTCACCATGTT
7040	AGAGACAGGGTTTCACCATGTTG
7041	GAGACAGGGTTTCACCATGTTGG
7042	AGACAGGGTTTCACCATGTTGGC
7043	GACAGGGTTTCACCATGTTGGCC
7044	ACAGGGTTTCACCATGTTGGCCA
7045	CAGGGTTTCACCATGTTGGCCAG
7046	AGGGTTTCACCATGTTGGCCAGG
7047	GGGTTTCACCATGTTGGCCAGGC
7048	GGTTTCACCATGTTGGCCAGGCT
7049	GTTTCACCATGTTGGCCAGGCTA
7050	TTTCACCATGTTGGCCAGGCTAG
7051	TTCACCATGTTGGCCAGGCTAGT
7052	TCACCATGTTGGCCAGGCTAGTC
7053	CACCATGTTGGCCAGGCTAGTCT
7054	ACCATGTTGGCCAGGCTAGTCTT
7055	CCATGTTGGCCAGGCTAGTCTTG
7056	CATGTTGGCCAGGCTAGTCTTGA

Fig. 29 cont'd (Sheet 147 of 170)

ID	SEQUENCE
7057	ATGTTGGCCAGGCTAGTCTTGAA
7058	TGTTGGCCAGGCTAGTCTTGAAT
7059	GTTGGCCAGGCTAGTCTTGAATT
7060	TTGGCCAGGCTAGTCTTGAATTT
7061	TGGCCAGGCTAGTCTTGAATTTC
7062	GGCCAGGCTAGTCTTGAATTTCT
7063	GCCAGGCTAGTCTTGAATTTCTG
7064	CCAGGCTAGTCTTGAATTTCTGA
7065	CAGGCTAGTCTTGAATTTCTGAC
7066	AGGCTAGTCTTGAATTTCTGACC
7067	GGCTAGTCTTGAATTTCTGACCT
7068	GCTAGTCTTGAATTTCTGACCTC
7069	CTAGTCTTGAATTTCTGACCTCA
7070	TAGTCTTGAATTTCTGACCTCAA
7071	AGTCTTGAATTTCTGACCTCAAG
7072	GTCTTGAATTTCTGACCTCAAGT
7073	TCTTGAATTTCTGACCTCAAGTG
7074	CTTGAATTTCTGACCTCAAGTGA
7075	TTGAATTTCTGACCTCAAGTGAT
7076	TGAATTTCTGACCTCAAGTGATT
7077	GAATTTCTGACCTCAAGTGATTC
7078	AATTTCTGACCTCAAGTGATTCA
7079	ATTTCTGACCTCAAGTGATTCAT
7080	TTTCTGACCTCAAGTGATTCATC
7081	TTCTGACCTCAAGTGATTCATCT
7082	TCTGACCTCAAGTGATTCATCTC
7083	CTGACCTCAAGTGATTCATCTCC
7084	TGACCTCAAGTGATTCATCTCCC
7085	GACCTCAAGTGATTCATCTCCCA
7086	ACCTCAAGTGATTCATCTCCCAA
7087	CCTCAAGTGATTCATCTCCCAAA
7088	CTCAAGTGATTCATCTCCCAAAG
7089	TCAAGTGATTCATCTCCCAAAGT
7090	CAAGTGATTCATCTCCCAAAGTG
7091	AAGTGATTCATCTCCCAAAGTGC
7092	AGTGATTCATCTCCCAAAGTGCT
7093	GTGATTCATCTCCCAAAGTGCTG
7094	TGATTCATCTCCCAAAGTGCTGG
7095	GATTCATCTCCCAAAGTGCTGGG
7096	ATTCATCTCCCAAAGTGCTGGGA
7097	TTCATCTCCCAAAGTGCTGGGAT
7098	TCATCTCCCAAAGTGCTGGGATT
7099	CATCTCCCAAAGTGCTGGGATTA
7100	ATCTCCCAAAGTGCTGGGATTAC
7101	TCTCCCAAAGTGCTGGGATTACA
7102	CTCCCAAAGTGCTGGGATTACAG
7103	TCCCAAAGTGCTGGGATTACAGG
7104	CCCAAAGTGCTGGGATTACAGGC

Fig. 29 cont'd (Sheet 148 of 170)

ID	SEQUENCE
7105	CCAAAGTGCTGGGATTACAGGCG
7106	CAAAGTGCTGGGATTACAGGCGT
7107	AAAGTGCTGGGATTACAGGCGTG
7108	AAGTGCTGGGATTACAGGCGTGA
7109	AGTGCTGGGATTACAGGCGTGAG
7110	GTGCTGGGATTACAGGCGTGAGC
7111	TGCTGGGATTACAGGCGTGAGCC
7112	GCTGGGATTACAGGCGTGAGCCA
7113	CTGGGATTACAGGCGTGAGCCAC
7114	TGGGATTACAGGCGTGAGCCACC
7115	GGGATTACAGGCGTGAGCCACCA
7116	GGATTACAGGCGTGAGCCACCAC
7117	GATTACAGGCGTGAGCCACCACG
7118	ATTACAGGCGTGAGCCACCACGG
7119	TTACAGGCGTGAGCCACCACGGC
7120	TACAGGCGTGAGCCACCACGGCC
7121	ACAGGCGTGAGCCACCACGGCCG
7122	CAGGCGTGAGCCACCACGGCCGG
7123	AGGCGTGAGCCACCACGGCCGGC
7124	GGCGTGAGCCACCACGGCCGGCT
7125	GCGTGAGCCACCACGGCCGGCTA
7126	CGTGAGCCACCACGGCCGGCTAA
7127	GTGAGCCACCACGGCCGGCTAAT
7128	TGAGCCACCACGGCCGGCTAATT
7129	GAGCCACCACGGCCGGCTAATTT
7130	AGCCACCACGGCCGGCTAATTTT
7131	GCCACCACGGCCGGCTAATTTTT
7132	CCACCACGGCCGGCTAATTTTTG
7133	CACCACGGCCGGCTAATTTTTGT
7134	ACCACGGCCGGCTAATTTTTGTA
7135	CCACGGCCGGCTAATTTTTGTAT
7136	CACGGCCGGCTAATTTTTGTATT
7137	ACGGCCGGCTAATTTTTGTATTT
7138	CGGCCGGCTAATTTTTGTATTTT
7139	GGCCGGCTAATTTTTGTATTTTT
7140	GCCGGCTAATTTTTGTATTTTTT
7141	CCGGCTAATTTTTGTATTTTTTA
7142	CGGCTAATTTTTGTATTTTTTAG
7143	GGCTAATTTTTGTATTTTTTAGT
7144	GCTAATTTTTGTATTTTTTAGTA
7145	CTAATTTTTGTATTTTTTAGTAG
7146	TAATTTTTGTATTTTTTAGTAGT
7147	AATTTTTGTATTTTTTAGTAGTG
7148	ATTTTTGTATTTTTTAGTAGTGA
7149	TTTTTGTATTTTTTAGTAGTGAC
7150	TTTTGTATTTTTTAGTAGTGACT
7151	TTTGTATTTTTTAGTAGTGACTG
7152	TTGTATTTTTTAGTAGTGACTGG

Fig. 29 cont'd (Sheet 149 of 170)

ID	SEQUENCE
7153	TGTATTTTTTAGTAGTGACTGGT
7154	GTATTTTTTAGTAGTGACTGGTT
7155	TATTTTTTAGTAGTGACTGGTTT
7156	ATTTTTTAGTAGTGACTGGTTTC
7157	TTTTTTAGTAGTGACTGGTTTCG
7158	TTTTTAGTAGTGACTGGTTTCGC
7159	TTTTAGTAGTGACTGGTTTCGCG
7160	TTTAGTAGTGACTGGTTTCGCGG
7161	TTAGTAGTGACTGGTTTCGCGGT
7162	TAGTAGTGACTGGTTTCGCGGTG
7163	AGTAGTGACTGGTTTCGCGGTGT
7164	GTAGTGACTGGTTTCGCGGTGTT
7165	TAGTGACTGGTTTCGCGGTGTTG
7166	AGTGACTGGTTTCGCGGTGTTGA
7167	GTGACTGGTTTCGCGGTGTTGAC
7168	TGACTGGTTTCGCGGTGTTGACC
7169	GACTGGTTTCGCGGTGTTGACCA
7170	ACTGGTTTCGCGGTGTTGACCAG
7171	CTGGTTTCGCGGTGTTGACCAGG
7172	TGGTTTCGCGGTGTTGACCAGGC
7173	GGTTTCGCGGTGTTGACCAGGCT
7174	GTTTCGCGGTGTTGACCAGGCTG
7175	TTTCGCGGTGTTGACCAGGCTGG
7176	TTCGCGGTGTTGACCAGGCTGGT
7177	TCGCGGTGTTGACCAGGCTGGTC
7178	CGCGGTGTTGACCAGGCTGGTCT
7179	GCGGTGTTGACCAGGCTGGTCTC
7180	CGGTGTTGACCAGGCTGGTCTCG
7181	GGTGTTGACCAGGCTGGTCTCGA
7182	GTGTTGACCAGGCTGGTCTCGAA
7183	TGTTGACCAGGCTGGTCTCGAAC
7184	GTTGACCAGGCTGGTCTCGAACT
7185	TTGACCAGGCTGGTCTCGAACTC
7186	TGACCAGGCTGGTCTCGAACTCC
7187	GACCAGGCTGGTCTCGAACTCCT
7188	ACCAGGCTGGTCTCGAACTCCTG
7189	CCAGGCTGGTCTCGAACTCCTGA
7190	CAGGCTGGTCTCGAACTCCTGAT
7191	AGGCTGGTCTCGAACTCCTGATC
7192	GGCTGGTCTCGAACTCCTGATCT
7193	GCTGGTCTCGAACTCCTGATCTC
7194	CTGGTCTCGAACTCCTGATCTCA
7195	TGGTCTCGAACTCCTGATCTCAG
7196	GGTCTCGAACTCCTGATCTCAGG
7197	GTCTCGAACTCCTGATCTCAGGT
7198	TCTCGAACTCCTGATCTCAGGTG
7199	CTCGAACTCCTGATCTCAGGTGA
7200	TCGAACTCCTGATCTCAGGTGAT

Fig. 29 cont'd (Sheet 150 of 170)

ID	SEQUENCE
7201	CGAACTCCTGATCTCAGGTGATC
7202	GAACTCCTGATCTCAGGTGATCT
7203	AACTCCTGATCTCAGGTGATCTG
7204	ACTCCTGATCTCAGGTGATCTGC
7205	CTCCTGATCTCAGGTGATCTGCC
7206	TCCTGATCTCAGGTGATCTGCCT
7207	CCTGATCTCAGGTGATCTGCCTG
7208	CTGATCTCAGGTGATCTGCCTGC
7209	TGATCTCAGGTGATCTGCCTGCC
7210	GATCTCAGGTGATCTGCCTGCCT
7211	ATCTCAGGTGATCTGCCTGCCTC
7212	TCTCAGGTGATCTGCCTGCCTCG
7213	CTCAGGTGATCTGCCTGCCTCGG
7214	TCAGGTGATCTGCCTGCCTCGGC
7215	CAGGTGATCTGCCTGCCTCGGCC
7216	AGGTGATCTGCCTGCCTCGGCCT
7217	GGTGATCTGCCTGCCTCGGCCTC
7218	GTGATCTGCCTGCCTCGGCCTCA
7219	TGATCTGCCTGCCTCGGCCTCAC
7220	GATCTGCCTGCCTCGGCCTCACA
7221	ATCTGCCTGCCTCGGCCTCACAA
7222	TCTGCCTGCCTCGGCCTCACAAA
7223	CTGCCTGCCTCGGCCTCACAAAG
7224	TGCCTGCCTCGGCCTCACAAAGT
7225	GCCTGCCTCGGCCTCACAAAGTG
7226	CCTGCCTCGGCCTCACAAAGTGC
7227	CTGCCTCGGCCTCACAAAGTGCT
7228	TGCCTCGGCCTCACAAAGTGCTG
7229	GCCTCGGCCTCACAAAGTGCTGG
7230	CCTCGGCCTCACAAAGTGCTGGG
7231	CTCGGCCTCACAAAGTGCTGGGA
7232	TCGGCCTCACAAAGTGCTGGGAT
7233	CGGCCTCACAAAGTGCTGGGATT
7234	GGCCTCACAAAGTGCTGGGATTA
7235	GCCTCACAAAGTGCTGGGATTAC
7236	CCTCACAAAGTGCTGGGATTACA
7237	CTCACAAAGTGCTGGGATTACAG
7238	TCACAAAGTGCTGGGATTACAGG
7239	CACAAAGTGCTGGGATTACAGGT
7240	ACAAAGTGCTGGGATTACAGGTG
7241	CAAAGTGCTGGGATTACAGGTGT
7242	AAAGTGCTGGGATTACAGGTGTG
7243	AAGTGCTGGGATTACAGGTGTGA
7244	AGTGCTGGGATTACAGGTGTGAA
7245	GTGCTGGGATTACAGGTGTGAAC
7246	TGCTGGGATTACAGGTGTGAACC
7247	GCTGGGATTACAGGTGTGAACCA
7248	CTGGGATTACAGGTGTGAACCAC

Fig. 29 cont'd (Sheet 151 of 170)

ID	SEQUENCE
7249	TGGGATTACAGGTGTGAACCACT
7250	GGGATTACAGGTGTGAACCACTG
7251	GGATTACAGGTGTGAACCACTGC
7252	GATTACAGGTGTGAACCACTGCT
7253	ATTACAGGTGTGAACCACTGCTC
7254	TTACAGGTGTGAACCACTGCTCC
7255	TACAGGTGTGAACCACTGCTCCC
7256	ACAGGTGTGAACCACTGCTCCCG
7257	CAGGTGTGAACCACTGCTCCCGG
7258	AGGTGTGAACCACTGCTCCCGGC
7259	GGTGTGAACCACTGCTCCCGGCC
7260	GTGTGAACCACTGCTCCCGGCCT
7261	TGTGAACCACTGCTCCCGGCCTT
7262	GTGAACCACTGCTCCCGGCCTTG
7263	TGAACCACTGCTCCCGGCCTTGT
7264	GAACCACTGCTCCCGGCCTTGTG
7265	AACCACTGCTCCCGGCCTTGTGT
7266	ACCACTGCTCCCGGCCTTGTGTG
7267	CCACTGCTCCCGGCCTTGTGTGA
7268	CACTGCTCCCGGCCTTGTGTGAT
7269	ACTGCTCCCGGCCTTGTGTGATT
7270	CTGCTCCCGGCCTTGTGTGATTT
7271	TGCTCCCGGCCTTGTGTGATTTT
7272	GCTCCCGGCCTTGTGTGATTTTA
7273	CTCCCGGCCTTGTGTGATTTTAT
7274	TCCCGGCCTTGTGTGATTTTATC
7275	CCCGGCCTTGTGTGATTTTATCT
7276	CCGGCCTTGTGTGATTTTATCTA
7277	CGGCCTTGTGTGATTTTATCTAA
7278	GGCCTTGTGTGATTTTATCTAAG
7279	GCCTTGTGTGATTTTATCTAAGG
7280	CCTTGTGTGATTTTATCTAAGGG
7281	CTTGTGTGATTTTATCTAAGGGA
7282	TTGTGTGATTTTATCTAAGGGAC
7283	TGTGTGATTTTATCTAAGGGACT
7284	GTGTGATTTTATCTAAGGGACTT
7285	TGTGATTTTATCTAAGGGACTTA
7286	GTGATTTTATCTAAGGGACTTAA
7287	TGATTTTATCTAAGGGACTTAAG
7288	GATTTTATCTAAGGGACTTAAGC
7289	ATTTTATCTAAGGGACTTAAGCG
7290	TTTTATCTAAGGGACTTAAGCGT
7291	TTTATCTAAGGGACTTAAGCGTC
7292	TTATCTAAGGGACTTAAGCGTCC
7293	TATCTAAGGGACTTAAGCGTCCT
7294	ATCTAAGGGACTTAAGCGTCCTC
7295	TCTAAGGGACTTAAGCGTCCTCA
7296	CTAAGGGACTTAAGCGTCCTCAG

Fig. 29 cont'd (Sheet 152 of 170)

ID	SEQUENCE
7297	TAAGGGACTTAAGCGTCCTCAGG
7298	AAGGGACTTAAGCGTCCTCAGGT
7299	AGGGACTTAAGCGTCCTCAGGTC
7300	GGGACTTAAGCGTCCTCAGGTCC
7301	GGACTTAAGCGTCCTCAGGTCCT
7302	GACTTAAGCGTCCTCAGGTCCTA
7303	ACTTAAGCGTCCTCAGGTCCTAG
7304	CTTAAGCGTCCTCAGGTCCTAGG
7305	TTAAGCGTCCTCAGGTCCTAGGG
7306	TAAGCGTCCTCAGGTCCTAGGGG
7307	AAGCGTCCTCAGGTCCTAGGGGG
7308	AGCGTCCTCAGGTCCTAGGGGGT
7309	GCGTCCTCAGGTCCTAGGGGGTC
7310	CGTCCTCAGGTCCTAGGGGGTCG
7311	GTCCTCAGGTCCTAGGGGGTCGT
7312	TCCTCAGGTCCTAGGGGGTCGTG
7313	CCTCAGGTCCTAGGGGGTCGTGA
7314	CTCAGGTCCTAGGGGGTCGTGAA
7315	TCAGGTCCTAGGGGGTCGTGAAA
7316	CAGGTCCTAGGGGGTCGTGAAAC
7317	AGGTCCTAGGGGGTCGTGAAACC
7318	GGTCCTAGGGGGTCGTGAAACCA
7319	GTCCTAGGGGGTCGTGAAACCAA
7320	TCCTAGGGGGTCGTGAAACCAAA
7321	CCTAGGGGGTCGTGAAACCAAAA
7322	CTAGGGGGTCGTGAAACCAAAAC
7323	TAGGGGGTCGTGAAACCAAAACC
7324	AGGGGGTCGTGAAACCAAAACCC
7325	GGGGGTCGTGAAACCAAAACCCC
7326	GGGGTCGTGAAACCAAAACCCCA
7327	GGGTCGTGAAACCAAAACCCCAG
7328	GGTCGTGAAACCAAAACCCCAGG
7329	GTCGTGAAACCAAAACCCCAGGG
7330	TCGTGAAACCAAAACCCCAGGGA
7331	CGTGAAACCAAAACCCCAGGGAT
7332	GTGAAACCAAAACCCCAGGGATA
7333	TGAAACCAAAACCCCAGGGATAG
7334	GAAACCAAAACCCCAGGGATAGC
7335	AAACCAAAACCCCAGGGATAGCA
7336	AACCAAAACCCCAGGGATAGCAA
7337	ACCAAAACCCCAGGGATAGCAAG
7338	CCAAAACCCCAGGGATAGCAAGG
7339	CAAAACCCCAGGGATAGCAAGGG
7340	AAAACCCCAGGGATAGCAAGGGA
7341	AAACCCCAGGGATAGCAAGGGAC
7342	AACCCCAGGGATAGCAAGGGACA
7343	ACCCCAGGGATAGCAAGGGACAA
7344	CCCCAGGGATAGCAAGGGACAAT

Fig. 29 cont'd (Sheet 153 of 170)

ID	SEQUENCE
7345	CCCAGGGATAGCAAGGGACAATT
7346	CCAGGGATAGCAAGGGACAATTG
7347	CAGGGATAGCAAGGGACAATTGT
7348	AGGGATAGCAAGGGACAATTGTA
7349	GGGATAGCAAGGGACAATTGTAT
7350	GGATAGCAAGGGACAATTGTATC
7351	GATAGCAAGGGACAATTGTATCT
7352	ATAGCAAGGGACAATTGTATCTT
7353	TAGCAAGGGACAATTGTATCTTC
7354	AGCAAGGGACAATTGTATCTTCA
7355	GCAAGGGACAATTGTATCTTCAA
7356	CAAGGGACAATTGTATCTTCAAA
7357	AAGGGACAATTGTATCTTCAAAG
7358	AGGGACAATTGTATCTTCAAAGT
7359	GGGACAATTGTATCTTCAAAGTA
7360	GGACAATTGTATCTTCAAAGTAG
7361	GACAATTGTATCTTCAAAGTAGA
7362	ACAATTGTATCTTCAAAGTAGAC
7363	CAATTGTATCTTCAAAGTAGACA
7364	AATTGTATCTTCAAAGTAGACAA
7365	ATTGTATCTTCAAAGTAGACAAA
7366	TTGTATCTTCAAAGTAGACAAAT
7367	TGTATCTTCAAAGTAGACAAATG
7368	GTATCTTCAAAGTAGACAAATGG
7369	TATCTTCAAAGTAGACAAATGGC
7370	ATCTTCAAAGTAGACAAATGGCG
7371	TCTTCAAAGTAGACAAATGGCGC
7372	CTTCAAAGTAGACAAATGGCGCC
7373	TTCAAAGTAGACAAATGGCGCCG
7374	TCAAAGTAGACAAATGGCGCCGG
7375	CGCCGGGCACGGTGGCTCACGCC
7376	GCCGGGCACGGTGGCTCACGCCT
7377	CCGGGCACGGTGGCTCACGCCTG
7378	CGGGCACGGTGGCTCACGCCTGT
7379	GGGCACGGTGGCTCACGCCTGTA
7380	GGCACGGTGGCTCACGCCTGTAA
7381	GCACGGTGGCTCACGCCTGTAAT
7382	CACGGTGGCTCACGCCTGTAATC
7383	ACGGTGGCTCACGCCTGTAATCC
7384	CGGTGGCTCACGCCTGTAATCCC
7385	GGTGGCTCACGCCTGTAATCCCA
7386	GTGGCTCACGCCTGTAATCCCAG
7387	TGGCTCACGCCTGTAATCCCAGC
7388	GGCTCACGCCTGTAATCCCAGCA
7389	GCTCACGCCTGTAATCCCAGCAG
7390	CTCACGCCTGTAATCCCAGCAGT
7391	TCACGCCTGTAATCCCAGCAGTT
7392	CACGCCTGTAATCCCAGCAGTTT

Fig. 29 cont'd (Sheet 154 of 170)

ID	SEQUENCE
7393	ACGCCTGTAATCCCAGCAGTTTC
7394	CGCCTGTAATCCCAGCAGTTTCC
7395	GCCTGTAATCCCAGCAGTTTCCG
7396	CCTGTAATCCCAGCAGTTTCCGA
7397	CTGTAATCCCAGCAGTTTCCGAG
7398	TGTAATCCCAGCAGTTTCCGAGG
7399	GTAATCCCAGCAGTTTCCGAGGC
7400	TAATCCCAGCAGTTTCCGAGGCT
7401	AATCCCAGCAGTTTCCGAGGCTG
7402	ATCCCAGCAGTTTCCGAGGCTGA
7403	TCCCAGCAGTTTCCGAGGCTGAG
7404	CCCAGCAGTTTCCGAGGCTGAGG
7405	CCAGCAGTTTCCGAGGCTGAGGC
7406	CAGCAGTTTCCGAGGCTGAGGCA
7407	AGCAGTTTCCGAGGCTGAGGCAG
7408	GCAGTTTCCGAGGCTGAGGCAGG
7409	CAGTTTCCGAGGCTGAGGCAGGC
7410	AGTTTCCGAGGCTGAGGCAGGCG
7411	GTTTCCGAGGCTGAGGCAGGCGG
7412	TTTCCGAGGCTGAGGCAGGCGGC
7413	TTCCGAGGCTGAGGCAGGCGGCT
7414	TCCGAGGCTGAGGCAGGCGGCTC
7415	CCGAGGCTGAGGCAGGCGGCTCA
7416	CGAGGCTGAGGCAGGCGGCTCAC
7417	GAGGCTGAGGCAGGCGGCTCACC
7418	AGGCTGAGGCAGGCGGCTCACCT
7419	GGCTGAGGCAGGCGGCTCACCTG
7420	GCTGAGGCAGGCGGCTCACCTGA
7421	CTGAGGCAGGCGGCTCACCTGAG
7422	TGAGGCAGGCGGCTCACCTGAGG
7423	GAGGCAGGCGGCTCACCTGAGGT
7424	AGGCAGGCGGCTCACCTGAGGTC
7425	GGCAGGCGGCTCACCTGAGGTCA
7426	GCAGGCGGCTCACCTGAGGTCAG
7427	CAGGCGGCTCACCTGAGGTCAGG
7428	AGGCGGCTCACCTGAGGTCAGGA
7429	GGCGGCTCACCTGAGGTCAGGAG
7430	GCGGCTCACCTGAGGTCAGGAGT
7431	CGGCTCACCTGAGGTCAGGAGTT
7432	GGCTCACCTGAGGTCAGGAGTTG
7433	GCTCACCTGAGGTCAGGAGTTGG
7434	CTCACCTGAGGTCAGGAGTTGGA
7435	TCACCTGAGGTCAGGAGTTGGAG
7436	CACCTGAGGTCAGGAGTTGGAGA
7437	ACCTGAGGTCAGGAGTTGGAGAC
7438	CCTGAGGTCAGGAGTTGGAGACC
7439	CTGAGGTCAGGAGTTGGAGACCA
7440	TGAGGTCAGGAGTTGGAGACCAG

Fig. 29 cont'd (Sheet 155 of 170)

ID	SEQUENCE
7441	GAGGTCAGGAGTTGGAGACCAGC
7442	AGGTCAGGAGTTGGAGACCAGCC
7443	GGTCAGGAGTTGGAGACCAGCCT
7444	GTCAGGAGTTGGAGACCAGCCTG
7445	TCAGGAGTTGGAGACCAGCCTGG
7446	CAGGAGTTGGAGACCAGCCTGGC
7447	AGGAGTTGGAGACCAGCCTGGCC
7448	GGAGTTGGAGACCAGCCTGGCCA
7449	GAGTTGGAGACCAGCCTGGCCAA
7450	AGTTGGAGACCAGCCTGGCCAAC
7451	GTTGGAGACCAGCCTGGCCAACA
7452	TTGGAGACCAGCCTGGCCAACAT
7453	TGGAGACCAGCCTGGCCAACATG
7454	GGAGACCAGCCTGGCCAACATGC
7455	GAGACCAGCCTGGCCAACATGCT
7456	AGACCAGCCTGGCCAACATGCTG
7457	GACCAGCCTGGCCAACATGCTGA
7458	ACCAGCCTGGCCAACATGCTGAA
7459	CCAGCCTGGCCAACATGCTGAAA
7460	CAGCCTGGCCAACATGCTGAAAC
7461	AGCCTGGCCAACATGCTGAAACC
7462	GCCTGGCCAACATGCTGAAACCC
7463	CCTGGCCAACATGCTGAAACCCT
7464	CTGGCCAACATGCTGAAACCCTG
7465	TGGCCAACATGCTGAAACCCTGT
7466	GGCCAACATGCTGAAACCCTGTC
7467	GCCAACATGCTGAAACCCTGTCT
7468	CCAACATGCTGAAACCCTGTCTG
7469	CAACATGCTGAAACCCTGTCTGT
7470	AACATGCTGAAACCCTGTCTGTA
7471	ACATGCTGAAACCCTGTCTGTAC
7472	CATGCTGAAACCCTGTCTGTACA
7473	ATGCTGAAACCCTGTCTGTACAA
7474	TGCTGAAACCCTGTCTGTACAAA
7475	GCTGAAACCCTGTCTGTACAAAA
7476	CTGAAACCCTGTCTGTACAAAAA
7477	TGAAACCCTGTCTGTACAAAAAT
7478	GAAACCCTGTCTGTACAAAAATA
7479	AAACCCTGTCTGTACAAAAATAC
7480	AACCCTGTCTGTACAAAAATACA
7481	ACCCTGTCTGTACAAAAATACAA
7482	CCCTGTCTGTACAAAAATACAAA
7483	CCTGTCTGTACAAAAATACAAAA
7484	CTGTCTGTACAAAAATACAAAAA
7485	TGTCTGTACAAAAATACAAAAAT
7486	GTCTGTACAAAAATACAAAAATA
7487	TCTGTACAAAAATACAAAAATAG
7488	CTGTACAAAAATACAAAAATAGC

Fig. 29 cont'd (Sheet 156 of 170)

ID	SEQUENCE
7489	TGTACAAAAATACAAAAATAGCT
7490	GTACAAAAATACAAAAATAGCTG
7491	TACAAAAATACAAAAATAGCTGG
7492	ACAAAAATACAAAAATAGCTGGG
7493	CAAAAATACAAAAATAGCTGGGC
7494	AAAAATACAAAAATAGCTGGGCA
7495	AAAATACAAAAATAGCTGGGCAT
7496	AAATACAAAAATAGCTGGGCATG
7497	AATACAAAAATAGCTGGGCATGG
7498	ATACAAAAATAGCTGGGCATGGT
7499	TACAAAAATAGCTGGGCATGGTG
7500	ACAAAAATAGCTGGGCATGGTGG
7501	CAAAAATAGCTGGGCATGGTGGC
7502	AAAAATAGCTGGGCATGGTGGCG
7503	AAAATAGCTGGGCATGGTGGCGC
7504	AAATAGCTGGGCATGGTGGCGCA
7505	AATAGCTGGGCATGGTGGCGCAT
7506	ATAGCTGGGCATGGTGGCGCATG
7507	TAGCTGGGCATGGTGGCGCATGC
7508	AGCTGGGCATGGTGGCGCATGCC
7509	GCTGGGCATGGTGGCGCATGCCT
7510	CTGGGCATGGTGGCGCATGCCTG
7511	TGGGCATGGTGGCGCATGCCTGT
7512	GGGCATGGTGGCGCATGCCTGTA
7513	GGCATGGTGGCGCATGCCTGTAG
7514	GCATGGTGGCGCATGCCTGTAGT
7515	CATGGTGGCGCATGCCTGTAGTC
7516	ATGGTGGCGCATGCCTGTAGTCC
7517	TGGTGGCGCATGCCTGTAGTCCC
7518	GGTGGCGCATGCCTGTAGTCCCA
7519	GTGGCGCATGCCTGTAGTCCCAG
7520	TGGCGCATGCCTGTAGTCCCAGC
7521	GGCGCATGCCTGTAGTCCCAGCT
7522	GCGCATGCCTGTAGTCCCAGCTA
7523	CGCATGCCTGTAGTCCCAGCTAC
7524	GCATGCCTGTAGTCCCAGCTACT
7525	CATGCCTGTAGTCCCAGCTACTA
7526	ATGCCTGTAGTCCCAGCTACTAG
7527	TGCCTGTAGTCCCAGCTACTAGA
7528	GCCTGTAGTCCCAGCTACTAGAG
7529	CCTGTAGTCCCAGCTACTAGAGC
7530	CTGTAGTCCCAGCTACTAGAGCG
7531	TGTAGTCCCAGCTACTAGAGCGA
7532	GTAGTCCCAGCTACTAGAGCGAC
7533	TAGTCCCAGCTACTAGAGCGACT
7534	AGTCCCAGCTACTAGAGCGACTG
7535	GTCCCAGCTACTAGAGCGACTGA
7536	TCCCAGCTACTAGAGCGACTGAG

Fig. 29 cont'd (Sheet 157 of 170)

ID	SEQUENCE
7537	CCCAGCTACTAGAGCGACTGAGG
7538	CCAGCTACTAGAGCGACTGAGGC
7539	CAGCTACTAGAGCGACTGAGGCA
7540	AGCTACTAGAGCGACTGAGGCAG
7541	GCTACTAGAGCGACTGAGGCAGG
7542	CTACTAGAGCGACTGAGGCAGGA
7543	TACTAGAGCGACTGAGGCAGGAG
7544	ACTAGAGCGACTGAGGCAGGAGA
7545	CTAGAGCGACTGAGGCAGGAGAA
7546	TAGAGCGACTGAGGCAGGAGAAT
7547	AGAGCGACTGAGGCAGGAGAATT
7548	GAGCGACTGAGGCAGGAGAATTG
7549	AGCGACTGAGGCAGGAGAATTGC
7550	GCGACTGAGGCAGGAGAATTGCT
7551	CGACTGAGGCAGGAGAATTGCTT
7552	GACTGAGGCAGGAGAATTGCTTG
7553	ACTGAGGCAGGAGAATTGCTTGA
7554	CTGAGGCAGGAGAATTGCTTGAA
7555	TGAGGCAGGAGAATTGCTTGAAC
7556	GAGGCAGGAGAATTGCTTGAACC
7557	AGGCAGGAGAATTGCTTGAACCT
7558	GGCAGGAGAATTGCTTGAACCTG
7559	GCAGGAGAATTGCTTGAACCTGG
7560	CAGGAGAATTGCTTGAACCTGGG
7561	AGGAGAATTGCTTGAACCTGGGA
7562	GGAGAATTGCTTGAACCTGGGAG
7563	GAGAATTGCTTGAACCTGGGAGG
7564	AGAATTGCTTGAACCTGGGAGGC
7565	GAATTGCTTGAACCTGGGAGGCG
7566	AATTGCTTGAACCTGGGAGGCGG
7567	ATTGCTTGAACCTGGGAGGCGGA
7568	TTGCTTGAACCTGGGAGGCGGAG
7569	TGCTTGAACCTGGGAGGCGGAGG
7570	GCTTGAACCTGGGAGGCGGAGGT
7571	CTTGAACCTGGGAGGCGGAGGTT
7572	TTGAACCTGGGAGGCGGAGGTTG
7573	TGAACCTGGGAGGCGGAGGTTGC
7574	GAACCTGGGAGGCGGAGGTTGCA
7575	AACCTGGGAGGCGGAGGTTGCAG
7576	ACCTGGGAGGCGGAGGTTGCAGG
7577	CCTGGGAGGCGGAGGTTGCAGGG
7578	CTGGGAGGCGGAGGTTGCAGGGA
7579	TGGGAGGCGGAGGTTGCAGGGAG
7580	GGGAGGCGGAGGTTGCAGGGAGC
7581	GGAGGCGGAGGTTGCAGGGAGCC
7582	GAGGCGGAGGTTGCAGGGAGCCA
7583	AGGCGGAGGTTGCAGGGAGCCAA
7584	GGCGGAGGTTGCAGGGAGCCAAG

Fig. 29 cont'd (Sheet 158 of 170)

ID	SEQUENCE
7585	GCGGAGGTTGCAGGGAGCCAAGA
7586	CGGAGGTTGCAGGGAGCCAAGAT
7587	GGAGGTTGCAGGGAGCCAAGATG
7588	GAGGTTGCAGGGAGCCAAGATGG
7589	AGGTTGCAGGGAGCCAAGATGGC
7590	GGTTGCAGGGAGCCAAGATGGCG
7591	GTTGCAGGGAGCCAAGATGGCGC
7592	TTGCAGGGAGCCAAGATGGCGCC
7593	TGCAGGGAGCCAAGATGGCGCCA
7594	GCAGGGAGCCAAGATGGCGCCAC
7595	CAGGGAGCCAAGATGGCGCCACC
7596	AGGGAGCCAAGATGGCGCCACCG
7597	GGGAGCCAAGATGGCGCCACCGC
7598	GGAGCCAAGATGGCGCCACCGCA
7599	GAGCCAAGATGGCGCCACCGCAC
7600	AGCCAAGATGGCGCCACCGCACT
7601	GCCAAGATGGCGCCACCGCACTC
7602	CCAAGATGGCGCCACCGCACTCC
7603	CAAGATGGCGCCACCGCACTCCA
7604	AAGATGGCGCCACCGCACTCCAG
7605	AGATGGCGCCACCGCACTCCAGC
7606	GATGGCGCCACCGCACTCCAGCC
7607	ATGGCGCCACCGCACTCCAGCCT
7608	TGGCGCCACCGCACTCCAGCCTA
7609	GGCGCCACCGCACTCCAGCCTAG
7610	GCGCCACCGCACTCCAGCCTAGG
7611	CGCCACCGCACTCCAGCCTAGGT
7612	GCCACCGCACTCCAGCCTAGGTG
7613	CCACCGCACTCCAGCCTAGGTGA
7614	CACCGCACTCCAGCCTAGGTGAT
7615	ACCGCACTCCAGCCTAGGTGATA
7616	CCGCACTCCAGCCTAGGTGATAG
7617	CGCACTCCAGCCTAGGTGATAGA
7618	GCACTCCAGCCTAGGTGATAGAG
7619	CACTCCAGCCTAGGTGATAGAGT
7620	ACTCCAGCCTAGGTGATAGAGTG
7621	CTCCAGCCTAGGTGATAGAGTGA
7622	TCCAGCCTAGGTGATAGAGTGAG
7623	CCAGCCTAGGTGATAGAGTGAGA
7624	CAGCCTAGGTGATAGAGTGAGAC
7625	AGCCTAGGTGATAGAGTGAGACT
7626	GCCTAGGTGATAGAGTGAGACTC
7627	CCTAGGTGATAGAGTGAGACTCC
7628	CTAGGTGATAGAGTGAGACTCCC
7629	TAGGTGATAGAGTGAGACTCCCT
7630	AGGTGATAGAGTGAGACTCCCTC
7631	GGTGATAGAGTGAGACTCCCTCT
7632	GTGATAGAGTGAGACTCCCTCTC

Fig. 29 cont'd (Sheet 159 of 170)

ID	SEQUENCE
7633	TGATAGAGTGAGACTCCCTCTCA
7634	GATAGAGTGAGACTCCCTCTCAA
7635	ATAGAGTGAGACTCCCTCTCAAA
7636	TAGAGTGAGACTCCCTCTCAAAA
7637	AGAGTGAGACTCCCTCTCAAAAA
7638	GAGTGAGACTCCCTCTCAAAAAC
7639	AGTGAGACTCCCTCTCAAAAACA
7640	GTGAGACTCCCTCTCAAAAACAA
7641	TGAGACTCCCTCTCAAAAACAAA
7642	GAGACTCCCTCTCAAAAACAAAA
7643	AGACTCCCTCTCAAAAACAAAAC
7644	GACTCCCTCTCAAAAACAAAACA
7645	ACTCCCTCTCAAAAACAAAACAA
7646	CTCCCTCTCAAAAACAAAACAAA
7647	TCCCTCTCAAAAACAAAACAAAA
7648	CCCTCTCAAAAACAAAACAAAAC
7649	CCTCTCAAAAACAAAACAAAACA
7650	CTCTCAAAAACAAAACAAAACAA
7651	TCTCAAAAACAAAACAAAACAAA
7652	CTCAAAAACAAAACAAAACAAAA
7653	TCAAAAACAAAACAAAACAAAAA
7654	CAAAAACAAAACAAAACAAAAAA
7655	AAAAACAAAACAAAACAAAAAAA
7656	AAAACAAAACAAAACAAAAAAAT
7657	AAACAAAACAAAACAAAAAAATT
7658	AACAAAACAAAACAAAAAAATTA
7659	ACAAAACAAAACAAAAAAATTAG
7660	CAAAACAAAACAAAAAAATTAGA
7661	AAAACAAAACAAAAAAATTAGAC
7662	AAACAAAACAAAAAAATTAGACA
7663	AACAAAACAAAAAAATTAGACAA
7664	ACAAAACAAAAAAATTAGACAAA
7665	CAAAACAAAAAAATTAGACAAAT
7666	AAAACAAAAAAATTAGACAAATG
7667	AAACAAAAAAATTAGACAAATGC
7668	AACAAAAAAATTAGACAAATGCT
7669	ACAAAAAAATTAGACAAATGCTA
7670	CAAAAAAATTAGACAAATGCTAC
7671	AAAAAAATTAGACAAATGCTACA
7672	AAAAAATTAGACAAATGCTACAT
7673	AAAAATTAGACAAATGCTACATT
7674	AAAATTAGACAAATGCTACATTA
7675	AAATTAGACAAATGCTACATTAA
7676	AATTAGACAAATGCTACATTAAT
7677	ATTAGACAAATGCTACATTAATG
7678	TTAGACAAATGCTACATTAATGT
7679	TAGACAAATGCTACATTAATGTT
7680	AGACAAATGCTACATTAATGTTT

Fig. 29 cont'd (Sheet 160 of 170)

ID	SEQUENCE
7681	GACAAATGCTACATTAATGTTTG
7682	ACAAATGCTACATTAATGTTTGG
7683	CAAATGCTACATTAATGTTTGGG
7684	AAATGCTACATTAATGTTTGGGT
7685	AATGCTACATTAATGTTTGGGTG
7686	ATGCTACATTAATGTTTGGGTGG
7687	TGCTACATTAATGTTTGGGTGGT
7688	GCTACATTAATGTTTGGGTGGTC
7689	CTACATTAATGTTTGGGTGGTCA
7690	TACATTAATGTTTGGGTGGTCAG
7691	ACATTAATGTTTGGGTGGTCAGA
7692	CATTAATGTTTGGGTGGTCAGAT
7693	ATTAATGTTTGGGTGGTCAGATT
7694	TTAATGTTTGGGTGGTCAGATTC
7695	TAATGTTTGGGTGGTCAGATTCT
7696	AATGTTTGGGTGGTCAGATTCTA
7697	ATGTTTGGGTGGTCAGATTCTAC
7698	TGTTTGGGTGGTCAGATTCTACT
7699	GTTTGGGTGGTCAGATTCTACTT
7700	TTTGGGTGGTCAGATTCTACTTT
7701	TTGGGTGGTCAGATTCTACTTTG
7702	TGGGTGGTCAGATTCTACTTTGA
7703	GGGTGGTCAGATTCTACTTTGAA
7704	GGTGGTCAGATTCTACTTTGAAT
7705	GTGGTCAGATTCTACTTTGAATC
7706	TGGTCAGATTCTACTTTGAATCT
7707	GGTCAGATTCTACTTTGAATCTG
7708	GTCAGATTCTACTTTGAATCTGA
7709	TCAGATTCTACTTTGAATCTGAA
7710	CAGATTCTACTTTGAATCTGAAG
7711	AGATTCTACTTTGAATCTGAAGT
7712	GATTCTACTTTGAATCTGAAGTT
7713	ATTCTACTTTGAATCTGAAGTTT
7714	TTCTACTTTGAATCTGAAGTTTG
7715	TCTACTTTGAATCTGAAGTTTGC
7716	CTACTTTGAATCTGAAGTTTGCA
7717	TACTTTGAATCTGAAGTTTGCAG
7718	ACTTTGAATCTGAAGTTTGCAGA
7719	CTTTGAATCTGAAGTTTGCAGAT
7720	TTTGAATCTGAAGTTTGCAGATA
7721	TTGAATCTGAAGTTTGCAGATAT
7722	TGAATCTGAAGTTTGCAGATATG
7723	GAATCTGAAGTTTGCAGATATGC
7724	AATCTGAAGTTTGCAGATATGCC
7725	ATCTGAAGTTTGCAGATATGCCT
7726	TCTGAAGTTTGCAGATATGCCTA
7727	CTGAAGTTTGCAGATATGCCTAT
7728	TGAAGTTTGCAGATATGCCTATA

Fig. 29 cont'd (Sheet 161 of 170)

ID	SEQUENCE
7729	GAAGTTTGCAGATATGCCTATAG
7730	AAGTTTGCAGATATGCCTATAGA
7731	AGTTTGCAGATATGCCTATAGAT
7732	GTTTGCAGATATGCCTATAGATT
7733	TTTGCAGATATGCCTATAGATTT
7734	TTGCAGATATGCCTATAGATTTT
7735	TGCAGATATGCCTATAGATTTTT
7736	GCAGATATGCCTATAGATTTTTG
7737	CAGATATGCCTATAGATTTTTGG
7738	AGATATGCCTATAGATTTTTGGA
7739	GATATGCCTATAGATTTTTGGAG
7740	ATATGCCTATAGATTTTTGGAGT
7741	TATGCCTATAGATTTTTGGAGTT
7742	ATGCCTATAGATTTTTGGAGTTT
7743	TGCCTATAGATTTTTGGAGTTTA
7744	GCCTATAGATTTTTGGAGTTTAC
7745	CCTATAGATTTTTGGAGTTTACC
7746	CTATAGATTTTTGGAGTTTACCA
7747	TATAGATTTTTGGAGTTTACCAC
7748	ATAGATTTTTGGAGTTTACCACT
7749	TAGATTTTTGGAGTTTACCACTT
7750	AGATTTTTGGAGTTTACCACTTT
7751	GATTTTTGGAGTTTACCACTTTC
7752	ATTTTTGGAGTTTACCACTTTCT
7753	TTTTTGGAGTTTACCACTTTCTT
7754	TTTTGGAGTTTACCACTTTCTTA
7755	TTTGGAGTTTACCACTTTCTTAT
7756	TTGGAGTTTACCACTTTCTTATT
7757	TGGAGTTTACCACTTTCTTATTC
7758	GGAGTTTACCACTTTCTTATTCT
7759	GAGTTTACCACTTTCTTATTCTG
7760	AGTTTACCACTTTCTTATTCTGT
7761	GTTTACCACTTTCTTATTCTGTA
7762	TTTACCACTTTCTTATTCTGTAT
7763	TTACCACTTTCTTATTCTGTATC
7764	TACCACTTTCTTATTCTGTATCA
7765	ACCACTTTCTTATTCTGTATCAT
7766	CCACTTTCTTATTCTGTATCATT
7767	CACTTTCTTATTCTGTATCATTA
7768	ACTTTCTTATTCTGTATCATTAA
7769	CTTTCTTATTCTGTATCATTAAT
7770	TTTCTTATTCTGTATCATTAATG
7771	TTCTTATTCTGTATCATTAATGT
7772	TCTTATTCTGTATCATTAATGTA
7773	CTTATTCTGTATCATTAATGTAA
7774	TTATTCTGTATCATTAATGTAAT
7775	TATTCTGTATCATTAATGTAATA
7776	ATTCTGTATCATTAATGTAATAT

Fig. 29 cont'd (Sheet 162 of 170)

ID	SEQUENCE
7777	TTCTGTATCATTAATGTAATATT
7778	TCTGTATCATTAATGTAATATTT
7779	CTGTATCATTAATGTAATATTTT
7780	TGTATCATTAATGTAATATTTTA
7781	GTATCATTAATGTAATATTTTAA
7782	TATCATTAATGTAATATTTTAAA
7783	ATCATTAATGTAATATTTTAAAT
7784	TCATTAATGTAATATTTTAAATT
7785	CATTAATGTAATATTTTAAATTA
7786	ATTAATGTAATATTTTAAATTAC
7787	TTAATGTAATATTTTAAATTACT
7788	TAATGTAATATTTTAAATTACTA
7789	AATGTAATATTTTAAATTACTAT
7790	ATGTAATATTTTAAATTACTATA
7791	TGTAATATTTTAAATTACTATAT
7792	GTAATATTTTAAATTACTATATA
7793	TAATATTTTAAATTACTATATAT
7794	AATATTTTAAATTACTATATATG
7795	ATATTTTAAATTACTATATATGT
7796	TATTTTAAATTACTATATATGTT
7797	ATTTTAAATTACTATATATGTTA
7798	TTTTAAATTACTATATATGTTAC
7799	TTTAAATTACTATATATGTTACC
7800	TTAAATTACTATATATGTTACCA
7801	TAAATTACTATATATGTTACCAT
7802	AAATTACTATATATGTTACCATT
7803	AATTACTATATATGTTACCATTT
7804	ATTACTATATATGTTACCATTTT
7805	TTACTATATATGTTACCATTTTT
7806	TACTATATATGTTACCATTTTTC
7807	ACTATATATGTTACCATTTTTCT
7808	CTATATATGTTACCATTTTTCTG
7809	TATATATGTTACCATTTTTCTGG
7810	ATATATGTTACCATTTTTCTGGA
7811	TATATGTTACCATTTTTCTGGAT
7812	ATATGTTACCATTTTTCTGGATT
7813	TATGTTACCATTTTTCTGGATTT
7814	ATGTTACCATTTTTCTGGATTTA
7815	TGTTACCATTTTTCTGGATTTAG
7816	GTTACCATTTTTCTGGATTTAGT
7817	TTACCATTTTTCTGGATTTAGTA
7818	TACCATTTTTCTGGATTTAGTAA
7819	ACCATTTTTCTGGATTTAGTAAG
7820	CCATTTTTCTGGATTTAGTAAGA
7821	CATTTTTCTGGATTTAGTAAGAA
7822	ATTTTTCTGGATTTAGTAAGAAA
7823	TTTTTCTGGATTTAGTAAGAAAT
7824	TTTTCTGGATTTAGTAAGAAATT

Fig. 29 cont'd (Sheet 163 of 170)

ID	SEQUENCE
7825	TTTCTGGATTTAGTAAGAAATTT
7826	TTCTGGATTTAGTAAGAAATTTG
7827	TCTGGATTTAGTAAGAAATTTGC
7828	CTGGATTTAGTAAGAAATTTGCA
7829	TGGATTTAGTAAGAAATTTGCAG
7830	GGATTTAGTAAGAAATTTGCAGT
7831	GATTTAGTAAGAAATTTGCAGTT
7832	ATTTAGTAAGAAATTTGCAGTTT
7833	TTTAGTAAGAAATTTGCAGTTTT
7834	TTAGTAAGAAATTTGCAGTTTTG
7835	TAGTAAGAAATTTGCAGTTTTGG
7836	AGTAAGAAATTTGCAGTTTTGGT
7837	GTAAGAAATTTGCAGTTTTGGTT
7838	TAAGAAATTTGCAGTTTTGGTTT
7839	AAGAAATTTGCAGTTTTGGTTTG
7840	AGAAATTTGCAGTTTTGGTTTGA
7841	GAAATTTGCAGTTTTGGTTTGAT
7842	AAATTTGCAGTTTTGGTTTGATG
7843	AATTTGCAGTTTTGGTTTGATGT
7844	ATTTGCAGTTTTGGTTTGATGTA
7845	TTTGCAGTTTTGGTTTGATGTAA
7846	TTGCAGTTTTGGTTTGATGTAAC
7847	TGCAGTTTTGGTTTGATGTAACA
7848	GCAGTTTTGGTTTGATGTAACAA
7849	CAGTTTTGGTTTGATGTAACAAG
7850	AGTTTTGGTTTGATGTAACAAGG
7851	GTTTTGGTTTGATGTAACAAGGG
7852	TTTTGGTTTGATGTAACAAGGGT
7853	TTTGGTTTGATGTAACAAGGGTT
7854	TTGGTTTGATGTAACAAGGGTTT
7855	TGGTTTGATGTAACAAGGGTTTT
7856	GGTTTGATGTAACAAGGGTTTTA
7857	GTTTGATGTAACAAGGGTTTTAA
7858	TTTGATGTAACAAGGGTTTTAAT
7859	TTGATGTAACAAGGGTTTTAATG
7860	TGATGTAACAAGGGTTTTAATGT
7861	GATGTAACAAGGGTTTTAATGTA
7862	ATGTAACAAGGGTTTTAATGTAA
7863	TGTAACAAGGGTTTTAATGTAAT
7864	GTAACAAGGGTTTTAATGTAATT
7865	TAACAAGGGTTTTAATGTAATTT
7866	AACAAGGGTTTTAATGTAATTTA
7867	ACAAGGGTTTTAATGTAATTTAT
7868	CAAGGGTTTTAATGTAATTTATG
7869	AAGGGTTTTAATGTAATTTATGT
7870	AGGGTTTTAATGTAATTTATGTT
7871	GGGTTTTAATGTAATTTATGTTA
7872	GGTTTTAATGTAATTTATGTTAG

Fig. 29 cont'd (Sheet 164 of 170)

ID	SEQUENCE
7873	GTTTTAATGTAATTTATGTTAGA
7874	TTTTAATGTAATTTATGTTAGAT
7875	TTTAATGTAATTTATGTTAGATT
7876	TTAATGTAATTTATGTTAGATTT
7877	TAATGTAATTTATGTTAGATTTT
7878	AATGTAATTTATGTTAGATTTTG
7879	ATGTAATTTATGTTAGATTTTGC
7880	TGTAATTTATGTTAGATTTTGCA
7881	GTAATTTATGTTAGATTTTGCAT
7882	TAATTTATGTTAGATTTTGCATT
7883	AATTTATGTTAGATTTTGCATTT
7884	ATTTATGTTAGATTTTGCATTTT
7885	TTTATGTTAGATTTTGCATTTTT
7886	TTATGTTAGATTTTGCATTTTTT
7887	TATGTTAGATTTTGCATTTTTTT
7888	ATGTTAGATTTTGCATTTTTTTC
7889	TGTTAGATTTTGCATTTTTTTCA
7890	GTTAGATTTTGCATTTTTTTCAT
7891	TTAGATTTTGCATTTTTTTCATT
7892	TAGATTTTGCATTTTTTTCATTA
7893	AGATTTTGCATTTTTTTCATTAC
7894	GATTTTGCATTTTTTTCATTACT
7895	ATTTTGCATTTTTTTCATTACTG
7896	TTTTGCATTTTTTTCATTACTGT
7897	TTTGCATTTTTTTCATTACTGTT
7898	TTGCATTTTTTTCATTACTGTTA
7899	TGCATTTTTTTCATTACTGTTAT
7900	GCATTTTTTTCATTACTGTTATA
7901	CATTTTTTTCATTACTGTTATAT
7902	ATTTTTTTCATTACTGTTATATT
7903	TTTTTTTCATTACTGTTATATTT
7904	TTTTTTCATTACTGTTATATTTT
7905	TTTTTCATTACTGTTATATTTTA
7906	TTTTCATTACTGTTATATTTTAA
7907	TTTCATTACTGTTATATTTTAAC
7908	TTCATTACTGTTATATTTTAACC
7909	TCATTACTGTTATATTTTAACCT
7910	CATTACTGTTATATTTTAACCTG
7911	ATTACTGTTATATTTTAACCTGA
7912	TTACTGTTATATTTTAACCTGAC
7913	TACTGTTATATTTTAACCTGACT
7914	ACTGTTATATTTTAACCTGACTG
7915	CTGTTATATTTTAACCTGACTGA
7916	TGTTATATTTTAACCTGACTGAC
7917	GTTATATTTTAACCTGACTGACT
7918	TTATATTTTAACCTGACTGACTG
7919	TATATTTTAACCTGACTGACTGA
7920	ATATTTTAACCTGACTGACTGAT

Fig. 29 cont'd (Sheet 165 of 170)

ID	SEQUENCE
7921	TATTTTAACCTGACTGACTGATC
7922	ATTTTAACCTGACTGACTGATCT
7923	TTTTAACCTGACTGACTGATCTA
7924	TTTAACCTGACTGACTGATCTAA
7925	TTAACCTGACTGACTGATCTAAT
7926	TAACCTGACTGACTGATCTAATT
7927	AACCTGACTGACTGATCTAATTG
7928	ACCTGACTGACTGATCTAATTGT
7929	CCTGACTGACTGATCTAATTGTA
7930	CTGACTGACTGATCTAATTGTAT
7931	TGACTGACTGATCTAATTGTATT
7932	GACTGACTGATCTAATTGTATTA
7933	ACTGACTGATCTAATTGTATTAG
7934	CTGACTGATCTAATTGTATTAGT
7935	TGACTGATCTAATTGTATTAGTA
7936	GACTGATCTAATTGTATTAGTAT
7937	ACTGATCTAATTGTATTAGTATT
7938	CTGATCTAATTGTATTAGTATTG
7939	TGATCTAATTGTATTAGTATTGT
7940	GATCTAATTGTATTAGTATTGTG
7941	ATCTAATTGTATTAGTATTGTGA
7942	TCTAATTGTATTAGTATTGTGAA
7943	CTAATTGTATTAGTATTGTGAAT
7944	TAATTGTATTAGTATTGTGAATA
7945	AATTGTATTAGTATTGTGAATAA
7946	ATTGTATTAGTATTGTGAATAAT
7947	TTGTATTAGTATTGTGAATAATC
7948	TGTATTAGTATTGTGAATAATCA
7949	GTATTAGTATTGTGAATAATCAT
7950	TATTAGTATTGTGAATAATCATG
7951	ATTAGTATTGTGAATAATCATGT
7952	TTAGTATTGTGAATAATCATGTG
7953	TAGTATTGTGAATAATCATGTGA
7954	AGTATTGTGAATAATCATGTGAA
7955	GTATTGTGAATAATCATGTGAAA
7956	TATTGTGAATAATCATGTGAAAT
7957	ATTGTGAATAATCATGTGAAATG
7958	TTGTGAATAATCATGTGAAATGT
7959	TGTGAATAATCATGTGAAATGTT
7960	GTGAATAATCATGTGAAATGTTT
7961	TGAATAATCATGTGAAATGTTTT
7962	GAATAATCATGTGAAATGTTTTG
7963	AATAATCATGTGAAATGTTTTGA
7964	ATAATCATGTGAAATGTTTTGAG
7965	TAATCATGTGAAATGTTTTGAGA
7966	AATCATGTGAAATGTTTTGAGAC
7967	ATCATGTGAAATGTTTTGAGACA
7968	TCATGTGAAATGTTTTGAGACAG

ID	SEQUENCE
7969	CATGTGAAATGTTTTGAGACAGA
7970	ATGTGAAATGTTTTGAGACAGAG
7971	TGTGAAATGTTTTGAGACAGAGT
7972	GTGAAATGTTTTGAGACAGAGTA
7973	TGAAATGTTTTGAGACAGAGTAC
7974	GAAATGTTTTGAGACAGAGTACT
7975	AAATGTTTTGAGACAGAGTACTA
7976	AATGTTTTGAGACAGAGTACTAT
7977	ATGTTTTGAGACAGAGTACTATA
7978	TGTTTTGAGACAGAGTACTATAT
7979	GTTTTGAGACAGAGTACTATATT
7980	TTTTGAGACAGAGTACTATATTT
7981	TTTGAGACAGAGTACTATATTTG
7982	TTGAGACAGAGTACTATATTTGT
7983	TGAGACAGAGTACTATATTTGTG
7984	GAGACAGAGTACTATATTTGTGA
7985	AGACAGAGTACTATATTTGTGAA
7986	GACAGAGTACTATATTTGTGAAT
7987	ACAGAGTACTATATTTGTGAATA
7988	CAGAGTACTATATTTGTGAATAT
7989	AGAGTACTATATTTGTGAATATA
7990	GAGTACTATATTTGTGAATATAA
7991	AGTACTATATTTGTGAATATAAT
7992	GTACTATATTTGTGAATATAATT
7993	TACTATATTTGTGAATATAATTT
7994	ACTATATTTGTGAATATAATTTT
7995	CTATATTTGTGAATATAATTTTA
7996	TATATTTGTGAATATAATTTTAT
7997	ATATTTGTGAATATAATTTTATG
7998	TATTTGTGAATATAATTTTATGG
7999	ATTTGTGAATATAATTTTATGGT
8000	TTTGTGAATATAATTTTATGGTT
8001	TTGTGAATATAATTTTATGGTTT
8002	TGTGAATATAATTTTATGGTTTT
8003	GTGAATATAATTTTATGGTTTTT
8004	TGAATATAATTTTATGGTTTTTT
8005	GAATATAATTTTATGGTTTTTTT
8006	AATATAATTTTATGGTTTTTTTC
8007	ATATAATTTTATGGTTTTTTTCA
8008	TATAATTTTATGGTTTTTTTCAC
8009	ATAATTTTATGGTTTTTTTCACT
8010	TAATTTTATGGTTTTTTTCACTT
8011	AATTTTATGGTTTTTTTCACTTA
8012	ATTTTATGGTTTTTTTCACTTAG
8013	TTTTATGGTTTTTTTCACTTAGA
8014	TTTATGGTTTTTTTCACTTAGAA
8015	TTATGGTTTTTTTCACTTAGAAC
8016	TATGGTTTTTTTCACTTAGAACC

Fig. 29 cont'd (Sheet 167 of 170)

ID	SEQUENCE
8017	ATGGTTTTTTTCACTTAGAACCT
8018	TGGTTTTTTTCACTTAGAACCTT
8019	GGTTTTTTTCACTTAGAACCTTT
8020	GTTTTTTTCACTTAGAACCTTTC
8021	TTTTTTTCACTTAGAACCTTTCT
8022	TTTTTTCACTTAGAACCTTTCTG
8023	TTTTTCACTTAGAACCTTTCTGT
8024	TTTTCACTTAGAACCTTTCTGTG
8025	TTTCACTTAGAACCTTTCTGTGT
8026	TTCACTTAGAACCTTTCTGTGTG
8027	TCACTTAGAACCTTTCTGTGTGG
8028	CACTTAGAACCTTTCTGTGTGGA
8029	ACTTAGAACCTTTCTGTGTGGAA
8030	CTTAGAACCTTTCTGTGTGGAAA
8031	TTAGAACCTTTCTGTGTGGAAAA
8032	TAGAACCTTTCTGTGTGGAAAAC
8033	AGAACCTTTCTGTGTGGAAAACT
8034	GAACCTTTCTGTGTGGAAAACTA
8035	AACCTTTCTGTGTGGAAAACTAA
8036	ACCTTTCTGTGTGGAAAACTAAG
8037	CCTTTCTGTGTGGAAAACTAAGA
8038	CTTTCTGTGTGGAAAACTAAGAA
8039	TTTCTGTGTGGAAAACTAAGAAA
8040	TTCTGTGTGGAAAACTAAGAAAA
8041	TCTGTGTGGAAAACTAAGAAAAT
8042	CTGTGTGGAAAACTAAGAAAATT
8043	TGTGTGGAAAACTAAGAAAATTG
8044	GTGTGGAAAACTAAGAAAATTGC
8045	TGTGGAAAACTAAGAAAATTGCT
8046	GTGGAAAACTAAGAAAATTGCTT
8047	TGGAAAACTAAGAAAATTGCTTT
8048	GGAAAACTAAGAAAATTGCTTTC
8049	GAAAACTAAGAAAATTGCTTTCT
8050	AAAACTAAGAAAATTGCTTTCTG
8051	AAACTAAGAAAATTGCTTTCTGC
8052	AACTAAGAAAATTGCTTTCTGCT
8053	ACTAAGAAAATTGCTTTCTGCTG
8054	CTAAGAAAATTGCTTTCTGCTGT
8055	TAAGAAAATTGCTTTCTGCTGTA
8056	AAGAAAATTGCTTTCTGCTGTAT
8057	AGAAAATTGCTTTCTGCTGTATA
8058	GAAAATTGCTTTCTGCTGTATAA
8059	AAAATTGCTTTCTGCTGTATAAT
8060	AAATTGCTTTCTGCTGTATAATC
8061	AATTGCTTTCTGCTGTATAATCT
8062	ATTGCTTTCTGCTGTATAATCTG
8063	TTGCTTTCTGCTGTATAATCTGG
8064	TGCTTTCTGCTGTATAATCTGGC

Fig. 29 cont'd (Sheet 168 of 170)

ID	SEQUENCE
8065	GCTTTCTGCTGTATAATCTGGCA
8066	CTTTCTGCTGTATAATCTGGCAT
8067	TTTCTGCTGTATAATCTGGCATT
8068	TTCTGCTGTATAATCTGGCATTC
8069	TCTGCTGTATAATCTGGCATTCA
8070	CTGCTGTATAATCTGGCATTCAT
8071	TGCTGTATAATCTGGCATTCATT
8072	GCTGTATAATCTGGCATTCATTG
8073	CTGTATAATCTGGCATTCATTGT
8074	TGTATAATCTGGCATTCATTGTA
8075	GTATAATCTGGCATTCATTGTAG
8076	TATAATCTGGCATTCATTGTAGA
8077	ATAATCTGGCATTCATTGTAGAT
8078	TAATCTGGCATTCATTGTAGATT
8079	AATCTGGCATTCATTGTAGATTA
8080	ATCTGGCATTCATTGTAGATTAA
8081	TCTGGCATTCATTGTAGATTAAA
8082	CTGGCATTCATTGTAGATTAAAG
8083	TGGCATTCATTGTAGATTAAAGC
8084	GGCATTCATTGTAGATTAAAGCT
8085	GCATTCATTGTAGATTAAAGCTT
8086	CATTCATTGTAGATTAAAGCTTA
8087	ATTCATTGTAGATTAAAGCTTAT
8088	TTCATTGTAGATTAAAGCTTATT
8089	TCATTGTAGATTAAAGCTTATTT
8090	CATTGTAGATTAAAGCTTATTTT
8091	ATTGTAGATTAAAGCTTATTTTT
8092	TTGTAGATTAAAGCTTATTTTTC
8093	TGTAGATTAAAGCTTATTTTTCT
8094	GTAGATTAAAGCTTATTTTTCTG
8095	TAGATTAAAGCTTATTTTTCTGT
8096	AGATTAAAGCTTATTTTTCTGTG
8097	GATTAAAGCTTATTTTTCTGTGA
8098	ATTAAAGCTTATTTTTCTGTGAA
8099	TTAAAGCTTATTTTTCTGTGAAT
8100	TAAAGCTTATTTTTCTGTGAATA
8101	AAAGCTTATTTTTCTGTGAATAA
8102	AAGCTTATTTTTCTGTGAATAAA
8103	AGCTTATTTTTCTGTGAATAAAA
8104	GCTTATTTTTCTGTGAATAAAAC
8105	CTTATTTTTCTGTGAATAAAACG
8106	TTATTTTTCTGTGAATAAAACGT
8107	TATTTTTCTGTGAATAAAACGTA
8108	ATTTTTCTGTGAATAAAACGTAT
8109	TTTTTCTGTGAATAAAACGTATT
8110	TTTTCTGTGAATAAAACGTATTC
8111	TTTCTGTGAATAAAACGTATTCA
8112	TTCTGTGAATAAAACGTATTCAA

Fig. 29 cont'd (Sheet 169 of 170)

ID	SEQUENCE
8113	TCTGTGAATAAAACGTATTCAAT
8114	CTGTGAATAAAACGTATTCAATA
8115	TGTGAATAAAACGTATTCAATAA
8116	GTGAATAAAACGTATTCAATAAA
8117	TGAATAAAACGTATTCAATAAAA
8118	GAATAAAACGTATTCAATAAAAT
8119	AATAAAACGTATTCAATAAAATA
8120	ATAAAACGTATTCAATAAAATAC
8121	TAAAACGTATTCAATAAAATACT
8122	AAAACGTATTCAATAAAATACTA
8123	AAACGTATTCAATAAAATACTAT
8124	AACGTATTCAATAAAATACTATT
8125	ACGTATTCAATAAAATACTATTC
8126	CGTATTCAATAAAATACTATTCT
8127	GTATTCAATAAAATACTATTCTT
8128	TATTCAATAAAATACTATTCTTT
8129	ATTCAATAAAATACTATTCTTTA
8130	TTCAATAAAATACTATTCTTTAA
8131	TCAATAAAATACTATTCTTTAAA
8132	CAATAAAATACTATTCTTTAAAA
8133	AATAAAATACTATTCTTTAAAAT
8134	ATAAAATACTATTCTTTAAAATT
8135	TAAAATACTATTCTTTAAAATTA

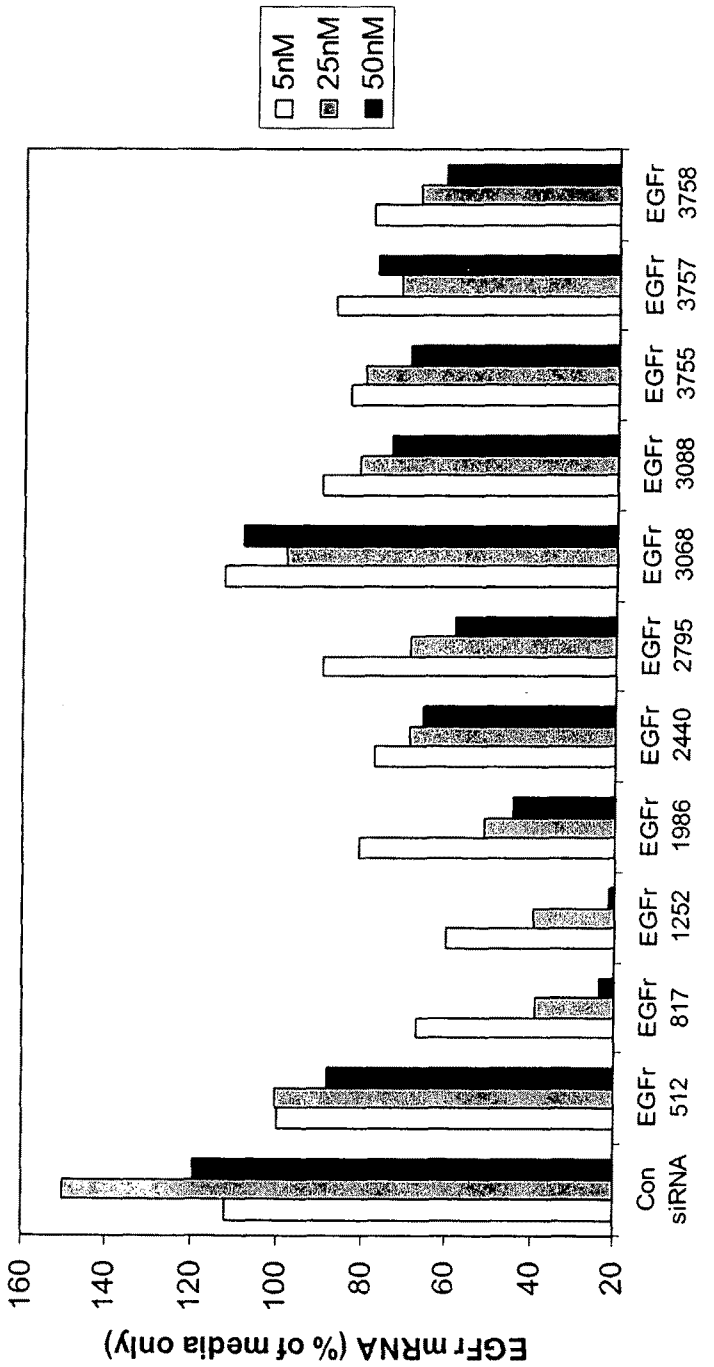

5nM
25nM
50nM
EGFr mRNA (% of media only)
160
140
120
100
80
60
40
20
Con siRNA
EGFr 512
EGFr 817
EGFr 1252
EGFr 1986
EGFr 2440
EGFr 2795
EGFr 3068
EGFr 3088
EGFr 3755
EGFr 3757
EGFr 3758

Figure 30

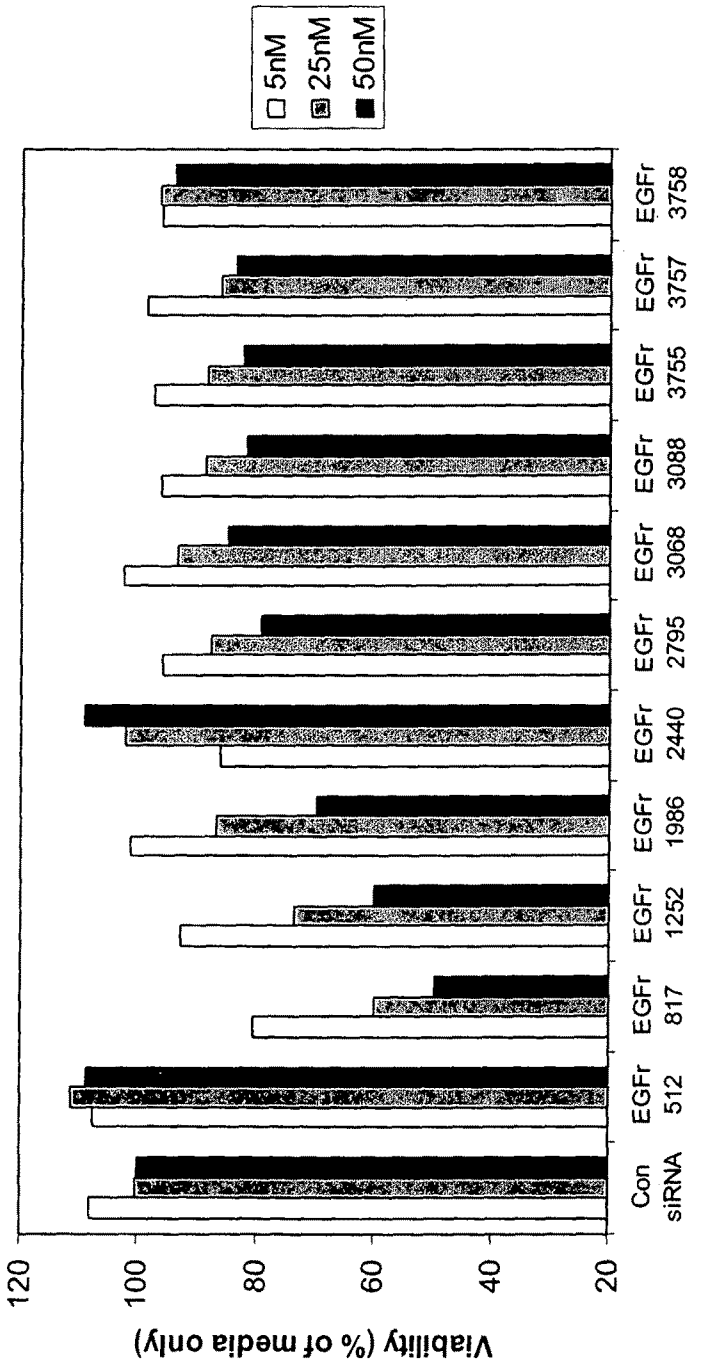

5nM
25nM
50nM
Viability (% of media only)
120
100
80
60
40
20
Con siRNA
EGFr 512
EGFr 817
EGFr 1252
EGFr 1986
EGFr 2440
EGFr 2795
EGFr 3068
EGFr 3088
EGFr 3755
EGFr 3757
EGFr 3758

Figure 31

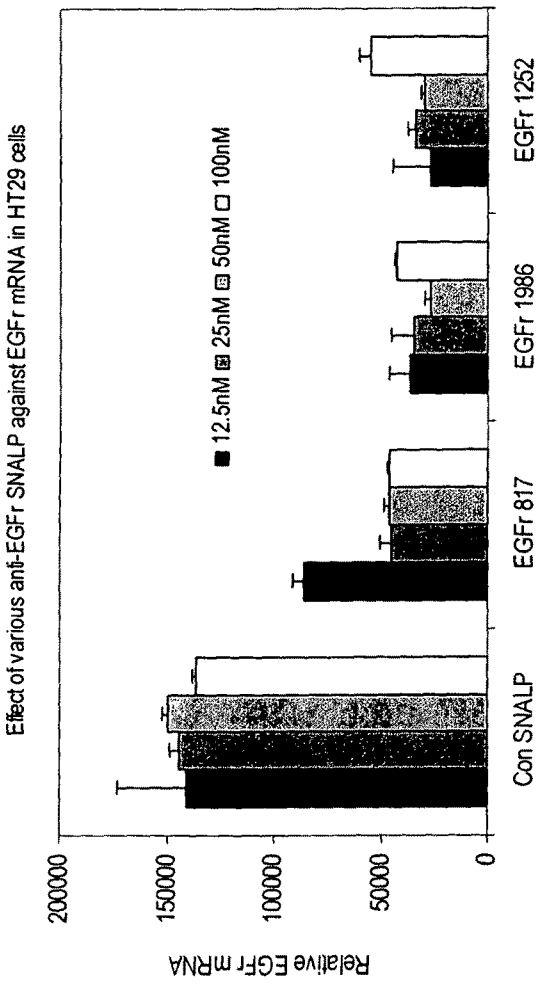

Effect of various anti-EGFr SNALP against EGFr mRNA in HT29 cells
12.5nM 25nM 50nM 100nM
Relative EGFr mRNA
200000
150000
100000
50000
0
Con SNALP
EGFr 817
EGFr 1986
EGFr 1252
siRNA SNALP

Figure 32

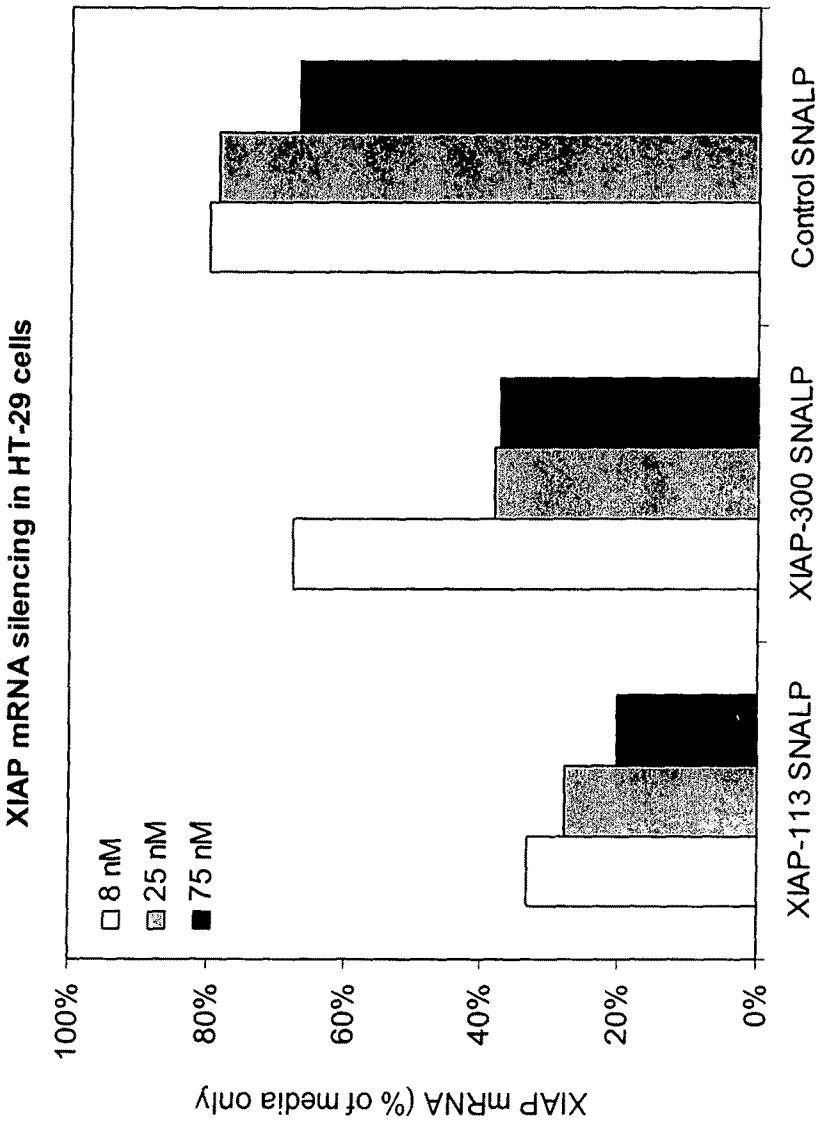

XIAP mRNA silencing in HT-29 cells
8 nM
25 nM
75 nM
100%
80%
60%
40%
20%
0%
XIAP mRNA (% of media only
XIAP-113 SNALP
XIAP-300 SNALP
Control SNALP

Figure 33

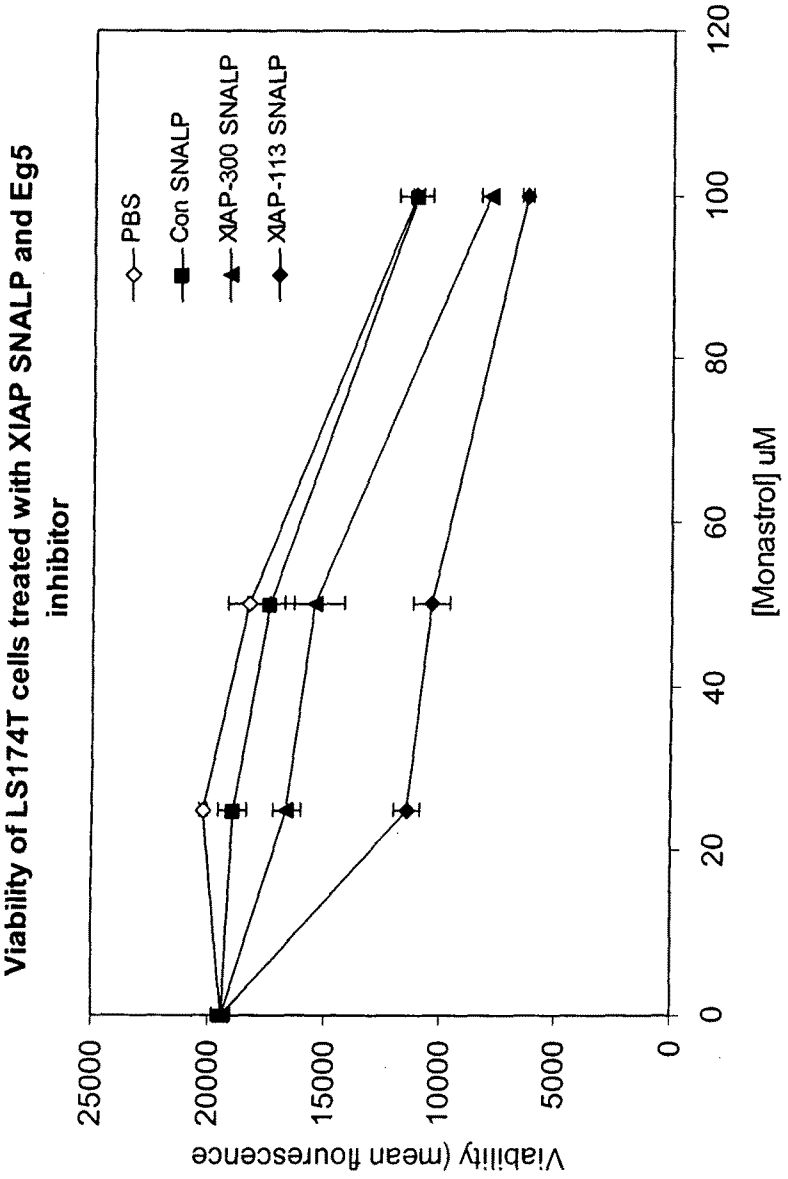

Viability of LS174T cells treated with XIAP SNALP and Eg5 inhibitor
PBS
Con SNALP
XIAP-300 SNALP
XIAP-113 SNALP
Viability (mean flourescence
25000
20000
15000
10000
5000
0
0
20
40
60
80
100
120
[Monastrol] uM

Figure 34

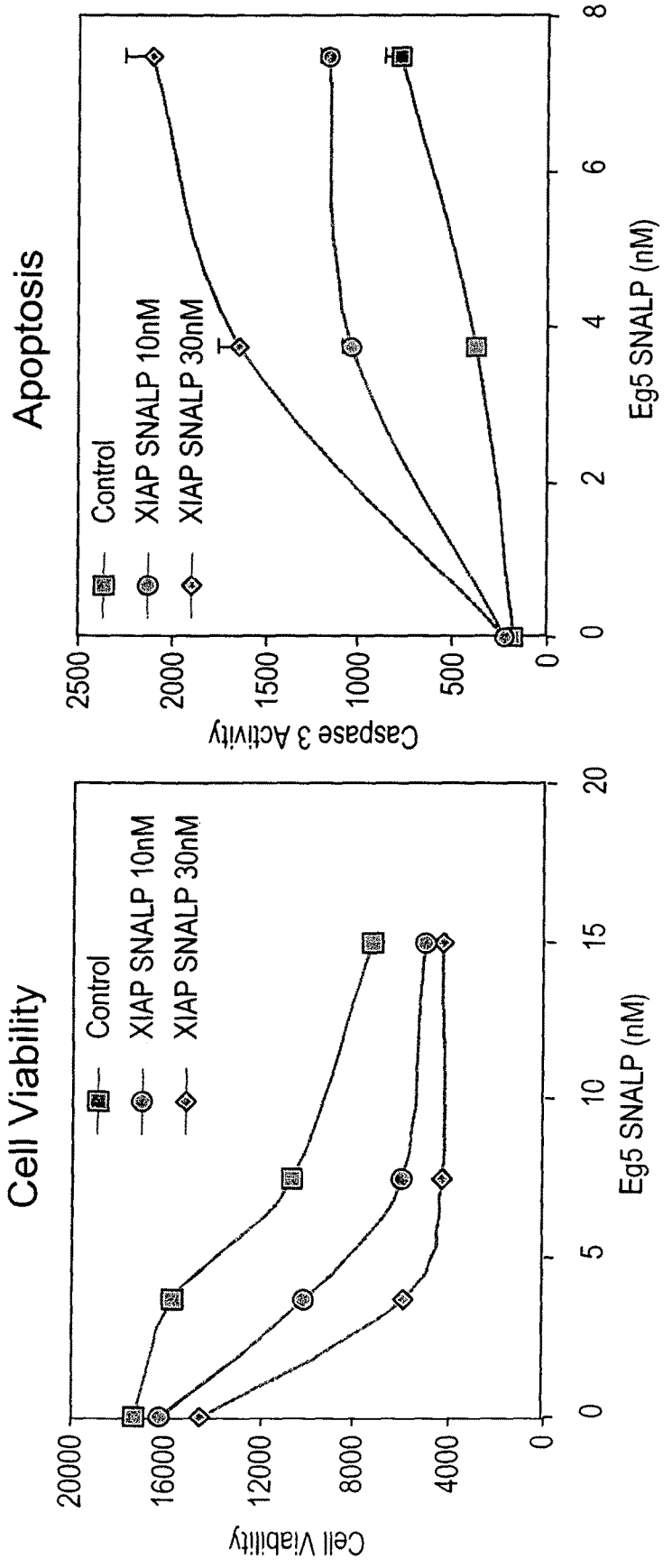

Apoptosis
Caspase 3 Activity
2500
2000
1500
1000
500
0
0
2
4
6
8
Eg5 SNALP (nM)
Control
XIAP SNALP 10nM
XIAP SNALP 30nM
Cell Viability
Cell Viability
20000
16000
12000
8000
4000
0
0
5
10
15
20
Eg5 SNALP (nM)
Control
XIAP SNALP 10nM
XIAP SNALP 30nM

Figure 35

SIRNA SILENCING OF GENES EXPRESSED IN CANCER

CROSS-REFERENCES TO RELATED APPLICATIONS

This application claims the benefit of U.S. Provisional Patent Application Nos. 60/808,859, filed May 26, 2006, and 60/817,556 filed Jun. 28, 2006, the disclosures of which are hereby incorporated by reference in their entirety for all purposes.

REFERENCE TO A "SEQUENCE LISTING," A TABLE, OR A COMPUTER PROGRAM LISTING APPENDIX SUBMITTED ON A COMPACT DISK

The Sequence Listing written in file -69-2.APP, 4,222,976 bytes, machine format IBM-PC, MS-Windows operating system, created on Oct. 7, 2008 on duplicate copies of compact disc of the written form of the Sequence Listing, i.e., "Copy 1 of 3" and "Copy 2 of 3", and the sequence information recorded in computer readable form on compact disc, i.e., "Copy 3 of 3" for application Ser. No. 11/807,872, MacLachlan et al., siRNA SILENCING OF GENES EXPRESSED IN CANCER, is hereby incorporated by reference.

BACKGROUND OF THE INVENTION

Cell proliferation and programmed cell death play important roles in the growth and development of an organism. In proliferative diseases such as cancer, the processes of cell proliferation and/or programmed cell death are often perturbed. For example, a cancer cell may have unregulated cell division through either the overexpression of a positive regulator of the cell cycle or the loss of a negative regulator of the cell cycle, perhaps by mutation. Alternatively, a cancer cell may have lost the ability to undergo programmed cell death through the overexpression of a negative regulator of apoptosis. Therefore, there is a need to develop new therapeutic agents that will restore the processes of checkpoint control and programmed cell death to cancerous cells.

RNA interference (RNAi) is an evolutionarily conserved process in which recognition of double-stranded RNA (dsRNA) ultimately leads to posttranscriptional suppression of gene expression. This suppression is mediated by short double stranded RNA (dsRNA), also called small interfering RNA (siRNA), which induces specific degradation of mRNA through complementary base pairing. In several model systems, i.e., mostly lower order animals, this natural response has been developed into a powerful tool for the investigation of gene function (Elbashir S M, et al., *Genes Dev,* 2001, 15:188-200; Hammond S M, et al., *Nat Rev Genet.,* 2001, 2:110-119). More recently it was discovered that introducing synthetic 21-nucleotide dsRNA duplexes into mammalian cells could efficiently silence gene expression. Although the precise mechanism is still unclear, RNAi offers a new way to inactivate genes of interest. In particular, for the treatment of neoplastic disorders (cancer), RNAi provides a potential new approach to modulate (e.g., reduce) the expression of certain genes, e.g., an anti-apoptotic molecule, a growth factor, a growth factor receptor, a mitotic spindle protein, a cell cycle protein, an angiogenic factor, an oncogene, an intracellular signal transducer, a molecular chaperone, and combinations thereof.

One such target is the Eg5 gene which produces the microtubule-associated protein, Eg5 (Kapoor, T. M., et al., *J. Cell Biol.,* 2001, 154, 1125-1133; Garrett, S. et al., *Curr Biol.,* 2003, 13, R810-812; Cassimeris, L., et al., *Curr Issues Mol. Biol.,* 2003, 5, 99-112; Houliston, E., et al., *Dev. Biol.* 1994, 164, 147-159). Generally, due to the clinical success seen with antimitotics in cancer therapy (e.g. taxanes), other proteins that that are also involved in the mitotic machinery, such as Eg5, have become desirable targets as next generation anti-cancer therapeutics. The mitotic kinesin, Eg5, contains an N-terminal motor domain which generates force along the microtubule, moving Eg5 to the microtubule plus end. During interphase in most epithelial cells, the plus ends of microtubules are oriented toward the plasma membrane while the minus ends are facing toward the nucleus. Upon entry into mitosis, microtubule plus ends reorient toward the chromosomes, while the minus ends are anchored at the spindle poles, forming a bipolar spindle. The homotetrameric structure of Eg5 has its motor domains arranged at two ends of a dumbbell such that it can bind and push apart spindle microtubules and generate and outward-directed force pushing spindle poles apart (Sawin, K. E., et al., *Prod Natl. Acad. Sci. USA,* 1995, 92, 4289-4293; Kapoor, T. M., et al., *J Cell Biol.,* 2000, 150, 975-988; Gaglio, T., et al., *J Cell Biol.,* 1996, 135, 399-414). Thus, Eg5 is critical for proper spindle formation during the mitotic process. Disruption of the process leads to activation of spindle assembly checkpoint, the major cell cycle control mechanism which prevents the cell undergoing mitosis to progress to anaphase and leads to cell cycle arrest. Inhibition of the production of the Eg5 protein, which is only expressed during mitosis, results in the induction of cancer cell apoptosis through a unique mechanism. In view of the important role of Eg5 has in the mitotic process, Eg5 has become an attractive therapeutic target for rapidly dividing cells, in particular, in cancer therapy.

The first small molecule inhibitors of Eg5 was identified in a phenotype-based screen and has been termed Monastrol, because of the formation of monoastral spindles due to Eg5 inhibition seen in cells treated with Monastrol (Mayer, T. U., et al., Science, 1999, 286, 971-974). Other small molecule inhibitors of Eg5 have been discovered since and are currently under development (Sakowicz, R., et al., *Cancer Res.,* 2004, 64, 3276-3280; Hotha, S. et al., Angew Chem. Intl. Ed. Engl., 2003, 42, 2379-2382). However, recent literature publications suggest that certain cancer cell lines, e.g., HT-29 colorectal cancer cells, are resistant toward small molecule Eg5 inhibitors, and thus suggest that small molecule Eg5 inhibitors may have be of more limited clinical use than previously thought.

A second target is the EGFR gene that encodes for the epidermal growth factor receptor (EGFR), a glycoprotein with a molecular weight of 170,000 to 180,000. EGFR is an intrinsic tyrosine-specific protein kinase, which is stimulated upon epidermal growth factor (EGF) binding. The known downstream effectors of EGFR include PI3-K, RAS-RAF-MAPK P44/P42, and protein kinase C signaling pathways. EGFR signaling involved in cell growth, angiogenesis, DNA repair, and autocrine growth regulation in a wide spectrum of human cancer cells (Wakeling A E., *Curr Opin Pharmacol* 2002, 2:382-387). Therefore, it has recently emerged as an innovative target for the development of new cancer therapy. Recently, a monoclonal antibody against EGFR called cetuximab has been developed. It has shown excellent clinical effects for the treatment of lung and head and neck cancer in a clinical trial in humans (Shin et al., *Clin Cancer Res,* 2001, 7:1204-1213). Other small chemical inhibitors, such as ZD-1839 have also been developed and demonstrated antitumor effects in in vitro and in vivo (Shawver L K, et al., Cancer Cell 2002, 1:117-123). However, clinical use of

ZD-1839 in humans has not been very successful. (Baselga *Eur J Cancer* 2001, 37:S16-22).

A third target is the XIAP (X-linked inhibitor of apoptosis protein) which is a member of the mammalian IAP gene family and encodes for the X-linked IAP (XIAP) protein. The anti-apoptotic function of XIAP is executed, at least in part, by inhibition of caspase-3 and caspase-7, two principal effectors of apoptosis. XIAP protein plays a critical role in regulating programmed cell death by suppressing activation of downstream caspase-3 and caspase-7. Interestingly, in pre-cancerous and cancerous cells, it is believed that expression or overexpression of XIAPs makes it difficult for cancer cells to eliminate themselves, instead allowing them to proliferate, metastasize and accumulate additional oncogenic mutations. Inhibition of XIAP activity using anti-sense oligonucleotides has demonstrates anti-tumor activity in human tumor xenograft animal model.

In view of the above, there is a need for compositions and methods for modulating the expression of genes involved in cancer. The present invention addresses these and other needs.

SUMMARY OF THE INVENTION

The present invention provides compositions comprising siRNA molecules that target genes expressed in cancer and methods of using such compositions to silence expression of such genes.

One embodiment of the invention provides a nucleic acid-lipid particle comprising an siRNA molecule that targets a gene expressed in cancer. In some embodiments, the gene is selected from an anti-apoptotic molecule, a growth factor, a growth factor receptor, a mitotic spindle protein, a cell cycle protein, an angiogenic factor, an oncogene, an intracellular signal transducer, a molecular chaperone, and combinations thereof. In some embodiments, the lipid portion of the particle comprises a cationic lipid and a non-cationic lipid. In some embodiments, the nucleic acid-lipid particle further comprises a conjugated lipid that prevents aggregation of the particles and/or a sterol (e.g., cholesterol).

Another embodiment of the invention provides a nucleic acid-lipid particle that targets expression of the Eg5, EGFR or XIAP gene. The nucleic acid-lipid particle comprises an siRNA molecule that silences expression of the Eg5, EGFR or XIAP gene; a cationic lipid; a non-cationic lipid; and a conjugated lipid that inhibits aggregation of particles. The siRNA molecules may comprise at least one sequence set forth in Tables 1-9 (i.e., Tables 1-2 and 7 for Eg5; Tables 3-4 and 8 for EGFR; or Tables 5-6 and 9 for XIAP). In some embodiments, nucleic acid-lipid particles comprise at least 2, 3, 4, 5, or 6 of the sequences set forth in Tables 1-2 and 7 for Eg5; Tables 3-4 and 8 for EGFR; or Tables 5-6 and 9 for XIAP. In some embodiments,

The cationic lipid may be, e.g., N,N-dioleyl-N,N-dimethylammonium chloride (DODAC), N,N-distearyl-N,N-dimethylammonium bromide (DDAB), N-(1-(2,3-dioleoyloxy) propyl)-N,N,N-trimethylammonium chloride (DOTAP), N-(1-(2,3-dioleyloxy)propyl)-N,N,N-trimethylammonium chloride (DOTMA), and N,N-dimethyl-2,3-dioleyloxy)propylamine (DODMA), 1,2-DiLinoleyloxy-N,N-dimethylaminopropane (DLinDMA), and 1,2-Dilinolenyloxy-N,N-dimethylaminopropane (DLendMA), or mixtures thereof. The cationic lipid may comprise from about 2 mol % to about 60 mol %, about 5 mol % to about 45 mol %, about 5 mol % to about 15 mol %, about 30 mol % to about 50 mol % or about 40 mol % to about 50 mol % of the total lipid present in the particle.

The non-cationic lipid may be an anionic lipid or a neutral lipid including, but not limited to, a non-cationic lipid is a member selected from the group consisting of dioleoylphosphatidylethanolamine (DOPE), palmitoyloleoylphosphatidylcholine (POPC), egg phosphatidylcholine (EPC), distearoylphosphatidylcholine (DSPC), palmitoyloleyolphosphatidylglycerol (POPG), dipalmitoyl phosphatidyl ethanolamine (DPPE), dimyristoylphosphoethanolamine (DMPE), distearoyl-phosphatidyl-ethanolamine (DSPE), 16-O-monomethyl PE, 16-O-dimethyl PE, 18-1-trans PE, palmitoyloleoyl-phosphatidylethanolamine (POPE), 1-stearoyl-2-oleoyl-phosphatidyethanolamine (SOPE), 1,2-dielaidoyl-sn-glycero-3-phophoethanolamine (transDOPE), cholesterol, or mixtures thereof. The non-cationic lipid comprises from about 5 mol % to about 90 mol % or about 20 mol % to about 85 mol % of the total lipid present in the particle.

The conjugated lipid that inhibits aggregation of particles may be a polyethyleneglycol (PEG)-lipid conjugate, a polyamide (ATTA)-lipid conjugate, a cationic-polymer-lipid conjugates (CPLs), or mixtures thereof. In one preferred embodiment, the nucleic acid-lipid particles comprise either a PEG-lipid conjugate or an ATTA-lipid conjugate together with a CPL. The conjugated lipid that inhibits aggregation of particles may comprise a polyethyleneglycol-lipid including, e.g., a PEG-diacylglycerol (DAG), a PEG dialkyloxypropyl (DAA), a PEG-phospholipid, a PEG-ceramide (Cer), or mixtures thereof. The PEG-DAA conjugate may be PEG-dilauryloxypropyl (C12), a PEG-dimyristyloxypropyl (C14), a PEG-dipalmityloxypropyl (C16), and a PEG-distearyloxypropyl (C18). In some embodiments, the conjugated lipid that inhibits aggregation of particles has the formula: A-W-Y, wherein: A is a lipid moiety; W is a hydrophilic polymer; and Y is a polycationic moiety. W may be a polymer selected from the group consisting of polyethyleneglycol (PEG), polyamide, polylactic acid, polyglycolic acid, polylactic acid/polyglycolic acid copolymers or combinations thereof, said polymer having a molecular weight of about 250 to about 7000 daltons. In some embodiments, Y has at least 4 positive charges at a selected pH. In some embodiments, Y may be lysine, arginine, asparagine, glutamine, derivatives thereof and combinations thereof. The conjugated lipid that prevents aggregation of particles may be about 0 mol % to about 20 mol %, about 1 mol % to about 15 mol %, about 4 mol % to about 10 mol %, or about 2 mol % of the total lipid present in said particle.

In some embodiments, the nucleic acid-lipid particle further comprises cholesterol at, e.g., about 0 mol % to about 10 mol %, about 2 mol % to about 10 mol %, about 10 mol % to about 60 mol % or about 20 mol % to about 45 mol % of the total lipid present in the particle.

In a specific embodiment of the invention, the nucleic acid-lipid particle comprises 48% cholesterol; 10% DSPC; 2% PEG-cDMA; and 40% DLinDMA.

In some embodiments, the siRNA in the nucleic acid-lipid particle is not substantially degraded after exposure of the particle to a nuclease at 37° C. for at least 20, 30, 45, or 60 minutes; or after incubation of the particle in serum at 37° C. for at least 30, 45, or 60 minutes, 2, 3, 4, 5, 6, 7, 8, 9, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, or 36 hours. In some embodiments, the siRNA is fully encapsulated in the nucleic acid-lipid particle. In some embodiments, the siRNA is complexed to the lipid portion of the particle.

The present invention further provides pharmaceutical compositions comprising the nucleic acid-lipid particles described herein and a pharmaceutically acceptable carrier.

The nucleic acid-lipid particles of the present invention are useful for the therapeutic delivery of nucleic acids comprising an interfering RNA sequence (i.e., an siRNA sequence that targets expression of an Eg5, EGFR or XIAP gene. In particular, it is an object of this invention to provide in vitro and in vivo methods for treatment of a disease in a mammal by downregulating or silencing the transcription and translation of a target nucleic acid sequence of interest. In these methods, an interfering RNA is formulated into a nucleic acid-lipid particle, and the particles are administered to patients requiring such treatment. Alternatively, cells are removed from a patient, the interfering RNA delivered in vitro, and reinjected into the patient. In one embodiment, the present invention provides for a method of introducing a nucleic acid into a cell by contacting a cell with a nucleic acid-lipid particle comprised of a cationic lipid, a non-cationic lipid, a conjugated lipid that inhibits aggregation, and an interfering RNA.

In one embodiment, at least 1%, 2%, 4%, 6%, 8%, 10%, 12%. 14%. 16% or 18% of the total injected dose of the nucleic acid-lipid particles is present in plasma 1, 2, 4, 6, 8, 12, 16, 18, or 24 hours after injection. In other embodiments, more than 20%, 30%, 40% and as much as 60%, 70% or 80% of the total injected dose of the nucleic acid-lipid particles is present in plasma 1, 4, 6, 8, 10, 12, 20, or 24 hours after injection. In one embodiment, the effect of an interfering RNA (e.g., downregulation of the target sequence) at a site proximal or distal to the site of administration is detectable at 12, 24, 48, 72, or 96 hours, 6, 8, 10, 12, 14, 16, 18, 19, 20, 22, 24, 26, or 28 days after administration of the nucleic acid-lipid particles. In one embodiment, downregulation of expression of the target sequence is detectable at 12, 24, 48, 72, or 96 hours, 6, 8, 10, 12, 14, 16, 18, 19, 20, 22, 24, 26, or 28 days after administration. In some embodiments, downregulation of Eg5, EGFR or XIAP gene is detected by detecting mRNA or protein levels in a biological sample from the mammal. In some embodiments, downregulation of expression of a Eg5, EGFR or XIAP sequence is detected by measuring the cell viability or the induction of apoptosis of cells in a biological sample from the mammal.

The particles are suitable for use in intravenous nucleic acid transfer as they are stable in circulation, of a size required for pharmacodynamic behavior resulting in access to extravascular sites and target cell populations. The invention also provides for pharmaceutically acceptable compositions comprising a nucleic acid-lipid particle.

Another embodiment of the present invention provides methods for in vivo delivery of interfering RNA (e.g., interfering RNA that silences expression of an Eg5, EGFR or XIAP gene). A nucleic acid-lipid particle comprising a cationic lipid, a non-cationic lipid, a conjugated lipid that inhibits aggregation of particles, and interfering RNA is administered (e.g., intravenously, intramuscularly, or subcutaneously) to a subject (e.g., a mammal such as a human or a rodent).

A further embodiment of the present invention provides a method of treating a disease or disorder in a mammalian subject. A therapeutically effective amount of a nucleic acid-lipid particle comprising a cationic lipid, a non-cationic lipid, a conjugated lipid that inhibits aggregation of particles, and interfering RNA (e.g., interfering RNA that silences expression of a Eg5, EGFR or XIAP gene) is administered to the mammalian subject (e.g., a rodent such as a mouse, a primate such as a human, a chimpanzee, or a monkey). In some embodiments, the mammalian subject has a cell proliferative disorder. In certain aspects of this embodiment, the mammalian subject has a said cell proliferative disorder is selected from the group consisting of neoplasia (cancer), hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation. Preferably, said cell proliferative disorder is a neoplastic disorder, i.e., cancer. In some embodiments, the cancer includes, but is not limited to papilloma, blastoglioma, Kaposi's sarcoma, melanoma, lung cancer, ovarian cancer, prostate cancer, squamous cell carcinoma, astrocytoma, head cancer, neck cancer, bladder cancer, breast cancer, lung cancer, colorectal cancer, thyroid cancer, pancreatic cancer, gastric cancer, hepatocellular carcinoma, leukemia, lymphoma, Hodgkin's disease, osteosarcoma, testicular cancer, and Burkitt's disease.

The invention further provides siRNA molecules having the sequences set forth in any one of Tables 1-9. In some embodiments, the siRNA molecules comprise modified nucleotides. The siRNA molecules comprising modified nucleotides are capable of silencing expression of a target sequence and are less immunostimulatory than a corresponding unmodified siRNA sequence. In some embodiments, less than about 20%, 15%, 10%, 5%, or 2% of the nucleotides in the siRNA comprise modified nucleotides. In some embodiments, the modified nucleotide is selected from a 2'-O-methyl (2'OMe) pyrimidine and a 2'OMe purine (e.g., a 2'OMe-guanosine, a 2'OMe-uridine, and a 2'OMe-adenosine). In some embodiments, the modified nucleotide is not 2'OMe-cytosine. In some embodiments, the modified nucleotides are present in one strand of the siRNA (e.g., in the sense strand). In some embodiments the corresponding unmodified siRNA sequence comprises at least one 5'-GU-3' motif. In some embodiments, the at least one 5'-GU-3' motif is in the sense strand of the unmodified siRNA sequence. In some embodiments, the double-stranded sequence comprises a hairpin loop structure.

The invention also provides compositions comprising the siRNA molecules described herein and a pharmaceutically acceptable carrier.

These and other embodiments of the invention are further described in the detailed description that follows.

BRIEF DESCRIPTION OF THE DRAWINGS

FIG. **1** illustrates data demonstrating RNAi activity of a Eg5 siRNA panel (at 1, 5, and 25 nM concentration) complexed with lipofectamine in HeLa cells (human).

FIG. **2** illustrates data demonstrating RNAi activity of a Eg5 siRNA panel (at 1, 5, and 25 nM concentration) complexed with lipofectamine in Neuro2A cells (mouse).

FIG. **3** illustrates data demonstrating RNAi activity of selected SNALP formulated Eg5 siRNA sequences in Neuro2A cells.

FIG. **4** illustrates data demonstrating that that the potent effects of Eg5 2263 U/U SNALP on cell viability is due to the silencing of Eg5 protein. Top panel: Eg5:GAPD mRNA ratios, bottom panel: Percent knockdown of Eg5 mRNA versus non-treated cells.

FIG. **5** illustrates data demonstrating certain characteristic changes seen in cell phenotype following treatment with Eg5 O/O siRNA.

FIG. **6** illustrates a list showing the sequences of various 2'-OMe modified Eg5 2263 siRNAs (SEQ ID NOS:1-3, 2, 3, 4, 2, 1, 5, 1, 6, 3, 5, 3, 6, 4, 6, 4 and 5, respectively).

FIG. **7** illustrates data demonstrating the activity of 2'-OMe modified Eg5 2263 siRNAs in HeLa cells (human).

FIG. **8** illustrates data demonstrating the activity of 2'-OMe modified Eg5 2263 siRNAs in Neuro2A cells (mouse).

FIG. **9** illustrates data demonstrating the Interferon induction activity for various 2'-OMe modified Eg5 2263 siRNAs, (i.e., U/O, G/O, U/U, G/G) in a SNALP formulation.

FIG. **10** illustrates data demonstrating the antibody response against the delivery vehicle for 2'-OMe modified Eg5 2663 U/U SNALP as compared to an unmodified Eg5 siRNA.

FIG. **11** illustrates data demonstrating the RNAi activity of 2'-OMe modified Eg5 2263 U/U SNALP against a range of tumor cells.

FIG. **12** illustrates data demonstrating the induction of apoptosis by Eg5 2263 U/U SNALP in human hepatocellular carcinoma cells.

FIG. **13** illustrates data demonstrating the induction of apoptosis by Eg5 2263 U/U SNALP in human colorectal cancer cells.

FIG. **14** illustrates data comparing the induction of apoptosis by Eg5 2263 U/U SNALP with a small molecule Eg5 inhibitor in human colorectal cells.

FIG. **15** illustrates data comparing the RNAi activity of Eg5 2263 U/U SNALP vs. a small molecule Eg5 inhibitor in a variety of cancer cells.

FIG. **16** illustrates data demonstrating the stability of naked Eg5 siRNA and SNALP encapsulated Eg5 O/O siRNA toward serum nuclease degradation.

FIG. **17** illustrates data demonstrating in vivo s.c. tumor growth of Neuro2A after treatment with Eg5 2263 U/U SNALP.

FIG. **18** illustrates data demonstrating that in vivo dosing with Eg5 2263 U/U SNALP in mice bearing s.c. Neuro2A tumors is well tolerated.

FIG. **19** illustrates data showing that the tumor histopathology of the intrahepatic Neuro2A tumor that was treated with Eg5 2263 U/U SNALP.

FIG. **20** illustrates data showing the tumor histopathology of the intrahepatic Neuro2A tumor that was treated with control SNALP

FIG. **21** is Table 1 which sets forth a list of Eg5 siRNA (SEQ ID NOS:7-32).

FIG. **22** is Table 2 which sets forth an additional list of Eg5 siRNA (SEQ ID NOS:33-62).

FIG. **23** is Table 3 which sets forth a list of EGFR siRNA (SEQ ID NOS:63-92).

FIG. **24** is Table 4 which sets forth an additional list of EGFR siRNA (SEQ ID NOS:93-118).

FIG. **25** is Table 5 which sets forth a list of XIAP siRNA (SEQ ID NOS:119-145).

FIG. **26** is Table 6 which sets forth an additional list of XIAP siRNA (SEQ ID NOS:146-173).

FIG. **27** is Table 7 which sets forth an additional list of Eg5 siRNA (SEQ ID NOS:174-4977).

FIG. **28** is Table 8 which sets forth an additional list of EGFR siRNA (SEQ ID NOS:4978-10362).

FIG. **29** is Table 9 which sets forth an additional list of XIAP siRNA (SEQ ID NOS:10363-18497).

FIG. **30** illustrates data showing in vitro silencing of EGFR mRNA by the panels of EGFR siRNA sequences set forth in Tables 3 and 4.

FIG. **31** illustrates data showing the silencing of EGFR mRNA correlates with a decrease in tumor cell viability.

FIG. **32** illustrates data showing in vitro silencing of EGFR mRNA by EGFR SNALP.

FIG. **33** illustrates data showing in vitro silencing of XIAP mRNA by XIAP SNALP.

FIG. **34** illustrates data showing the cells treated with XIAP SNALP are sensitized to Eg5 inhibitors.

FIG. **35** illustrates data showing that silencing of XIAP mRNA with XIAP SNALP sensitizes tumor cells to killing by Eg5 SNALP.

DETAILED DESCRIPTION OF THE INVENTION

I. Introduction

The invention provides compositions and methods for treating cancer. In particular, the invention provides nucleic acid-lipid particles comprising siRNA molecules that silence genes expressed in cancer including, e.g., growth factors (e.g. epidermal growth factor ("EGF") and insulin growth factor-1 ("IGF-1")), growth factor receptors (e.g., epidermal growth factor receptor ("EGFR") and hepatocyte growth factor receptor (i.e. c-Met)), mitotic spindle proteins (e.g., kinesins such as kinesin family member 11 ("Eg5" or "KIF11"), anti-apoptotic molecules (e.g., caspase inhibitors such as XIAP and CrmA, survivin, bcl-2), cell cycle proteins (e.g., cyclin E and aurora kinase), angiogenic factors (e.g., vascular endothelial growth factor ("VEGF") and vascular endothelial growth factor receptor ("VEGFR")); oncogenes (e.g., src, fyn, ras and myc), intracellular signal transducers (e.g., mammalian target of rapamycin ("mTOR"), MAP kinase kinases ("MEK") and nuclear factor kappa-B ("NFkB")), and molecular chaperones (e.g., HSP90). The lipid portion of the nucleic acid-lipid particles comprise a cationic lipid, a non-cationic lipid, optionally a lipid that prevents aggregation of particles. It is a discovery of the invention that the nucleic acid-lipid particles described herein are particularly effective for encapsulating and delivering siRNA molecules that target cancer cells.

This invention is based in part on the discovery that silencing Eg5, EGFR and/or XIAP gene expression is an effective means to halt proliferation of rapidly dividing cells, e.g., cancer cells. Accordingly, the present invention also provides nucleic acid-lipid particles that target Eg5, EGFR and/or XIAP gene expression comprising an siRNA that silences Eg5, EGFR and/or XIAP gene expression; a cationic lipid; a non-cationic lipid; and a conjugated lipid that inhibits aggregation of particles. The invention further provides methods of silencing Eg5, EGFR or XIAP gene expression by administering the nucleic acid-lipid particles described herein to a mammalian subject. In addition, the invention provides methods of treating a subject who suffers from a cell proliferative disorder, e.g., cancer, by administering the nucleic acid-lipid particles described herein.

II. Definitions

The term "Eg5" refers to the kif11 gene product, a member in a class of kinesin-related proteins that are involved in functions related to movements of organelles, microtubules, or chromosomes along microtubules. These functions include axonal transport, microtubule sliding during nuclear fusion or division, and chromosome disjunction during meiosis and early mitosis. Eg5 appears to play a critical role in mitosis of mammalian cells. Sequences for Eg5 are set forth in, e.g., Genbank Accession Nos. NM_004523 (human) and NM_010615 (mouse).

The term "EGFR" refers to the cell surface receptor, epidermal growth factor receptor, also known as ERBB1, that is a member of the ERBB tyrosine kinase family. EGF has 3 regions: one projects outside the cell and contains the site for binding epidermal growth factor (EGF) and related growth factors; the second is embedded in the membrane; the third projects into the cytoplasm of the cell's interior. EGFR is a phosphotyrosinekinase. Binding of EGFR by EGF has a profound effect on the differentiation of specific cells in vivo and is a potent mitogenic factor for a variety of cultured cells of both ectodermal and mesodermal origin. Sequences for the

EGF gene are set forth in Genbank Accession Nos. NM_005228 (human) and NM_207655 (mouse).

The term "XIAP" or "X-linked inhibitor of apoptosis" is a potent member of the inhibitor of apoptosis (IAP) family. All members of this family possess baculoviral IAP (BIR) repeats, cysteine-rich domains of approximately 80 amino acids that bind and inhibit caspases. XIAP has 3 BIR domains and a C-terminal RING zinc finger that possesses E3 ubiquitin ligase activity. The anticaspase activity of XIAP and is important in mediating apoptosis resistance in cancer cells. Sequences for XIAP are set forth in Genbank Accession Nos. NM_001167 (human) and NM_009688 (mouse).

The term "interfering RNA" or "RNAi" or "interfering RNA sequence" refers to double-stranded RNA (i.e., duplex RNA) that targets (i.e., silences, reduces, or inhibits) expression of a target gene (i.e., by mediating the degradation of mRNAs which are complementary to the sequence of the interfering RNA) when the interfering RNA is in the same cell as the target gene. Interfering RNA thus refers to the double stranded RNA formed by two complementary strands or by a single, self-complementary strand. Interfering RNA typically has substantial or complete identity to the target gene. The sequence of the interfering RNA can correspond to the full length target gene, or a subsequence thereof. Interfering RNA includes small-interfering RNA" or "siRNA," i.e., interfering RNA of about 15-60, 15-50, 15-50, or 15-40 (duplex) nucleotides in length, more typically about, 15-30, 15-25 or 19-25 (duplex) nucleotides in length, and is preferably about 20-24 or about 21-22 or 21-23 (duplex) nucleotides in length (e.g., each complementary sequence of the double stranded siRNA is 15-60, 15-50, 15-50, 15-40, 15-30, 15-25 or 19-25 nucleotides in length, preferably about 20-24 or about 21-22 or 21-23 nucleotides in length, and the double stranded siRNA is about 15-60, 15-50, 15-50, 15-40, 15-30, 15-25 or 19-25 preferably about 20-24 or about 21-22 or 21-23 base pairs in length). siRNA duplexes may comprise 3' overhangs of about 1 to about 4 nucleotides, preferably of about 2 to about 3 nucleotides and 5' phosphate termini. The siRNA can be chemically synthesized or maybe encoded by a plasmid (e.g., transcribed as sequences that automatically fold into duplexes with hairpin loops). siRNA can also be generated by cleavage of longer dsRNA (e.g., dsRNA greater than about 25 nucleotides in length) with the *E. coli* RNase III or Dicer. These enzymes process the dsRNA into biologically active siRNA (see, e.g., Yang et al., *PNAS USA* 99: 9942-7 (2002); Calegari et al., *PNAS USA* 99: 14236 (2002); Byrom et al., *Ambion TechNotes* 10(1): 4-6 (2003); Kawasaki et al., *Nucleic Acids Res.* 31: 981-7 (2003); Knight and Bass, *Science* 293: 2269-71 (2001); and Robertson et al., *J. Biol. Chem.* 243: 82 (1968)). Preferably, dsRNA are at least 50 nucleotides to about 100, 200, 300, 400 or 500 nucleotides in length. A dsRNA may be as long as 1000, 1500, 2000, 5000 nucleotides in length, or longer. The dsRNA can encode for an entire gene transcript or a partial gene transcript.

"Substantial identity" refers to a sequence that hybridizes to a reference sequence under stringent conditions, or to a sequence that has a specified percent identity over a specified region of a reference sequence.

The phrase "stringent hybridization conditions" refers to conditions under which a probe will hybridize to its target subsequence, typically in a complex mixture of nucleic acids, but to no other sequences. Stringent conditions are sequence-dependent and will be different in different circumstances. Longer sequences hybridize specifically at higher temperatures. An extensive guide to the hybridization of nucleic acids is found in Tijssen, *Techniques in Biochemistry and Molecular Biology—Hybridization with Nucleic Probes*, "Overview of principles of hybridization and the strategy of nucleic acid assays" (1993). Generally, stringent conditions are selected to be about 5-10° C. lower than the thermal melting point (T_m) for the specific sequence at a defined ionic strength pH. The T_m is the temperature (under defined ionic strength, pH, and nucleic concentration) at which 50% of the probes complementary to the target hybridize to the target sequence at equilibrium (as the target sequences are present in excess, at T_m, 50% of the probes are occupied at equilibrium). Stringent conditions may also be achieved with the addition of destabilizing agents such as formamide. For selective or specific hybridization, a positive signal is at least two times background, preferably 10 times background hybridization.

Exemplary stringent hybridization conditions can be as following: 50% formamide, 5×SSC, and 1% SDS, incubating at 42° C., or, 5×SSC, 1% SDS, incubating at 65° C., with wash in 0.2×SSC, and 0.1% SDS at 65° C. For PCR, a temperature of about 36° C. is typical for low stringency amplification, although annealing temperatures may vary between about 32° C. and 48° C. depending on primer length. For high stringency PCR amplification, a temperature of about 62° C. is typical, although high stringency annealing temperatures can range from about 50° C. to about 65° C., depending on the primer length and specificity. Typical cycle conditions for both high and low stringency amplifications include a denaturation phase of 90° C.-95° C. for 30 sec-2 min., an annealing phase lasting 30 sec.-2 min., and an extension phase of about 72° C. for 1-2 min. Protocols and guidelines for low and high stringency amplification reactions are provided, e.g., in Innis et al. (1990) *PCR Protocols, A Guide to Methods and Applications*, Academic Press, Inc. N.Y.).

Nucleic acids that do not hybridize to each other under stringent conditions are still substantially identical if the polypeptides which they encode are substantially identical. This occurs, for example, when a copy of a nucleic acid is created using the maximum codon degeneracy permitted by the genetic code. In such cases, the nucleic acids typically hybridize under moderately stringent hybridization conditions. Exemplary "moderately stringent hybridization conditions" include a hybridization in a buffer of 40% formamide, 1 M NaCl, 1% SDS at 37° C., and a wash in 1×SSC at 45° C. A positive hybridization is at least twice background. Those of ordinary skill will readily recognize that alternative hybridization and wash conditions can be utilized to provide conditions of similar stringency. Additional guidelines for determining hybridization parameters are provided in numerous reference, e.g., and Current Protocols in Molecular Biology, ed. Ausubel, et al.

The terms "substantially identical" or "substantial identity," in the context of two or more nucleic acids, refer to two or more sequences or subsequences that are the same or have a specified percentage of nucleotides that are the same (i.e., at least about 60%, preferably 65%, 70%, 75%, preferably 80%, 85%, 90%, or 95% identity over a specified region), when compared and aligned for maximum correspondence over a comparison window, or designated region as measured using one of the following sequence comparison algorithms or by manual alignment and visual inspection. This definition, when the context indicates, also refers analogously to the complement of a sequence. Preferably, the substantial identity exists over a region that is at least about 5, 10, 15, 20, 25, 30, 35, 40, 45, 50, 75, or 100 nucleotides in length.

For sequence comparison, typically one sequence acts as a reference sequence, to which test sequences are compared. When using a sequence comparison algorithm, test and reference sequences are entered into a computer, subsequence coordinates are designated, if necessary, and sequence algo-

rithm program parameters are designated. Default program parameters can be used, or alternative parameters can be designated. The sequence comparison algorithm then calculates the percent sequence identities for the test sequences relative to the reference sequence, based on the program parameters.

A "comparison window", as used herein, includes reference to a segment of any one of the number of contiguous positions selected from the group consisting of from 20 to 600, usually about 50 to about 200, more usually about 100 to about 150 in which a sequence may be compared to a reference sequence of the same number of contiguous positions after the two sequences are optimally aligned. Methods of alignment of sequences for comparison are well-known in the art. Optimal alignment of sequences for comparison can be conducted, e.g., by the local homology algorithm of Smith & Waterman, *Adv. Appl. Math.* 2:482 (1981), by the homology alignment algorithm of Needleman & Wunsch, *J. Mol. Biol.* 48:443 (1970), by the search for similarity method of Pearson & Lipman, *Proc. Nat'l. Acad. Sci. USA* 85:2444 (1988), by computerized implementations of these algorithms (GAP, BESTFIT, FASTA, and TFASTA in the Wisconsin Genetics Software Package, Genetics Computer Group, 575 Science Dr., Madison, Wis.), or by manual alignment and visual inspection (see, e.g., *Current Protocols in Molecular Biology* (Ausubel et al., eds. 1995 supplement)).

A preferred example of algorithm that is suitable for determining percent sequence identity and sequence similarity are the BLAST and BLAST 2.0 algorithms, which are described in Altschul et al., *Nuc. Acids Res.* 25:3389-3402 (1977) and Altschul et al., *J. Mol. Biol.* 215:403-410 (1990), respectively. BLAST and BLAST 2.0 are used, with the parameters described herein, to determine percent sequence identity for the nucleic acids and proteins of the invention. Software for performing BLAST analyses is publicly available through the National Center for Biotechnology Information. This algorithm involves first identifying high scoring sequence pairs (HSPs) by identifying short words of length W in the query sequence, which either match or satisfy some positive-valued threshold score T when aligned with a word of the same length in a database sequence. T is referred to as the neighborhood word score threshold (Altschul et al., supra). These initial neighborhood word hits act as seeds for initiating searches to find longer HSPs containing them. The word hits are extended in both directions along each sequence for as far as the cumulative alignment score can be increased. Cumulative scores are calculated using, for nucleotide sequences, the parameters M (reward score for a pair of matching residues; always >0) and N (penalty score for mismatching residues; always <0). For amino acid sequences, a scoring matrix is used to calculate the cumulative score. Extension of the word hits in each direction are halted when: the cumulative alignment score falls off by the quantity X from its maximum achieved value; the cumulative score goes to zero or below, due to the accumulation of one or more negative-scoring residue alignments; or the end of either sequence is reached. The BLAST algorithm parameters W, T, and X determine the sensitivity and speed of the alignment. The BLASTN program (for nucleotide sequences) uses as defaults a wordlength (W) of 11, an expectation (E) or 10, M=5, N=−4 and a comparison of both strands. For amino acid sequences, the BLASTP program uses as defaults a wordlength of 3, and expectation (E) of 10, and the BLOSUM62 scoring matrix (see Henikoff & Henikoff, *Proc. Natl. Acad. Sci. USA* 89:10915 (1989)) alignments (B) of 50, expectation (E) of 10, M=5, N=−4, and a comparison of both strands.

The BLAST algorithm also performs a statistical analysis of the similarity between two sequences (see, e.g., Karlin & Altschul, *Proc. Nat'l. Acad. Sci. USA* 90:5873-5787 (1993)). One measure of similarity provided by the BLAST algorithm is the smallest sum probability (P(N)), which provides an indication of the probability by which a match between two nucleotide or amino acid sequences would occur by chance. For example, a nucleic acid is considered similar to a reference sequence if the smallest sum probability in a comparison of the test nucleic acid to the reference nucleic acid is less than about 0.2, more preferably less than about 0.01, and most preferably less than about 0.001.

The phrase "inhibiting expression of a target gene" refers to the ability of a siRNA of the invention to silence, reduce, or inhibit expression of a target gene (e.g., an Eg5, EGFR or XIAP gene). To examine the extent of gene silencing, a test sample (e.g., a biological sample from organism of interest expressing the target gene or a sample of cells in culture expressing the target gene) is contacted with an siRNA that silences, reduces, or inhibits expression of the target gene. Expression of the target gene in the test sample is compared to expression of the target gene in a control sample (e.g., a biological sample from organism of interest expressing the target gene or a sample of cells in culture expressing the target gene) that is not contacted with the siRNA. Control samples (i.e., samples expressing the target gene) are assigned a value of 100%. Silencing, inhibition, or reduction of expression of a target gene is achieved when the value of the test sample relative to the control sample is about 95%, 90%, 85%, 80%, 75%, 70%, 65%, 60%, 55%, 50%, 45%, 40%, 35%, 30%, 25%, 20%, or 10%. Suitable assays include, e.g., examination of protein or mRNA levels using techniques known to those of skill in the art such as dot blots, northern blots, in situ hybridization, ELISA, immunoprecipitation, enzyme function, as well as phenotypic assays known to those of skill in the art.

"Nucleic acid" refers to deoxyribonucleotides or ribonucleotides and polymers thereof in single- or double-stranded form. The term encompasses nucleic acids containing known nucleotide analogs or modified backbone residues or linkages, which are synthetic, naturally occurring, and non-naturally occurring, which have similar binding properties as the reference nucleic acid, and which are metabolized in a manner similar to the reference nucleotides. Examples of such analogs include, without limitation, phosphorothioates, phosphoramidates, methyl phosphonates, chiral-methyl phosphonates, 2-O-methyl ribonucleotides, peptide-nucleic acids (PNAs).

An "effective amount" or "therapeutically effective amount" of a siRNA is an amount sufficient to produce the desired effect, e.g., a decrease in the expression of a target sequence in comparison to the normal expression level detected in the absence of the siRNA.

The term "lipid" refers to a group of organic compounds that include, but are not limited to, esters of fatty acids and are characterized by being insoluble in water, but soluble in many organic solvents. They are usually divided into at least three classes: (1) "simple lipids' which include fats and oils as well as waxes; (2) "compound lipids" which include phospholipids and glycolipids; (3) "derived lipids" such as steroids.

"Lipid vesicle" refers to any lipid composition that can be used to deliver a compound including, but not limited to, liposomes, wherein an aqueous volume is encapsulated by an amphipathic lipid bilayer; or wherein the lipids coat an interior comprising a large molecular component, such as a plasmid comprising an interfering RNA sequence, with a reduced

aqueous interior; or lipid aggregates or micelles, wherein the encapsulated component is contained within a relatively disordered lipid mixture.

As used herein, "lipid encapsulated" can refer to a lipid formulation that provides a compound with full encapsulation, partial encapsulation, or both. In some embodiments, the nucleic acid is fully encapsulated in the lipid formulation (e.g., to form an SPLP, pSPLP, SNALP, or other nucleic acid-lipid particle).

As used herein, the term "cell proliferative disorder" includes disorders involving the undesired proliferation of a cell. Non-limiting examples of such disorders include neoplasias (i.e., cancer), hyperplasias, restenosis, cardiac hypertrophy, immune disorders and inflammation.

The nucleic acid-lipid particles of the present invention typically have a mean diameter of less than about 150 nm and are substantially nontoxic. In addition, the nucleic acids when present in the nucleic acid-lipid particles of the present invention are resistant in aqueous solution to degradation with a nuclease. Nucleic acid-lipid particles and their method of preparation are disclosed in U.S. Pat. No. 5,976,567, U.S. Pat. No. 5,981,501 and PCT Patent Publication No. WO 96/40964.

Various suitable cationic lipids may be used in the present invention, either alone or in combination with one or more other cationic lipid species or non-cationic lipid species.

The cationic lipids of Formula I and Formula II described herein typically carry a net positive charge at a selected pH, such as physiological pH. It has been surprisingly found that cationic lipids comprising alkyl chains with multiple sites of unsaturation, e.g., at least two or three sites of unsaturation, are particularly useful for forming lipid-nucleic acid particles with increased membrane fluidity. A number of cationic lipids and related analogs, which are also useful in the present invention, have been described in U.S. Pat. Nos. 5,208,036, 5,264,618, 5,279,833 and 5,283,185, and WO 96/10390, the disclosures of which are incorporated herein by reference.

The noncationic lipids used in the present invention can be any of a variety of neutral uncharged, zwitterionic or anionic lipids capable of producing a stable complex. They are preferably neutral, although they can alternatively be negatively charged. Examples of noncationic lipids useful in the present invention include: phospholipid-related materials, such as lecithin, phosphatidylethanolamine, lysolecithin, lysophosphatidylethanolamine, phosphatidylserine, phosphatidylinositol, sphingomyelin, cephalin, cardiolipin, phosphatidic acid, cerebrosides, dicetylphosphate, distearoylphosphatidylcholine (DSPC), dioleoylphosphatidylcholine (DOPC), dipalmitoylphosphatidylcholine (DPPC), dioleoylphosphatidylglycerol (DOPG), dipalmitoylphosphatidylglycerol (DPPG), dioleoyl-phosphatidylethanolamine (DOPE), palmitoyloleoylphosphatidylcholine (POPC), palmitoyloleoyl-phosphatidylethanolamine (POPE) and dioleoyl-phosphatidylethanolamine 4-(N-maleimidomethyl)-cyclohexane-1-carboxylate (DOPE-mal). Noncationic lipids or sterols such as cholesterol may be present. Additional nonphosphorous containing lipids are, e.g., stearylamine, dodecylamine, hexadecylamine, acetyl palmitate, glycerolricinoleate, hexadecyl stereate, isopropyl myristate, amphoteric acrylic polymers, triethanolamine-lauryl sulfate, alkyl-aryl sulfate polyethyloxylated fatty acid amides, dioctadecyldimethyl ammonium bromide and the like, diacylphosphatidylcholine, diacylphosphatidylethanolamine, ceramide, sphingomyelin, cephalin, and cerebrosides. Other lipids such as lysophosphatidylcholine and lysophosphatidylethanolamine may be present. Noncationic lipids also include polyethylene glycol-based polymers such as PEG 2000, PEG 5000 and polyethylene glycol conjugated to phospholipids or to ceramides (referred to as PEG-Cer).

In preferred embodiments, the noncationic lipids are diacylphosphatidylcholine (e.g., distearoylphosphatidylcholine, dioleoylphosphatidylcholine, dipalmitoylphosphatidylcholine and dilinoleoylphosphatidylcholine), diacylphosphatidylethanolamine (e.g. dioleoylphosphatidylethanolamine and palmitoyloleoylphosphatidylethanolamine), ceramide or sphingomyelin. The acyl groups in these lipids are preferably acyl groups derived from fatty acids having C_{10}-C_{24} carbon chains. More preferably the acyl groups are lauroyl, myristoyl, palmitoyl, stearoyl or oleoyl. In particularly preferred embodiments, the noncationic lipid will be cholesterol, 1,2-sn-dioleoylphosphatidylethanolamine, or egg sphingomyelin (ESM).

In addition to cationic and non-cationic lipids, the nucleic acid-lipid particles (e.g., SPLPs and SNALPs of the present invention comprise bilayer stabilizing component (BSC) such as an ATTA-lipid or a PEG-lipid, such as PEG coupled to dialkyloxypropyls (PEG-DAA) (see, copending U.S. Patent Application No. 60/503,239), PEG coupled to diacylglycerol (PEG-DAG) (see, copending U.S. patent application Ser. No. 10/136,707), PEG coupled to phosphatidylethanolamine (PE) (PEG-PE), or PEG conjugated to ceramides, or a mixture thereof (see, U.S. Pat. No. 5,885,613, which is incorporated herein by reference). In one preferred embodiment, the BSC is a conjugated lipid that inhibits aggregation of the nucleic acid-lipid particles. Suitable conjugated lipids include, but are not limited to PEG-lipid conjugates, ATTA-lipid conjugates, cationic-polymer-lipid conjugates (CPLs) or mixtures thereof. In one preferred embodiment, the nucleic acid-lipid particles comprise either a PEG-lipid conjugate or an ATTA-lipid conjugate together with a CPL.

PEG is a polyethylene glycol, a linear, water-soluble polymer of ethylene PEG repeating units with two terminal hydroxyl groups. PEGs are classified by their molecular weights; for example, PEG 2000 has an average molecular weight of about 2,000 daltons, and PEG 5000 has an average molecular weight of about 5,000 daltons. PEGs are commercially available from Sigma Chemical Co. and other companies and include, for example, the following: monomethoxypolyethylene glycol (MePEG-OH), monomethoxypolyethylene glycol-succinate (MePEG-S), monomethoxypolyethylene glycol-succinimidyl succinate (MePEG-S-NHS), monomethoxypolyethylene glycol-amine (MePEG-NH_2), monomethoxypolyethylene glycol-tresylate (MePEG-TRES), and monomethoxypolyethylene glycol-imidazolyl-carbonyl (MePEG-IM). In addition, monomethoxypolyethyleneglycol-acetic acid (MePEG-CH_2COOH), is particularly useful for preparing the PEG-lipid conjugates including, e.g., PEG-DAA conjugates.

In some embodiments, the PEG has an average molecular weight of from about 1000 to about 5000 daltons, more preferably, from about 1,000 to about 3,000 daltons and, even more preferably, of about 2,000 daltons. The PEG can be optionally substituted by an alkyl, alkoxy, acyl or aryl group. PEG can be conjugated directly to the lipid or may be linked to the lipid via a linker moiety. Any linker moiety suitable for coupling the PEG to a lipid can be used including, e.g., non-ester containing linker moieties and ester-containing linker moieties.

As used herein, the term "non-ester containing linker moiety" refers to a linker moiety that does not contain a carboxylic ester bond (—OC(O)—). Suitable non-ester containing linker moieties include, but are not limited to, amido (—C(O)NH—), amino (—NR—), carbonyl (—C(O)—), carbamate

(—NHC(O)O—), urea (—NHC(O)NH—), disulphide (—S—S—), ether (—O—), succinyl (—(O)CCH$_2$CH$_2$C(O)—), succinamidyl (—NHC(O)CH$_2$CH$_2$C(O)NH—), ether, disulphide, etc. as well as combinations thereof (such as a linker containing both a carbamate linker moiety and an amido linker moiety). In some embodiments, a carbamate linker is used to couple the PEG to the lipid.

In other embodiments, an ester containing linker moiety is used to couple the PEG to the lipid. Suitable ester containing linker moieties include, e.g., carbonate (—OC(O)O—), succinoyl, phosphate esters (—O—(O)POH—O—), sulfonate esters, and combinations thereof.

As used herein, the term "SNALP" refers to a stable nucleic acid-lipid particle, including SPLP. A SNALP represents a vesicle of lipids coating a reduced aqueous interior comprising a nucleic acid (e.g., ssDNA, dsDNA, ssRNA, dsRNA, siRNA, or a plasmid, including plasmids from which an interfering RNA is transcribed). As used herein, the term "SPLP" refers to a nucleic acid-lipid particle comprising a nucleic acid (e.g., a plasmid) encapsulated within a lipid vesicle. SNALPs and SPLPs typically contain a cationic lipid, a noncationic lipid, and a lipid that prevents aggregation of the particle (e.g., a PEG-lipid conjugate). SNALPs and SPLPs have systemic application as they exhibit extended circulation lifetimes following intravenous (i.v.) injection, accumulate at distal sites (e.g., sites physically separated from the administration site) and can mediate gene silencing or gene expression of a transfected nucleic acid at these distal sites. SPLPs include "pSPLP" which comprise an encapsulated condensing agent-nucleic acid complex as set forth in WO 00/03683.

The term "vesicle-forming lipid" is intended to include any amphipathic lipid having a hydrophobic moiety and a polar head group, and which by itself can form spontaneously into bilayer vesicles in water, as exemplified by most phospholipids.

The term "vesicle-adopting lipid" is intended to include any amphipathic lipid that is stably incorporated into lipid bilayers in combination with other amphipathic lipids, with its hydrophobic moiety in contact with the interior, hydrophobic region of the bilayer membrane, and its polar head group moiety oriented toward the exterior, polar surface of the membrane. Vesicle-adopting lipids include lipids that on their own tend to adopt a nonlamellar phase, yet which are capable of assuming a bilayer structure in the presence of a bilayer-stabilizing component. A typical example is DOPE (dioleoylphosphatidylethanolamine). Bilayer stabilizing components include, but are not limited to, conjugated lipids that inhibit aggregation of the SNALPs, polyamide oligomers (e.g., ATTA-lipid derivatives), peptides, proteins, detergents, lipid-derivatives, PEG-lipid derivatives such as PEG coupled to dialkyloxypropyls, PEG coupled to diacylglycerols, PEG coupled to phosphatidyl-ethanolamines, and PEG conjugated to ceramides (see, U.S. Pat. No. 5,885,613, which is incorporated herein by reference).

The term "amphipathic lipid" refers, in part, to any suitable material wherein the hydrophobic portion of the lipid material orients into a hydrophobic phase, while the hydrophilic portion orients toward the aqueous phase. Amphipathic lipids are usually the major component of a lipid vesicle. Hydrophilic characteristics derive from the presence of polar or charged groups such as carbohydrates, phosphate, carboxylic, sulfato, amino, sulfhydryl, nitro, hydroxy and other like groups. Hydrophobicity can be conferred by the inclusion of apolar groups that include, but are not limited to, long chain saturated and unsaturated aliphatic hydrocarbon groups and such groups substituted by one or more aromatic, cycloaliphatic or heterocyclic group(s). Examples of amphipathic compounds include, but are not limited to, phospholipids, aminolipids and sphingolipids. Representative examples of phospholipids include, but are not limited to, phosphatidylcholine, phosphatidylethanolamine, phosphatidylserine, phosphatidylinositol, phosphatidic acid, palmitoyloleoyl phosphatidylcholine, lysophosphatidylcholine, lysophosphatidylethanolamine, dipalmitoylphosphatidylcholine, dioleoylphosphatidylcholine, distearoylphosphatidylcholine or dilinoleoylphosphatidylcholine. Other compounds lacking in phosphorus, such as sphingolipid, glycosphingolipid families, diacylglycerols and .beta.-acyloxyacids, are also within the group designated as amphipathic lipids. Additionally, the amphipathic lipid described above can be mixed with other lipids including triglycerides and sterols.

The term "neutral lipid" refers to any of a number of lipid species that exist either in an uncharged or neutral zwitterionic form at a selected pH. At physiological pH, such lipids include, for example, diacylphosphatidylcholine, diacylphosphatidylethanolamine, ceramide, sphingomyelin, cephalin, cholesterol, cerebrosides and diacylglycerols.

The term "noncationic lipid" refers to any neutral lipid as described above as well as anionic lipids.

The term "anionic lipid" refers to any lipid that is negatively charged at physiological pH. These lipids include, but are not limited to, phosphatidylglycerol, cardiolipin, diacylphosphatidylserine, diacylphosphatidic acid, N-dodecanoyl phosphatidylethanolamines, N-succinyl phosphatidylethanolamines, N-glutarylphosphatidylethanolamines, lysylphosphatidylglycerols, palmitoyloleyolphosphatidylglycerol (POPG), and other anionic modifying groups joined to neutral lipids.

The term "cationic lipid" refers to any of a number of lipid species that carry a net positive charge at a selected pH, such as physiological pH (e.g., pH of about 7.0). As used herein, physiological pH refers to the pH of a biological fluid such as blood or lymph as well as the pH of a cellular compartment such as an endosome, an acidic endosome, or a lysosome). Such lipids include, but are not limited to, N,N-dioleyl-N,N-dimethylammonium chloride ("DODAC"); N-(2,3-dioleyloxy)propyl)-N,N,N-trimethylammonium chloride ("DOTMA"); N,N-distearyl-N,N-dimethylammonium bromide ("DDAB"); N-(2,3-dioleoyloxy)propyl)-N,N,N-trimethylammonium chloride ("DOTAP"); 3-(N—(N',N'-dimethylaminoethane)-carbamoyl)cholesterol ("DC-Chol"); N-(1,2-dimyristyloxyprop-3-yl)-N,N-dimethyl-N-hydroxyethyl ammonium bromide ("DMRIE"); 1,2-DiLinoleyloxy-N,N-dimethylaminopropane (DLinDMA); and 1,2-Dilinolenyloxy-N,N-dimethylaminopropane (DLenDMA). The following lipids are cationic and have a positive charge at below physiological pH or at physiological pH: DODAP, DODMA, DLinDMA and the like.

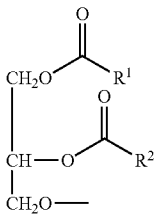
The term "hydrophobic lipid" refers to compounds having apolar groups that include, but are not limited to, long chain saturated and unsaturated aliphatic hydrocarbon groups and such groups optionally substituted by one or more aromatic, cycloaliphatic or heterocyclic group(s). Suitable examples include, but are not limited to, diacylglycerol, dialkylglycerol, N-N-dialkylamino, 1,2-diacyloxy-3-aminopropane and 1,2-dialkyl-3-aminopropane.

The term "fusogenic" refers to the ability of a liposome, an SNALP or other drug delivery system to fuse with membranes of a cell. The membranes can be either the plasma membrane or membranes surrounding organelles, e.g., endosome, nucleus, etc.

The term "diacylglycerol" refers to a compound having 2-fatty acyl chains, R^1 and R^2, both of which have indepen-

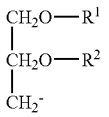
dently between 2 and 30 carbons bonded to the 1- and 2-position of glycerol by ester linkages. The acyl groups can be saturated or have varying degrees of unsaturation. Diacylglycerols have the following general formula:

(III)



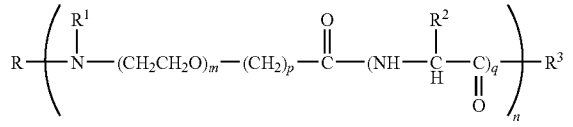
The term "dialkyloxypropyl" refers to a compound having 2-alkyl chains, R^1 and R^2, both of which have independently between 2 and 30 carbons. The alkyl groups can be saturated or have varying degrees of unsaturation. Dialkyloxypropyls have the following general formula:

(IV)



The term "ATTA" or "polyamide" refers to, but is not limited to, compounds disclosed in U.S. Pat. Nos. 6,320,017 and 6,586,559, both of which are incorporated herein by reference. These compounds include a compound having the formula

(V)



wherein: R is a member selected from the group consisting of hydrogen, alkyl and acyl; R^1 is a member selected from the group consisting of hydrogen and alkyl; or optionally, R and R^1 and the nitrogen to which they are bound form an azido moiety; R^2 is a member of the group selected from hydrogen, optionally substituted alkyl, optionally substituted aryl and a side chain of an amino acid; R^3 is a member selected from the group consisting of hydrogen, halogen, hydroxy, alkoxy, mercapto, hydrazino, amino and NR^4R^5, wherein R^4 and R^5 are independently hydrogen or alkyl; n is 4 to 80; m is 2 to 6; p is 1 to 4; and q is 0 or 1. It will be apparent to those of skill in the art that other polyamides can be used in the compounds of the present invention.

The term "nucleic acid" or "polynucleotide" refers to a polymer containing at least two ribonucleotides (e.g. deoxy or ribo) in either single- or double-stranded form. Unless specifically limited, the terms encompasses nucleic acids containing known analogues of natural nucleotides that have similar binding properties as the reference nucleic acid and are metabolized in a manner similar to naturally occurring nucleotides. Unless otherwise indicated, a particular nucleic acid sequence also implicitly encompasses conservatively modified variants thereof (e.g., degenerate codon substitutions), alleles, orthologs, SNPs, and complementary sequences as well as the sequence explicitly indicated. Specifically, degenerate codon substitutions may be achieved by generating sequences in which the third position of one or more selected (or all) codons is substituted with mixed-base and/or deoxyinosine residues (Batzer et al., *Nucleic Acid Res.* 19:5081 (1991); Ohtsuka et al., *J. Biol. Chem.* 260:2605-2608 (1985); and Cassol et al. (1992); Rossolini et al., *Mol. Cell. Probes* 8:91-98 (1994)). "Nucleotides" contain a sugar deoxyribose (DNA) or ribose (RNA), a base, and a phosphate group. Nucleotides are linked together through the phosphate groups. "Bases" include purines and pyrimidines, which further include natural compounds adenine, thymine, guanine, cytosine, uracil, inosine, and natural analogs, and synthetic derivatives of purines and pyrimidines, which include, but are not limited to, modifications which place new reactive groups such as, but not limited to, amines, alcohols, thiols, carboxylates, and alkylhalides. DNA may be in the form of antisense, plasmid DNA, parts of a plasmid DNA, pre-condensed DNA, product of a polymerase chain reaction (PCR), vectors (P1, PAC, BAC, YAC, artificial chromosomes), expression cassettes, chimeric sequences, chromosomal DNA, or derivatives of these groups. The term nucleic acid is used interchangeably with gene, cDNA, mRNA encoded by a gene, and an interfering RNA molecule.

The term "gene" refers to a nucleic acid (e.g., DNA or RNA) sequence that comprises partial length or entire length coding sequences necessary for the production of a polypeptide or precursor (e.g., Eg5, EGFR or XIAP).

"Gene product," as used herein, refers to a product of a gene such as an RNA transcript.

As used herein, the term "aqueous solution" refers to a composition comprising in whole, or in part, water.

As used herein, the term "organic lipid solution" refers to a composition comprising in whole, or in part, an organic solvent having a lipid.

"Distal site," as used herein, refers to a physically separated site, which is not limited to an adjacent capillary bed, but includes sites broadly distributed throughout an organism.

"Serum-stable" in relation to nucleic acid-lipid particles means that the particle is not significantly degraded after exposure to a serum or nuclease assay that would significantly degrade free DNA. Suitable assays include, for example, a standard serum assay or a DNAse assay such as those described in the Examples below.

"Fully encapsulated" in relation to nucleic acid-lipid particles means that the nucleic acid portion of the particle is serum stable and is not accessible to a fluorescent dye (e.g., such as RiboGreen™). In contrast to a nucleic acid that forms a complex with the lipid vehicle (e.g., a liposome or multilammelar vesicle), a nucleic acid fully encapsulated in the lipid portion of a particle does not fluoresce in the presence of a fluorescent dye.

"Systemic delivery," as used herein, refers to delivery that leads to a broad biodistribution of a compound within an organism. Some techniques of administration can lead to the systemic delivery of certain compounds, but not others. Systemic delivery means that a useful, preferably therapeutic, amount of a compound is exposed to most parts of the body. To obtain broad biodistribution generally requires a blood lifetime such that the compound is not rapidly degraded or cleared (such as by first pass organs (liver, lung, etc.) or by rapid, nonspecific cell binding) before reaching a disease site distal to the site of administration. Systemic delivery of nucleic acid-lipid particles can be by any means known in the art including, for example, intravenous, subcutaneous, intra-

peritoneal, In some embodiments, systemic delivery of nucleic acid-lipid particles is by intravenous delivery.

"Local delivery" as used herein refers to delivery of a compound directly to a target site within an organism. For example, a compound can be locally delivered by direct injection into a disease site such as a tumor or other target site such as a site of inflammation or a target organ such as the liver, heart, pancreas, kidney, and the like.

III. Carrier Systems Containing siRNA

In one aspect, the present invention provides carrier systems containing the siRNA molecules described herein. In some embodiments, the carrier system is a lipid-based carrier system such as a stabilized nucleic acid-lipid particle (e.g., SNALP or SPLP), cationic lipid or liposome nucleic acid complexes (i.e., lipoplexes), a liposome, a micelle, a virosome, or a mixture thereof. In other embodiments, the carrier system is a polymer-based carrier system such as a cationic polymer-nucleic acid complex (i.e., polyplex). In additional embodiments, the carrier system is a cyclodextrin-based carrier system such as a cyclodextrin polymer-nucleic acid complex. In further embodiments, the carrier system is a protein-based carrier system such as a cationic peptide-nucleic acid complex. Preferably, the carrier system is a stabilized nucleic acid-lipid particle such as a SNALP or SPLP. One skilled in the art will appreciate that the siRNA molecules of the present invention can also be delivered as naked siRNA.

IV. Stable Nucleic Acid-Lipid Particles (SNALPs) and Properties Thereof

The stable nucleic acid-lipid particles or, alternatively, SNALPs typically comprise an siRNA molecule that targets expression of a gene expressed in cancer (e.g., an Eg5, EGFR or XIAP gene), a cationic lipid (e.g., a cationic lipid of Formula I or II), a noncationic lipid and a bilayer stabilizing component (i.e., a conjugated lipid that inhibits aggregation of the SNALPs) The nucleic acid-lipid particles may comprise at least 1, 2, 3, 4, 5, or more of the sequences set forth in Tables 1-9.

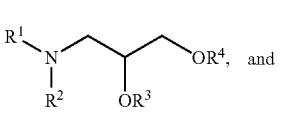
The SNALPs of the present invention typically have a mean diameter of about 50 nm to about 150 nm, more typically about 60 nm to about 130 nm, more typically about 70 nm to about 110 nm, most typically about 70 to about 90 nm and are substantially nontoxic. In addition, the nucleic acids present in the SNALPs of the present invention are resistant in aqueous solution to degradation with a nuclease.

In one embodiment, the present invention provides stabilized nucleic acid-lipid particles (SPLPs or SNALPs) and other lipid-based carrier systems (e.g., a liposome, a micelle, a virosome, a lipid-nucleic acid particle, a nucleic acid complex and mixtures thereof) containing cationic lipids. The lipid-nucleic acid particles of the present invention typically comprise a nucleic acid, a cationic lipid, a non-cationic lipid and a PEG-lipid conjugate. The cationic lipid typically comprises from about 2 mol % to about 60 mol %, from about 5 mol % to about 50 mol %, from about 10 mol % to about 45 mol %, from about 20 mol % to about 40 mol %, or from about 30 mol % to about 40 mol % of the total lipid present in said particle. The non-cationic lipid typically comprises from about 5 mol % to about 90 mol %, from about 10 mol % to about 85 mol %, from about 20 mol % to about 80 mol %, from about 30 mol % to about 70 mol %, from about 40 mol % to about 60 mol % or about 48 mol % of the total lipid present in said particle. The PEG-lipid conjugate typically comprises from about 0.5 mol % to about 20 mol %, from about 1.5 mol % to about 18 mol %, from about 4 mol % to about 15 mol %, from about 5 mol % to about 12 mol %, or about 2 mol % of the total lipid present in said particle. The nucleic acid-lipid particles of the present invention may further comprise cholesterol. If present, the cholesterol typically comprises from about 0 mol % to about 10 mol %, about 2 mol % to about 10 mol %, about 10 mol % to about 60 mol %, from about 12 mol % to about 58 mol %, from about 20 mol % to about 55 mol %, or about 48 mol % of the total lipid present in said particle. It will be readily apparent to one of skill in the art that the proportions of the components of the nucleic acid-lipid particles may be varied. In a specific formulation, the total lipid in the nucleic acid-lipid particle comprises 48 mol % cholesterol; 10 mol % DSPC; 2 mol % PEG-cDMA; and 40 mol % DLinDMA of the total lipid present in said particle.

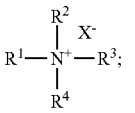
A. Cationic Lipids

Various suitable cationic lipids may be used in the present invention, either alone or in combination with one or more other cationic lipid species or neutral lipid species.

Suitable cationic lipids include, for example, DLinDMA, DLenDMA, DODAC, DOTMA, DDAB, DOTAP, DOSPA, DOGS, DC-Chol and DMRIE, or combinations thereof. A number of these lipids and related analogs, which are also useful in the present invention, have been described in U.S. Pat. Nos. 5,208,036, 5,264,618, 5,279,833, 5,283,185, 5,753,613 and 5,785,992. Additionally, a number of commercial preparations of cationic lipids are available and can be used in the present invention. These include, for example, LIPOFECTIN® (commercially available cationic liposomes comprising DOTMA and DOPE, from GIBCO/BRL, Grand Island, N.Y., USA); LIPOFECTAMINE® (commercially available cationic liposomes comprising DOSPA and DOPE, from GIBCO/BRL); and TRANSFECTAM® (commercially available cationic liposomes comprising DOGS from Promega Corp., Madison, Wis., USA). In addition, cationic lipids of Formula I and Formula II can be used in the present invention. Cationic lipids of Formula I and II have the following structures:



(I)



(II)

wherein R^1 and R^2 are independently selected and are H or C_1-C_3 alkyls. R^3 and R^4 are independently selected and are alkyl groups having from about 10 to about 20 carbon atoms; at least one of R^3 and R^4 comprises at least two sites of unsaturation. In one embodiment, R^3 and R^4 are both the same, i.e., R^3 and R^4 are both linoleyl (C18), etc. In another embodiment, R^3 and R^4 are different, i.e., R^3 is myristyl (C14) and R^4 is linoleyl (C18). In some embodiments, the cationic lipids of the present invention are symmetrical, i.e., R^3 and R^4 are both the same. In another preferred embodiment, both R^3 and R^4 comprise at least two sites of unsaturation. In some embodiments, R^3 and R^4 are independently selected from dodecadienyl, tetradecadienyl, hexadecadienyl, linoleyl, and icosadienyl. In some embodiments, R^3 and R^4 are both lino-

leyl. In some embodiments, R^3 and R^4 comprise at least three sites of unsaturation and are independently selected from, e.g., dodecatrienyl, tetradectrienyl, hexadecatrienyl, linolenyl, and icosatrienyl.

The cationic lipids of Formula I and Formula II described herein typically carry a net positive charge at a selected pH, such as physiological pH. It has been surprisingly found that cationic lipids comprising alkyl chains with multiple sites of unsaturation, e.g., at least two or three sites of unsaturation, are particularly useful for forming lipid-nucleic acid particles with increased membrane fluidity. A number of cationic lipids and related analogs, which are also useful in the present invention, have been described in U.S. Pat. Nos. 5,208,036, 5,264,618, 5,279,833 and 5,283,185, and WO 96/10390.

Additional suitable cationic lipids include, e.g., dioctadecyldimethylammonium ("DODMA"), Distearyldimethylammonium ("DSDMA"), N,N-dioleyl-N,N-dimethylammonium chloride ("DODAC"); N-(2,3-dioleyloxy)propyl)-N,N,N-trimethylammonium chloride ("DOTMA"); N,N-distearyl-N,N-dimethylammonium bromide ("DDAB"); N-(2,3-dioleoyloxy)propyl)-N,N,N-trimethylammonium chloride ("DOTAP"); 3-(N—(N',N'-dimethylaminoethane)-carbamoyl)cholesterol ("DC-Chol") and N-(1,2-dimyristyloxyprop-3-yl)-N,N-dimethyl-N-hydroxyethyl ammonium bromide ("DMRIE"). A number of these lipids and related analogs, which are also useful in the present invention, have been described in U.S. Pat. Nos. 5,208,036, 5,264,618, 5,279,833, 5,283,185, 5,753,613 and 5,785,992.

B. Non-Cationic Lipids

The noncationic lipids used in the present invention can be any of a variety of neutral uncharged, zwitterionic or anionic lipids capable of producing a stable complex. They are preferably neutral, although they can alternatively be negatively charged. Examples of noncationic lipids useful in the present invention include: phospholipid-related materials, such as lecithin, phosphatidylethanolamine, lysolecithin, lysophosphatidylethanolamine, phosphatidylserine, phosphatidylinositol, sphingomyelin, cephalin, cardiolipin, phosphatidic acid, cerebrosides, dicetylphosphate, distearoylphosphatidylcholine (DSPC), dioleoylphosphatidylcholine (DOPC), dipalmitoylphosphatidylcholine (DPPC), dioleoylphosphatidylglycerol (DOPG), dipalmitoylphosphatidylglycerol (DPPG), dioleoyl-phosphatidylethanolamine (DOPE), palmitoyloleoylphosphatidylcholine (POPC), palmitoyloleoyl-phosphatidylethanolamine (POPE) and dioleoyl-phosphatidylethanolamine 4-(N-maleimidomethyl)-cyclohexane-1-carboxylate (DOPE-mal), dipalmitoyl phosphatidyl ethanolamine (DPPE), dimyristoylphosphoethanolamine (DMPE), distearoyl-phosphatidyl-ethanolamine (DSPE), 16-O-monomethyl PE, 16-O-dimethyl PE, 18-1-trans PE, 1-stearoyl-2-oleoyl-phosphatidyethanolamine (SOPE), and 1,2-dielaidoyl-sn-glycero-3-phophoethanolamine (trans-DOPE). Noncationic lipids or sterols such as cholesterol may be present. Additional nonphosphorous containing lipids are, e.g., stearylamine, dodecylamine, hexadecylamine, acetyl palmitate, glycerolricinoleate, hexadecyl stereate, isopropyl myristate, amphoteric acrylic polymers, triethanolamine-lauryl sulfate, alkyl-aryl sulfate polyethyloxylated fatty acid amides, dioctadecyldimethyl ammonium bromide and the like, diacylphosphatidylcholine, diacylphosphatidylethanolamine, ceramide, sphingomyelin, cephalin, and cerebrosides. Other lipids such as lysophosphatidylcholine and lysophosphatidylethanolamine may be present. Noncationic lipids also include polyethylene glycol-based polymers such as PEG 2000, PEG 5000 and polyethylene glycol conjugated to phospholipids or to ceramides (referred to as PEG-Cer).

In preferred embodiments, the noncationic lipids are diacylphosphatidylcholine (e.g., distearoylphosphatidylcholine, dioleoylphosphatidylcholine, dipalmitoylphosphatidylcholine and dilinoleoylphosphatidylcholine), diacylphosphatidylethanolamine (e.g., dioleoylphosphatidylethanolamine and palmitoyloleoylphosphatidylethanolamine), ceramide or sphingomyelin. The acyl groups in these lipids are preferably acyl groups derived from fatty acids having C_{10}-C_{24} carbon chains. More preferably the acyl groups are lauroyl, myristoyl, palmitoyl, stearoyl or oleoyl. In particularly preferred embodiments, the noncationic lipid will be cholesterol, 1,2-sn-dioleoylphosphatidylethanolamine, or egg sphingomyelin (ESM).

C. Bilayer Stabilizing Component

In addition to cationic and non-cationic lipids, the nucleic acid-lipid particles (e.g., SNALPs and SPLPs) of the present invention comprise bilayer stabilizing component (BSC) such as an ATTA-lipid or a PEG-lipid, such as PEG coupled to dialkyloxypropyls (PEG-DAA) as described in, e.g., WO 05/026372, PEG coupled to diacylglycerol (PEG-DAG) as described in, e.g., U.S. Patent Publication Nos. 20030077829 and 2005008689), PEG coupled to phosphatidylethanolamine (PE) (PEG-PE), or PEG conjugated to ceramides, or a mixture thereof (see, U.S. Pat. No. 5,885,613). In one preferred embodiment, the BSC is a conjugated lipid that inhibits aggregation of the nucleic acid-lipid particles. Suitable conjugated lipids include, but are not limited to PEG-lipid conjugates, ATTA-lipid conjugates, cationic-polymer-lipid conjugates (CPLs) or mixtures thereof. In one preferred embodiment, the nucleic acid-lipid particles comprise either a PEG-lipid conjugate or an ATTA-lipid conjugate together with a CPL.

PEG is a polyethylene glycol, a linear, water-soluble polymer of ethylene PEG repeating units with two terminal hydroxyl groups. PEGs are classified by their molecular weights; for example, PEG 2000 has an average molecular weight of about 2,000 daltons, and PEG 5000 has an average molecular weight of about 5,000 daltons. PEGs are commercially available from Sigma Chemical Co. and other companies and include, for example, the following: monomethoxypolyethylene glycol (MePEG-OH), monomethoxypolyethylene glycol-succinate (MePEG-S), monomethoxypolyethylene glycol-succinimidyl succinate (MePEG-S-NHS), monomethoxypolyethylene glycol-amine (MePEG-NH_2), monomethoxypolyethylene glycol-tresylate (MePEG-TRES), and monomethoxypolyethylene glycol-imidazolyl-carbonyl (MePEG-IM). In addition, monomethoxypolyethyleneglycol-acetic acid (MePEG-CH_2COOH), is particularly useful for preparing the PEG-lipid conjugates including, e.g., PEG-DAA conjugates.

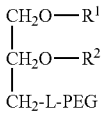
In some embodiments, the PEG has an average molecular weight of from about 550 daltons to about 10,000 daltons, more preferably of about 750 daltons to about 5,000 daltons, more preferably of about 1,000 daltons to about 5,000 daltons, more preferably of about 1,500 daltons to about 3,000 daltons and, even more preferably, of about 2,000 daltons, or about 750 daltons. The PEG can be optionally substituted by an alkyl, alkoxy, acyl or aryl group. PEG can be conjugated directly to the lipid or may be linked to the lipid via a linker moiety. Any linker moiety suitable for coupling the PEG to a lipid can be used including, e.g., non-ester containing linker moieties and ester-containing linker moieties. In some embodiments, the linker moiety is a non-ester containing linker moiety. As used herein, the term "non-ester containing linker moiety" refers to a linker moiety that does not contain a carboxylic ester bond (—OC(O)—). Suitable non-ester containing linker moieties include, but are not limited to,

amido (—C(O)NH—), amino (—NR—), carbonyl (—C(O)—), carbamate (—NHC(O)O—), urea (—NHC(O)NH—), disulphide (—S—S—), ether (—O—), succinyl (—(O)CCH$_2$CH$_2$C(O)—), succinamidyl (—NHC(O)CH$_2$CH$_2$C(O)NH—), ether, disulphide, etc. as well as combinations thereof (such as a linker containing both a carbamate linker moiety and an amido linker moiety). In some embodiments, a carbamate linker is used to couple the PEG to the lipid.

In other embodiments, an ester containing linker moiety is used to couple the PEG to the lipid. Suitable ester containing linker moieties include, e.g., carbonate (—OC(O)O—), succinoyl, phosphate esters (—O—(O)POH—O—), sulfonate esters, and combinations thereof.

Phosphatidylethanolamines having a variety of acyl chain groups of varying chain lengths and degrees of saturation can be conjugated to polyethyleneglycol to form the bilayer stabilizing component. Such phosphatidylethanolamines are commercially available, or can be isolated or synthesized using conventional techniques known to those of skilled in the art. Phosphatidylethanolamines containing saturated or unsaturated fatty acids with carbon chain lengths in the range of C_{10} to C_{20} are preferred. Phosphatidylethanolamines with mono- or diunsaturated fatty acids and mixtures of saturated and unsaturated fatty acids can also be used. Suitable phosphatidylethanolamines include, but are not limited to, the following: dimyristoylphosphatidylethanolamine (DMPE), dipalmitoylphosphatidylethanolamine (DPPE), dioleoylphosphatidylethanolamine (DOPE) and distearoylphosphatidylethanolamine (DSPE).

In some embodiments, the PEG-lipid is a PEG-DAA conjugate has the following formula:



(VI)

In Formula VI, R^1 and R^2 are independently selected and are alkyl groups having from about 10 to about 22 carbon atoms. The long-chain alkyl groups can be saturated or unsaturated. Suitable alkyl groups include, but are not limited to, lauryl (C12), myristyl (C14), palmityl (C16), stearyl (C18) and icosyl (C20). In some embodiments, R^1 and R^2 are the same, i.e., R^1 and R^2 are both myristyl (i.e., dimyristyl), R^1 and R^2 are both stearyl (i.e., distearyl), etc. In some embodiments, the alkyl groups are saturated.

In Formula VI above, "PEG" is a polyethylene glycol having an average molecular weight ranging of about 550 daltons to about 10,000 daltons, about 750 daltons to about 5,000 daltons, about 1,000 daltons to about 5,000 daltons, about 1,500 daltons to about 3,000 daltons, about 2,000 daltons, or about 750 daltons. The PEG can be optionally substituted with alkyl, alkoxy, acyl or aryl. In some embodiments, the terminal hydroxyl group is substituted with a methoxy or methyl group.

In Formula VI, above, "L" is a non-ester containing linker moiety or an ester containing linker moiety. In some embodiments, L is a non-ester containing linker moiety. Suitable non-ester containing linkers include, but are not limited to, an amido linker moiety, an amino linker moiety, a carbonyl linker moiety, a carbamate linker moiety, a urea linker moiety, an ether linker moiety, a disulphide linker moiety, a succinamidyl linker moiety and combinations thereof. In some embodiments, the non-ester containing linker moiety is a carbamate linker moiety (i.e., a PEG-C-DAA conjugate), an amido linker moiety (i.e., a PEG-A-DAA conjugate), or a succinamidyl linker moiety (i.e., a PEG-S-DAA conjugate).

The PEG-DAA conjugates are synthesized using standard techniques and reagents known to those of skill in the art. It will be recognized that the PEG-DAA conjugates will contain various amide, amine, ether, thio, carbamate and urea linkages. T hose of skill in the art will recognize that methods and reagents for forming these bonds are well known and readily available. See, e.g., March, ADVANCED ORGANIC CHEMISTRY (Wiley 1992), Larock, COMPREHENSIVE ORGANIC TRANSFORMATIONS (VCH 1989); and Fumiss, VOGEL'S TEXTBOOK OF PRACTICAL ORGANIC CHEMISTRY 5th ed. (Longman 1989). It will also be appreciated that any functional groups present may require protection and deprotection at different points in the synthesis of the PEG-DAA conjugates. Those of skill in the art will recognize that such techniques are well known. See, e.g., Green and Wuts, PROTECTIVE GROUPS IN ORGANIC SYNTHESIS (Wiley 1991).

In some embodiments, the PEG-DAA conjugate is a dilauryloxypropyl (C12)-PEG conjugate, dimyristyloxypropyl (C14)-PEG conjugate, a dipalmitoyloxypropyl (C16)-PEG conjugate or a disteryloxypropyl (C18)-PEG conjugate. Those of skill in the art will readily appreciate that other dialkyloxypropyls can be used in the PEG-DAA conjugates of the present invention.

In addition to the foregoing, it will be readily apparent to those of skill in the art that other hydrophilic polymers can be used in place of PEG. Examples of suitable polymers that can be used in place of PEG include, but are not limited to, polyvinylpyrrolidone, polymethyloxazoline, polyethyloxazoline, polyhydroxypropyl methacrylamide, polymethacrylamide and polydimethylacrylamide, polylactic acid, polyglycolic acid, and derivatized celluloses, such as hydroxymethylcellulose or hydroxyethylcellulose.

In addition to the foregoing components, the SNALPs and SPLPs of the present invention can further comprise cationic poly(ethylene glycol) (PEG) lipids, or CPLs, that have been designed for insertion into lipid bilayers to impart a positive charge(see, Chen, et al., *Bioconj. Chem.* 11:433-437 (2000)). Suitable SPLPs and SPLP-CPLs for use in the present invention, and methods of making and using SPLPs and SPLP-CPLs, are disclosed, e.g., in U.S. Pat. No. 6,852,334 and WO 00/62813. Cationic polymer lipids (CPLs) useful in the present invention have the following architectural features: (1) a lipid anchor, such as a hydrophobic lipid, for incorporating the CPLs into the lipid bilayer; (2) a hydrophilic spacer, such as a polyethylene glycol, for linking the lipid anchor to a cationic head group; and (3) a polycationic moiety, such as a naturally occurring amino acid, to produce a protonizable cationic head group.

Suitable CPL include compounds of Formula VII:

A-W-Y (VII)

wherein A, W and Y are as described below.

With reference to Formula VII, "A" is a lipid moiety such as an amphipathic lipid, a neutral lipid or a hydrophobic lipid that acts as a lipid anchor. Suitable lipid examples include vesicle-forming lipids or vesicle adopting lipids and include, but are not limited to, diacylglycerolyls, dialkylglycerolyls, N-N-dialkylaminos, 1,2-diacyloxy-3-aminopropanes and 1,2-dialkyl-3-aminopropanes.

"W" is a polymer or an oligomer, such as a hydrophilic polymer or oligomer. Typically, the hydrophilic polymer is a biocompatable polymer that is nonimmunogenic or possesses

low inherent immunogenicity. Alternatively, the hydrophilic polymer can be weakly antigenic if used with appropriate adjuvants. Suitable nonimmunogenic polymers include, but are not limited to, PEG, polyamides, polylactic acid, polyglycolic acid, polylactic acid/polyglycolic acid copolymers and combinations thereof. In some embodiments, the polymer has a molecular weight of about 250 to about 7000 daltons.

"Y" is a polycationic moiety. The term polycationic moiety refers to a compound, derivative, or functional group having a positive charge, typically at least 2 positive charges at a selected pH, typically physiological pH. Suitable polycationic moieties include basic amino acids and their derivatives such as arginine, asparagine, glutamine, lysine and histidine; spermine; spermidine; cationic dendrimers; polyamines; polyamine sugars; and amino polysaccharides. The polycationic moieties can be linear, such as linear tetralysine, branched or dendrimeric in structure. Polycationic moieties have between about 2 to about 15 positive charges, between about 2 to about 12 positive charges, or between about 2 to about 8 positive charges at selected pH values. The selection of which polycationic moiety to employ may be determined by the type of liposome application which is desired.

The charges on the polycationic moieties can be either distributed around the entire liposome moiety, or alternatively, they can be a discrete concentration of charge density in one particular area of the liposome moiety e.g., a charge spike. If the charge density is distributed on the liposome, the charge density can be equally distributed or unequally distributed. All variations of charge distribution of the polycationic moiety are encompassed by the present invention.

The lipid "A," and the nonimmunogenic polymer "W," can be attached by various methods and preferably, by covalent attachment. Methods known to those of skill in the art can be used for the covalent attachment of "A" and "W." Suitable linkages include, but are not limited to, amide, amine, carboxyl, carbonate, carbamate, ester and hydrazone linkages. It will be apparent to those skilled in the art that "A" and "W" must have complementary functional groups to effectuate the linkage. The reaction of these two groups, one on the lipid and the other on the polymer, will provide the desired linkage. For example, when the lipid is a diacylglycerol and the terminal hydroxyl is activated, for instance with NHS and DCC, to form an active ester, and is then reacted with a polymer which contains an amino group, such as with a polyamide (see, U.S. Pat. Nos. 6,320,017 and 6,586,559), an amide bond will form between the two groups.

In certain instances, the polycationic moiety can have a ligand attached, such as a targeting ligand or a chelating moiety for complexing calcium. Preferably, after the ligand is attached, the cationic moiety maintains a positive charge. In certain instances, the ligand that is attached has a positive charge. Suitable ligands include, but are not limited to, a compound or device with a reactive functional group and include lipids, amphipathic lipids, carrier compounds, bioaffinity compounds, biomaterials, biopolymers, biomedical devices, analytically detectable compounds, therapeutically active compounds, enzymes, peptides, proteins, antibodies, immune stimulators, radiolabels, fluorogens, biotin, drugs, haptens, DNA, RNA, polysaccharides, liposomes, virosomes, micelles, immunoglobulins, functional groups, other targeting moieties, or toxins.

D. Nucleic Acid Component

The nucleic acid component of the present invention comprises an interfering RNA that silences (e.g., partially or completely inhibits) expression of a gene of interest (e.g., an Eg5, EGFR and/or XIAP gene). An interfering RNA can be provided in several forms. For example an interfering RNA can be provided as one or more isolated small-interfering RNA (siRNA) duplexes, longer double-stranded RNA (dsRNA) or as siRNA or dsRNA transcribed from a transcriptional cassette in a DNA plasmid. The interfering RNA can be administered alone or in combination with the administration of conventional agents used to treat the disease or disorder associated with the gene of interest including, e.g., cancer. Genes of interest include, but are not limited to, genes associated with viral infection and survival, genes associated with liver and kidney diseases and disorders, genes associated with tumorigenesis and cell transformation, angiogenic genes, immunomodulator genes, such as those associated with inflammatory and autoimmune responses, ligand receptor genes, and genes associated with neurodegenerative disorders.

E. siRNAs

The siRNAs of the invention are capable of silencing expression of a target sequence such as, e.g., Eg5, EGFR or XIAP mRNA. Suitable siRNA sequences are set forth in, e.g., Tables 1-2 and 7 for Eg5; Tables 3-4 and 9 for EGFR; or Tables 5-6 and 9 for XIAP. For any of the sequences set forth in the Tables above, thymines (i.e., T) can substituted with uracil ("U") and uracil can be substituted with ("T"). In some embodiments, the siRNA are about 15 to 30 nucleotides in length.

1. Selecting siRNA Sequences

Suitable siRNA sequences can be identified using any means known in the art. Typically, the methods described in Elbashir et al., *Nature,* 411:494-498 (2001) and Elbashir et al., *EMBO J,* 20:6877-6888 (2001) are combined with rational design rules set forth in Reynolds et al., *Nature Biotech.,* 22:326-330 (2004).

Generally, the nucleotide sequence 3' of the AUG start codon of a transcript from the target gene of interest is scanned for dinucleotide sequences (e.g., AA, NA, CC, GG, or UU, wherein N=C, G, or U) (see, e.g., Elbashir et al., *EMBO J,* 20:6877-6888 (2001)). The nucleotides immediately 3' to the dinucleotide sequences are identified as potential siRNA sequences (i.e., a target sequence or a sense strand sequence). Typically, the 19, 21, 23, 25, 27, 29, 31, 33, 35, or more nucleotides immediately 3' to the dinucleotide sequences are identified as potential siRNA sequences. In some embodiments, the dinucleotide sequence is an AA or NA sequence and the 19 nucleotides immediately 3' to the AA or NA dinucleotide are identified as a potential siRNA sequences. siRNA sequences are usually spaced at different positions along the length of the target gene. To further enhance silencing efficiency of the siRNA sequences, potential siRNA sequences may be analyzed to identify sites that do not contain regions of homology to other coding sequences, e.g., in the target cell or organism. For example, a suitable siRNA sequence of about 21 base pairs typically will not have more than 16-17 contiguous base pairs of homology to coding sequences in the target cell or organism. If the siRNA sequences are to be expressed from an RNA Pol III promoter, siRNA sequences lacking more than 4 contiguous A's or T's are selected.

Once a potential siRNA sequence has been identified, the sequence can be analyzed using a variety of criteria known in the art. For example, to enhance their silencing efficiency, the siRNA sequences may be analyzed by a rational design algorithm to identify sequences that have one or more of the following features: (1) G/C content of about 25% to about 60% G/C; (2) at least 3 A/Us at positions 15-19 of the sense strand; (3) no internal repeats; (4) an A at position 19 of the sense strand; (5) an A at position 3 of the sense strand; (6) a U

at position 10 of the sense strand; (7) no G/C at position 19 of the sense strand; and (8) no G at position 13 of the sense strand. siRNA design tools that incorporate algorithms that assign suitable values of each of these features are useful for selection of siRNA. One of skill in the art will appreciate that sequences with one or more of the foregoing characteristics may be selected for further analysis and testing as potential siRNA sequences.

Additionally, potential siRNA target sequences with one or more of the following criteria can often be eliminated as siRNA: (1) sequences comprising a stretch of 4 or more of the same base in a row; (2) sequences comprising homopolymers of Gs (i.e., to reduce possible non-specific effects due to structural characteristics of these polymers; (3) sequences comprising triple base motifs (e.g., GGG, CCC, AAA, or TTT); (4) sequences comprising stretches of 7 or more G/Cs in a row; and (5) sequences comprising direct repeats of 4 or more bases within the candidates resulting in internal fold-back structures. However, one of skill in the art will appreciate that sequences with one or more of the foregoing characteristics may still be selected for further analysis and testing as potential siRNA sequences.

In some embodiments, potential siRNA target sequences may be further analyzed based on siRNA duplex asymmetry as described in, e.g., Khvorova et al., *Cell,* 115:209-216 (2003); and Schwarz et al., *Cell,* 115:199-208 (2003). In other embodiments, potential siRNA target sequences may be further analyzed based on secondary structure at the mRNA target site as described in, e.g., Luo et al., *Biophys. Res. Commun.,* 318:303-310 (2004). For example, mRNA secondary structure can be modeled using the Mfold algorithm to select siRNA sequences which favor accessibility at the mRNA target site where less secondary structure in the form of base-pairing and stem-loops is present.

Once a potential siRNA sequence has been identified, the sequence can be analyzed for the presence of any immunostimulatory properties, e.g., using an in vitro cytokine assay or an in vivo animal model. Motifs in the sense and/or antisense strand of the siRNA sequence such as GU-rich motifs (e.g., 5'-GU-3',5'-UGU-3',5'-GUGU-3',5'-UGUGU-3', etc.) can also provide an indication of whether the sequence may be immunostimulatory. Once an siRNA molecule is found to be immunostimulatory, it can then be modified to decrease its immunostimulatory properties as described herein. As a non-limiting example, an siRNA sequence can be contacted with a mammalian responder cell under conditions such that the cell produces a detectable immune response to determine whether the siRNA is an immunostimulatory or a non-immunostimulatory siRNA. The mammalian responder cell may be from a naïve mammal (i.e., a mammal that has not previously been in contact with the siRNA sequence). The mammalian responder cell may be, e.g., a peripheral blood mononuclear cell (PBMC), a macrophage, and the like. The detectable immune response may comprise production of a cytokine or growth factor such as, e.g., TNF-α, IFN-α, IFN-β, IFN-γ, IL-6, IL-12, or a combination thereof. An siRNA molecule identified as being immunostimulatory can then be modified to decrease its immunostimulatory properties by replacing at least one of the nucleotides on the sense and/or antisense strand with modified nucleotides. For example, less than about 30% (e.g., less than about 30%, 25%, 20%, 15%, 10%, or 5%) of the nucleotides in the double-stranded region of the siRNA duplex can be replaced with modified nucleotides such as 2'OMe nucleotides. The modified siRNA can then be contacted with a mammalian responder cell as described above to confirm that its immunostimulatory properties have been reduced or abrogated.

Suitable in vitro assays for detecting an immune response include, but are not limited to, the double monoclonal antibody sandwich immunoassay technique of David et al. (U.S. Pat. No. 4,376,110); monoclonal-polyclonal antibody sandwich assays (Wide et al., in Kirkham and Hunter, eds., *Radioimmunoassay Methods*, E. and S. Livingstone, Edinburgh (1970)); the "Western blot" method of Gordon et al. (U.S. Pat. No. 4,452,901); immunoprecipitation of labeled ligand (Brown et al., *J. Biol. Chem.,* 255:4980-4983 (1980)); enzyme-linked immunosorbent assays (ELISA) as described, for example, by Raines et al., *J. Biol. Chem.,* 257:5154-5160 (1982); immunocytochemical techniques, including the use of fluorochromes (Brooks et al., *Clin. Exp. Immunol.,* 39:477 (1980)); and neutralization of activity (Bowen-Pope et al., *Proc. Natl. Acad. Sci. USA,* 81:2396-2400 (1984)). In addition to the immunoassays described above, a number of other immunoassays are available, including those described in U.S. Pat. Nos. 3,817,827; 3,850,752; 3,901,654; 3,935,074; 3,984,533; 3,996,345; 4,034,074; and 4,098,876.

A non-limiting example of an in vivo model for detecting an immune response includes an in vivo mouse cytokine induction assay that can be performed as follows: (1) siRNA can be administered by standard intravenous injection in the lateral tail vein; (2) blood can be collected by cardiac puncture about 6 hours after administration and processed as plasma for cytokine analysis; and (3) cytokines can be quantified using sandwich ELISA kits according to the manufacturer's instructions (e.g., mouse and human IFN-α (PBL Biomedical; Piscataway, N.J.); human IL-6 and TNF-α (eBioscience; San Diego, Calif.); and mouse IL-6, TNF-α, and IFN-γ (BD Biosciences; San Diego, Calif.)).

Monoclonal antibodies that specifically bind cytokines and growth factors are commercially available from multiple sources and can be generated using methods known in the art (see, e.g., Kohler and Milstein, *Nature,* 256: 495-497 (1975); and Harlow and Lane, ANTIBODIES, A LABORATORY MANUAL, Cold Spring Harbor Publication, New York (1999)). Generation of monoclonal antibodies has been previously described and can be accomplished by any means known in the art (see, e.g., Buhring et al. in Hybridoma, Vol. 10, No. 1, pp. 77-78 (1991)). In some methods, the monoclonal antibody is labeled (e.g., with any composition detectable by spectroscopic, photochemical, biochemical, electrical, optical, chemical means, and the like) to facilitate detection.

F. Generating siRNA Molecules

siRNA molecules can be provided in several forms including, e.g., as one or more isolated small-interfering RNA (siRNA) duplexes, as longer double-stranded RNA (dsRNA), or as siRNA or dsRNA transcribed from a transcriptional cassette in a DNA plasmid. The siRNA sequences may have overhangs (e.g., 3' or 5' overhangs as described in Elbashir et al., *Genes Dev.,* 15:188 (2001) or Nykänen et al., *Cell,* 107: 309 (2001)), or may lack overhangs (i.e., have blunt ends).

An RNA population can be used to provide long precursor RNAs, or long precursor RNAs that have substantial or complete identity to a selected target sequence can be used to make the siRNA. The RNAs can be isolated from cells or tissue, synthesized, and/or cloned according to methods well known to those of skill in the art. The RNA can be a mixed population (obtained from cells or tissue, transcribed from cDNA, subtracted, selected, etc.), or can represent a single target sequence. RNA can be naturally occurring (e.g., isolated from tissue or cell samples), synthesized in vitro (e.g., using T7 or SP6 polymerase and PCR products or a cloned cDNA), or chemically synthesized.

To form a long dsRNA, for synthetic RNAs, the complement is also transcribed in vitro and hybridized to form a dsRNA. If a naturally occurring RNA population is used, the RNA complements are also provided (e.g., to form dsRNA for digestion by *E. coli* RNAse III or Dicer), e.g., by transcribing cDNAs corresponding to the RNA population, or by using RNA polymerases. The precursor RNAs are then hybridized to form double stranded RNAs for digestion. The dsRNAs can be directly administered to a subject or can be digested in vitro prior to administration.

Alternatively, one or more DNA plasmids encoding one or more siRNA templates are used to provide siRNA. siRNA can be transcribed as sequences that automatically fold into duplexes with hairpin loops from DNA templates in plasmids having RNA polymerase III transcriptional units, for example, based on the naturally occurring transcription units for small nuclear RNA U6 or human RNase P RNA H1 (see, Brummelkamp et al., *Science,* 296:550 (2002); Donzé et al., *Nucleic Acids Res.,* 30:e46 (2002); Paddison et al., *Genes Dev.,* 16:948 (2002); Yu et al., *Proc. Natl. Acad. Sci. USA,* 99:6047 (2002); Lee et al., *Nat. Biotech.,* 20:500 (2002); Miyagishi et al., *Nat. Biotech.,* 20:497 (2002); Paul et al., *Nat. Biotech.,* 20:505 (2002); and Sui et al., *Proc. Natl. Acad. Sci. USA,* 99:5515 (2002)). Typically, a transcriptional unit or cassette will contain an RNA transcript promoter sequence, such as an H1-RNA or a U6 promoter, operably linked to a template for transcription of a desired siRNA sequence and a termination sequence, comprised of 2-3 uridine residues and a polythymidine (T5) sequence (polyadenylation signal) (Brummelkamp et al., supra). The selected promoter can provide for constitutive or inducible transcription. Compositions and methods for DNA-directed transcription of RNA interference molecules is described in detail in U.S. Pat. No. 6,573,099. The transcriptional unit is incorporated into a plasmid or DNA vector from which the interfering RNA is transcribed. Plasmids suitable for in vivo delivery of genetic material for therapeutic purposes are described in detail in U.S. Pat. Nos. 5,962,428 and 5,910,488. The selected plasmid can provide for transient or stable delivery of a target cell. It will be apparent to those of skill in the art that plasmids originally designed to express desired gene sequences can be modified to contain a transcriptional unit cassette for transcription of siRNA.

Methods for isolating RNA, synthesizing RNA, hybridizing nucleic acids, making and screening cDNA libraries, and performing PCR are well known in the art (see, e.g., Gubler and Hoffman, *Gene* 25:263-269 (1983); Sambrook et al., supra; Ausubel et al., supra), as are PCR methods (see, U.S. Pat. Nos. 4,683,195 and 4,683,202; *PCR Protocols: A Guide to Methods and Applications* (Innis et al., eds, 1990)). Expression libraries are also well known to those of skill in the art. Additional basic texts disclosing the general methods of use in this invention include Sambrook et al., *Molecular Cloning, A Laboratory Manual* (2nd ed. 1989); Kriegler, *Gene Transfer and Expression: A Laboratory Manual* (1990); and *Current Protocols in Molecular Biology* (Ausubel et al., eds., 1994).

Preferably, siRNA molecules are chemically synthesized. The single-stranded molecules that comprise the siRNA molecule can be synthesized using any of a variety of techniques known in the art, such as those described in Usman et al., *J. Am. Chem. Soc.,* 109:7845 (1987); Scaringe et al., *Nuc. Acids Res.,* 18:5433 (1990); Wincott et al., *Nucl. Acids Res.,* 23:2677-2684 (1995); and Wincott et al., *Methods Mol. Bio.,* 74:59 (1997). The synthesis of the single-stranded molecules makes use of common nucleic acid protecting and coupling groups, such as dimethoxytrityl at the 5'-end and phosphoramidites at the 3'-end. As a non-limiting example, small scale syntheses can be conducted on an Applied Biosystems synthesizer using a 0.2 μmol scale protocol with a 2.5 min coupling step for 2'-O-methylated nucleotides. Alternatively, syntheses at the 0.2 μmol scale can be performed on a 96-well plate synthesizer from Protogene (Palo Alto, Calif.). However, a larger or smaller scale of synthesis is also within the scope of the present invention. Suitable reagents for synthesis of the siRNA single-stranded molecules, methods for RNA deprotection, and methods for RNA purification are known to those of skill in the art.

The siRNA molecules can also be synthesized via a tandem synthesis technique, wherein both strands are synthesized as a single continuous fragment or strand separated by a cleavable linker that is subsequently cleaved to provide separate fragments or strands that hybridize to form the siRNA duplex. The linker can be a polynucleotide linker or a non-nucleotide linker. The tandem synthesis of siRNA can be readily adapted to both multiwell/multiplate synthesis platforms as well as large scale synthesis platforms employing batch reactors, synthesis columns, and the like. Alternatively, the siRNA molecules can be assembled from two distinct single-stranded molecules, wherein one strand comprises the sense strand and the other comprises the antisense strand of the siRNA. For example, each strand can be synthesized separately and joined together by hybridization or ligation following synthesis and/or deprotection. In certain other instances, the siRNA molecules can be synthesized as a single continuous fragment, where the self-complementary sense and antisense regions hybridize to form an siRNA duplex having hairpin secondary structure.

C. Modifying siRNA Sequences

In certain aspects, the siRNA molecules of the present invention comprise a duplex having two strands and at least one modified nucleotide in the double-stranded region, wherein each strand is about 15 to about 60 nucleotides in length. Advantageously, the modified siRNA is less immunostimulatory than a corresponding unmodified siRNA sequence, but retains the capability of silencing the expression of a target sequence.

Examples of modified nucleotides suitable for use in the present invention include, but are not limited to, ribonucleotides having a 2'-O-methyl (2'OMe), 2'-deoxy-2'-fluoro (2° F.), 2'-deoxy, 5-C-methyl, 2'-O-(2-methoxyethyl) (MOE), 4'-thio, 2'-amino, or 2'-C-allyl group. Modified nucleotides having a Northern conformation such as those described in, e.g., Saenger, *Principles of Nucleic Acid Structure*, Springer-Verlag Ed. (1984), are also suitable for use in the siRNA molecules of the present invention. Such modified nucleotides include, without limitation, locked nucleic acid (LNA) nucleotides (e.g., 2'-O, 4'-C-methylene-(D-ribofuranosyl) nucleotides), 2'-O-(2-methoxyethyl) (MOE) nucleotides, 2'-methyl-thio-ethyl nucleotides, 2'-deoxy-2'-fluoro (2° F.) nucleotides, 2'-deoxy-2'-chloro (2'Cl) nucleotides, and 2'-azido nucleotides. In certain instances, the siRNA molecules of the present invention include one or more G-clamp nucleotides. A G-clamp nucleotide refers to a modified cytosine analog wherein the modifications confer the ability to hydrogen bond both Watson-Crick and Hoogsteen faces of a complementary guanine nucleotide within a duplex (see, e.g., Lin et al., *J. Am. Chem. Soc.,* 120:8531-8532 (1998)). In addition, nucleotides having a nucleotide base analog such as, for example, C-phenyl, C-naphthyl, other aromatic derivatives, inosine, azole carboxamides, and nitroazole derivatives such as 3-nitropyrrole, 4-nitroindole, 5-nitroindole, and 6-ni-

troindole (see, e.g., Loakes, *Nucl. Acids Res.,* 29:2437-2447 (2001)) can be incorporated into the siRNA molecules of the present invention.

In certain embodiments, the siRNA molecules of the present invention further comprise one or more chemical modifications such as terminal cap moieties, phosphate backbone modifications, and the like. Examples of terminal cap moieties include, without limitation, inverted deoxy abasic residues, glyceryl modifications, 4',5'-methylene nucleotides, 1-(β-D-erythrofuranosyl) nucleotides, 4'-thio nucleotides, carbocyclic nucleotides, 1,5-anhydrohexitol nucleotides, L-nucleotides, α-nucleotides, modified base nucleotides, threo-pentofuranosyl nucleotides, acyclic 3',4'-seco nucleotides, acyclic 3,4-dihydroxybutyl nucleotides, acyclic 3,5-dihydroxypentyl nucleotides, 3'-3'-inverted nucleotide moieties, 3'-3'-inverted abasic moieties, 3'-2'-inverted nucleotide moieties, 3'-2'-inverted abasic moieties, 5'-5'-inverted nucleotide moieties, 5'-5'-inverted abasic moieties, 3'-5'-inverted deoxy abasic moieties, 5'-amino-alkyl phosphate, 1,3-diamino-2-propyl phosphate, 3-aminopropyl phosphate, 6-aminohexyl phosphate, 1,2-aminododecyl phosphate, hydroxypropyl phosphate, 1,4-butanediol phosphate, 3'-phosphoramidate, 5'-phosphoramidate, hexylphosphate, aminohexyl phosphate, 3'-phosphate, 5'-amino, 3'-phosphorothioate, 5'-phosphorothioate, phosphorodithioate, and bridging or non-bridging methylphosphonate or 5'-mercapto moieties (see, e.g., U.S. Pat. No. 5,998,203; Beaucage et al., *Tetrahedron* 49:1925 (1993)). Non-limiting examples of phosphate backbone modifications (i.e., resulting in modified internucleotide linkages) include phosphorothioate, phosphorodithioate, methylphosphonate, phosphotriester, morpholino, amidate, carbamate, carboxymethyl, acetamidate, polyamide, sulfonate, sulfonamide, sulfamate, formacetal, thioformacetal, and alkylsilyl substitutions (see, e.g., Hunziker et al., *Nucleic Acid Analogues: Synthesis and Properties, in Modern Synthetic Methods*, VCH, 331-417 (1995); Mesmaeker et al., *Novel Backbone Replacements for Oligonucleotides, in Carbohydrate Modifications in Antisense Research*, ACS, 24-39 (1994)). Such chemical modifications can occur at the 5'-end and/or 3'-end of the sense strand, antisense strand, or both strands of the siRNA.

In some embodiments, the sense and/or antisense strand can further comprise a 3'-terminal overhang having about 1 to about 4 (e.g., 1, 2, 3, or 4) 2'-deoxy ribonucleotides and/or any combination of modified and unmodified nucleotides. Additional examples of modified nucleotides and types of chemical modifications that can be introduced into the modified siRNA molecules of the present invention are described, e.g., in UK Patent No. GB 2,397,818 B and U.S. Patent Publication Nos. 20040192626 and 20050282188.

The siRNA molecules of the present invention can optionally comprise one or more non-nucleotides in one or both strands of the siRNA. As used herein, the term "non-nucleotide" refers to any group or compound that can be incorporated into a nucleic acid chain in the place of one or more nucleotide units, including sugar and/or phosphate substitutions, and allows the remaining bases to exhibit their activity. The group or compound is abasic in that it does not contain a commonly recognized nucleotide base such as adenosine, guanine, cytosine, uracil, or thymine and therefore lacks a base at the 1'-position.

In other embodiments, chemical modification of the siRNA comprises attaching a conjugate to the siRNA molecule. The conjugate can be attached at the 5'- and/or 3'-end of the sense and/or antisense strand of the siRNA via a covalent attachment such as, e.g., a biodegradable linker. The conjugate can also be attached to the siRNA, e.g., through a carbamate group or other linking group (see, e.g., U.S. Patent Publication Nos. 20050074771, 20050043219, and 20050158727). In certain instances, the conjugate is a molecule that facilitates the delivery of the siRNA into a cell. Examples of conjugate molecules suitable for attachment to the siRNA of the present invention include, without limitation, steroids such as cholesterol, glycols such as polyethylene glycol (PEG), human serum albumin (HSA), fatty acids, carotenoids, terpenes, bile acids, folates (e.g., folic acid, folate analogs and derivatives thereof), sugars (e.g., galactose, galactosamine, N-acetyl galactosamine, glucose, mannose, fructose, fucose, etc.), phospholipids, peptides, ligands for cellular receptors capable of mediating cellular uptake, and combinations thereof (see, e.g., U.S. Patent Publication Nos. 20030130186, 20040110296, and 20040249178; U.S. Pat. No. 6,753,423). Other examples include the lipophilic moiety, vitamin, polymer, peptide, protein, nucleic acid, small molecule, oligosaccharide, carbohydrate cluster, intercalator, minor groove binder, cleaving agent, and cross-linking agent conjugate molecules described in U.S. Patent Publication Nos. 20050119470 and 20050107325. Yet other examples include the 2'-O-alkyl amine, 2'-O-alkoxyalkyl amine, polyamine, C5-cationic modified pyrimidine, cationic peptide, guanidinium group, amidininium group, cationic amino acid conjugate molecules described in U.S. Patent Publication No. 20050153337. Additional examples include the hydrophobic group, membrane active compound, cell penetrating compound, cell targeting signal, interaction modifier, and steric stabilizer conjugate molecules described in U.S. Patent Publication No. 20040167090. Further examples include the conjugate molecules described in U.S. Patent Publication No. 20050239739. The type of conjugate used and the extent of conjugation to the siRNA molecule can be evaluated for improved pharmacokinetic profiles, bioavailability, and/or stability of the siRNA while retaining RNAi activity. As such, one skilled in the art can screen siRNA molecules having various conjugates attached thereto to identify ones having improved properties and RNAi activity using any of a variety of well-known in vitro cell culture or in vivo animal models.

V. Additional Carrier Systems

Non-limiting examples of additional lipid-based carrier systems suitable for use in the present invention include lipoplexes (see, e.g., U.S. Patent Publication No. 20030203865; and Zhang et al., *J. Control Release,* 100:165-180 (2004)), pH-sensitive lipoplexes (see, e.g., U.S. Patent Publication No. 20020192275), reversibly masked lipoplexes (see, e.g., U.S. Patent Publication Nos. 20030180950), cationic lipid-based compositions (see, e.g., U.S. Pat. No. 6,756,054; and U.S. Patent Publication No. 20050234232), cationic liposomes (see, e.g., U.S. Patent Publication Nos. 20030229040, 20020160038, and 20020012998; U.S. Pat. No. 5,908,635; and PCT Publication No. WO 01/72283), anionic liposomes (see, e.g., U.S. Patent Publication No. 20030026831), pH-sensitive liposomes (see, e.g., U.S. Patent Publication No. 20020192274; and AU 2003210303), antibody-coated liposomes (see, e.g., U.S. Patent Publication No. 20030108597; and PCT Publication No. WO 00/50008), cell-type specific liposomes (see, e.g., U.S. Patent Publication No. 20030198664), liposomes containing nucleic acid and peptides (see, e.g., U.S. Pat. No. 6,207,456), liposomes containing lipids derivatized with releasable hydrophilic polymers (see, e.g., U.S. Patent Publication No. 20030031704), lipid-entrapped nucleic acid (see, e.g., PCT Publication Nos. WO

03/057190 and WO 03/059322), lipid-encapsulated nucleic acid (see, e.g., U.S. Patent Publication No. 20030129221; and U.S. Pat. No. 5,756,122), other liposomal compositions (see, e.g., U.S. Patent Publication Nos. 20030035829 and 20030072794; and U.S. Pat. No. 6,200,599), stabilized mixtures of liposomes and emulsions (see, e.g., EP1304160), emulsion compositions (see, e.g., U.S. Pat. No. 6,747,014), and nucleic acid micro-emulsions (see, e.g., U.S. Patent Publication No. 20050037086).

Examples of polymer-based carrier systems suitable for use in the present invention include, but are not limited to, cationic polymer-nucleic acid complexes (i.e., polyplexes). To form a polyplex, a nucleic acid (e.g., siRNA) is typically complexed with a cationic polymer having a linear, branched, star, or dendritic polymeric structure that condenses the nucleic acid into positively charged particles capable of interacting with anionic proteoglycans at the cell surface and entering cells by endocytosis. In some embodiments, the polyplex comprises nucleic acid (e.g., siRNA) complexed with a cationic polymer such as polyethylenimine (PEI) (see, e.g., U.S. Pat. No. 6,013,240; commercially available from Qbiogene, Inc. (Carlsbad, Calif.) as In vivo jetPEI™, a linear form of PEI), polypropylenimine (PPI), polyvinylpyrrolidone (PVP), poly-L-lysine (PLL), diethylaminoethyl (DEAE)-dextran, poly(β-amino ester) (PAE) polymers (see, e.g., Lynn et al., *J. Am. Chem. Soc.,* 123:8155-8156 (2001)), chitosan, polyamidoamine (PAMAM) dendrimers (see, e.g., Kukowska-Latallo et al., *Proc. Natl. Acad. Sci. USA,* 93:4897-4902 (1996)), porphyrin (see, e.g., U.S. Pat. No. 6,620,805), polyvinylether (see, e.g., U.S. Patent Publication No. 20040156909), polycyclic amidinium (see, e.g., U.S. Patent Publication No. 20030220289), other polymers comprising primary amine, imine, guanidine, and/or imidazole groups (see, e.g., U.S. Pat. No. 6,013,240; PCT Publication No. WO/9602655; PCT Publication No. WO95/21931; Zhang et al., *J. Control Release,* 100:165-180 (2004); and Tiera et al., *Curr. Gene Ther.,* 6:59-71 (2006)), and a mixture thereof. In other embodiments, the polyplex comprises cationic polymer-nucleic acid complexes as described in U.S. Patent Publication Nos. 20060211643, 20050222064, 20030125281, and 20030185890, and PCT Publication No. WO 03/066069; biodegradable poly(β-amino ester) polymer-nucleic acid complexes as described in U.S. Patent Publication No. 20040071654; microparticles containing polymeric matrices as described in U.S. Patent Publication No. 20040142475; other microparticle compositions as described in U.S. Patent Publication No. 20030157030; condensed nucleic acid complexes as described in U.S. Patent Publication No. 20050123600; and nanocapsule and microcapsule compositions as described in AU 2002358514 and PCT Publication No. WO 02/096551.

In certain instances, the nucleic acid (e.g., siRNA) may be complexed with cyclodextrin or a polymer thereof. Non-limiting examples of cyclodextrin-based carrier systems include the cyclodextrin-modified polymer-nucleic acid complexes described in U.S. Patent Publication No. 20040087024; the linear cyclodextrin copolymer-nucleic acid complexes described in U.S. Pat. Nos. 6,509,323, 6,884,789, and 7,091,192; and the cyclodextrin polymer-complexing agent-nucleic acid complexes described in U.S. Pat. No. 7,018,609. In certain other instances, the nucleic acid (e.g., siRNA) may be complexed with a peptide or polypeptide. An example of a protein-based carrier system includes, but is not limited to, the cationic oligopeptide-nucleic acid complex described in PCT Publication No. WO95/21931.

VI. Preparation of SNALPs

The present invention provides a method of preparing serum-stable nucleic acid-lipid particles in which the siRNA, plasmid or other nucleic acid is encapsulated in a lipid bilayer and is protected from degradation. The particles made by the methods of this invention typically have a size of about 50 nm to about 150 nm, about 60 nm to about 130 nm, about 70 nm to about 110 nm, or about 70 to about 90 nm. The particles can be formed by any method known in the art including, but not limited to: a continuous mixing method, a detergent dialysis method, or a modification of a reverse-phase method which utilizes organic solvents to provide a single phase during mixing of the components.

In preferred embodiments, the cationic lipids are lipids of Formula I and II or combinations thereof. In other preferred embodiments, the noncationic lipids are ESM, DOPE, DOPC, DPPE, DMPE, 16:0 Monomethyl Phosphatidylethanolamine, 16:0 Dimethyl Phosphatidylethanolamine, 18:1 Trans Phosphatidylethanolamine, 18:0 18:1 Phosphatidylethanolamine (SOPE), 1,2-dielaidoyl-sn-glycero-3-phophoethanolamine (transDOPE), 16:0 18:1 Phosphatidylethanolamine, DSPE, polyethylene glycol-based polymers (e.g., PEG 2000, PEG 5000, PEG-modified diacylglycerols, or PEG-modified dialkyloxypropyls), distearoylphosphatidylcholine (DSPC), cholesterol, or combinations thereof. In still other preferred embodiments, the organic solvents are methanol, chloroform, methylene chloride, ethanol, diethyl ether or combinations thereof.

In a particularly preferred embodiment, the nucleic acid is an siRNA molecule; the cationic lipid is a lipid of Formula I or II or combinations thereof; the noncationic lipid is ESM, DOPE, PEG-DAAs, distearoylphosphatidylcholine (DSPC), cholesterol, or combinations thereof (e.g. DSPC and PEG-DAAs); and the organic solvent is methanol, chloroform, methylene chloride, ethanol, diethyl ether or combinations thereof.

In a particularly preferred embodiment, the present invention provides for nucleic acid-lipid particles produced via a continuous mixing method, e.g., process that includes providing an aqueous solution comprising a nucleic acid such as an siRNA or a plasmid, in a first reservoir, and providing an organic lipid solution in a second reservoir, and mixing the aqueous solution with the organic lipid solution such that the organic lipid solution mixes with the aqueous solution so as to substantially instantaneously produce a liposome encapsulating the nucleic acid (e.g., siRNA). This process and the apparatus for carrying this process is described in detail in U.S. Patent Publication No. 20040142025.

The action of continuously introducing lipid and buffer solutions into a mixing environment, such as in a mixing chamber, causes a continuous dilution of the lipid solution with the buffer solution, thereby producing a liposome substantially instantaneously upon mixing. As used herein, the phrase "continuously diluting a lipid solution with a buffer solution" (and variations) generally means that the lipid solution is diluted sufficiently rapidly in a hydration process with sufficient force to effectuate vesicle generation. By mixing the aqueous solution comprising a nucleic acid with the organic lipid solution, the organic lipid solution undergoes a continuous stepwise dilution in the presence of the buffer solution (i.e., aqueous solution) to produce a nucleic acid-lipid particle.

In another embodiment, the present invention provides for nucleic acid-lipid particles produced via a direct dilution process that includes forming a liposome solution and immediately and directly introducing the liposome solution into a collection vessel containing a controlled amount of dilution buffer. In preferred aspects, the collection vessel includes one or more elements configured to stir the contents of the collection vessel to facilitate dilution. In one aspect, the amount

of dilution buffer present in the collection vessel is substantially equal to the volume of liposome solution introduced thereto. As an example, liposome solution in 45% ethanol when introduced into the collection vessel containing an equal volume of aqueous solution will advantageously yield smaller particles in about 22.5%, about 20%, or about 15% ethanol.

In even another embodiment, the present invention provides for nucleic acid-lipid particles produced via a direct dilution process in which a third reservoir containing dilution buffer is fluidly coupled to a second mixing region. In this embodiment, the liposome solution formed in a first mixing region is immediately and directly mixed with dilution buffer in the second mixing region. In preferred aspects, the second mixing region includes a T-connector arranged so that the liposome solution and the dilution buffer flows meet as opposing 180° flows, however, connectors providing shallower angles can be used, e.g., 27° to about 180°. A pump mechanism delivers a controllable flow of buffer to the second mixing region. In one aspect, the flow rate of dilution buffer provided to the second mixing region is controlled to be substantially equal to the flow rate of liposome solution introduced thereto from the first mixing region. This embodiment advantageously allows for more control of the flow of dilution buffer mixing with the liposome solution in the second mixing region, and therefore also the concentration of liposome solution in buffer throughout the second mixing process. Such control of the dilution buffer flow rate advantageously allows for small particle size formation at reduced concentrations.

These processes and the apparati for carrying these direct dilution processes is described in detail in U.S. Provisional Patent Application No. 60/703,380 filed Jul. 27, 2005 (Systems and Methods for Manufacturing Liposomes, which is incorporated herein by reference.

The serum-stable nucleic acid-lipid particles formed using the continuous mixing method typically have a size of from about 50 nm to about 150 nm, about 100 nm to about 130 nm, about 110 nm to about 115 nm, about 65 nm to about 95 nm, or about 50 nm to about 75 nm. The particles thus formed do not aggregate and are optionally sized to achieve a uniform particle size.

In some embodiments, the particles are formed using detergent dialysis. Without intending to be bound by any particular mechanism of formation, a plasmid or other nucleic acid (e.g., siRNA) is contacted with a detergent solution of cationic lipids to form a coated nucleic acid complex. These coated nucleic acids can aggregate and precipitate. However, the presence of a detergent reduces this aggregation and allows the coated nucleic acids to react with excess lipids (typically, non-cationic lipids) to form particles in which the plasmid or other nucleic acid is encapsulated in a lipid bilayer. Thus, the present invention provides a method for the preparation of serum-stable nucleic acid-lipid particles, comprising:

(a) combining a nucleic acid with cationic lipids in a detergent solution to form a coated nucleic acid-lipid complex;

(b) contacting non-cationic lipids with the coated nucleic acid-lipid complex to form a detergent solution comprising a nucleic acid-lipid complex and non-cationic lipids; and

(c) dialyzing the detergent solution of step (b) to provide a solution of serum-stable nucleic acid-lipid particles, wherein the nucleic acid is encapsulated in a lipid bilayer and the particles are serum-stable and have a size of from about 50 to about 150 nm.

An initial solution of coated nucleic acid-lipid complexes is formed by combining the nucleic acid with the cationic lipids in a detergent solution.

In these embodiments, the detergent solution is preferably an aqueous solution of a neutral detergent having a critical micelle concentration of 15-300 mM, more preferably 20-50 mM. Examples of suitable detergents include, for example, N,N'-((octanoylimino)-bis-(trimethylene))-bis-(D-gluconamide) (BIGCHAP); BRIJ 35; Deoxy-BIGCHAP; dodecylpoly(ethylene glycol) ether; Tween 20; Tween 40; Tween 60; Tween 80; Tween 85; Mega 8; Mega 9; Zwittergent® 3-08; Zwittergent® 3-10; Triton X-405; hexyl-, heptyl-, octyl- and nonyl-β-D-glucopyranoside; and heptylthioglucopyranoside; with octyl β-D-glucopyranoside and Tween-20 being the most preferred. The concentration of detergent in the detergent solution is typically about 100 mM to about 2 M, preferably from about 200 mM to about 1.5 M.

The cationic lipids and nucleic acids will typically be combined to produce a charge ratio (+/−) of about 1:1 to about 20:1, in a ratio of about 1:1 to about 12:1, or in a ratio of about 2:1 to about 6:1. Additionally, the overall concentration of nucleic acid in solution will typically be from about 25 μg/mL to about 1 mg/mL, from about 25 μg/mL to about 200 μg/mL, or from about 50 μg/mL to about 100 μg/mL. The combination of nucleic acids and cationic lipids in detergent solution is kept, typically at room temperature, for a period of time which is sufficient for the coated complexes to form. Alternatively, the nucleic acids and cationic lipids can be combined in the detergent solution and warmed to temperatures of up to about 37° C., about 50° C., about 60° C., or about 70° C. For nucleic acids which are particularly sensitive to temperature, the coated complexes can be formed at lower temperatures, typically down to about 4° C.

In some embodiments, the nucleic acid to lipid ratios (mass/mass ratios) in a formed nucleic acid-lipid particle will range from about 0.01 to about 0.2, from about 0.03 to about 0.01 or about 0.01 to about 0.08. The ratio of the starting materials also falls within this range. In another preferred embodiment, the nucleic acid-lipid particle preparation uses about 400 μg nucleic acid per 10 mg total lipid or a nucleic acid to lipid ratio of about 0.01 to about 0.08 or about 0.04, which corresponds to 1.25 mg of total lipid per 50 μg of nucleic acid.

The detergent solution of the coated nucleic acid-lipid complexes is then contacted with non-cationic lipids to provide a detergent solution of nucleic acid-lipid complexes and non-cationic lipids. The non-cationic lipids which are useful in this step include, diacylphosphatidylcholine, diacylphosphatidylethanolamine, ceramide, sphingomyelin, cephalin, cardiolipin, and cerebrosides. In preferred embodiments, the non-cationic lipids are diacylphosphatidylcholine, diacylphosphatidylethanolamine, ceramide or sphingomyelin. The acyl groups in these lipids are preferably acyl groups derived from fatty acids having C_{10}-C_{24} carbon chains. More preferably the acyl groups are lauroyl, myristoyl, palmitoyl, stearoyl or oleoyl. In particularly preferred embodiments, the non-cationic lipid will be 1,2-sn-dioleoylphosphatidylethanolamine (DOPE), palmitoyl oleoyl phosphatidylcholine (POPC), egg phosphatidylcholine (EPC), distearoylphosphatidylcholine (DSPC), cholesterol, or a mixture thereof. In the most preferred embodiments, the nucleic acid-lipid particles will be fusogenic particles with enhanced properties in vivo and the non-cationic lipid will be DSPC or DOPE. In addition, the nucleic acid-lipid particles of the present invention may further comprise cholesterol. In other preferred embodiments, the non-cationic lipids will further comprise polyethylene glycol-based polymers such as PEG 2000, PEG

5000 and polyethylene glycol conjugated to a diacylglycerol, a ceramide or a phospholipid, as described in U.S. Pat. No. 5,820,873 and U.S. Patent Publication No. 20030077829. In further preferred embodiments, the non-cationic lipids will further comprise polyethylene glycol-based polymers such as PEG 2000, PEG 5000 and polyethylene glycol conjugated to a dialkyloxypropyl.

Following formation of the detergent solution of nucleic acid-lipid complexes and non-cationic lipids, the detergent is removed, preferably by dialysis. The removal of the detergent results in the formation of a lipid-bilayer which surrounds the nucleic acid providing serum-stable nucleic acid-lipid particles which have a size of from about 50 nm to about 150 nm, more typically about 60 nm to about 130 nm, more typically about 70 nm to about 110 nm, most typically about 70 to about 90 nm. The particles thus formed do not aggregate and are optionally sized to achieve a uniform particle size.

The serum-stable nucleic acid-lipid particles can be sized by any of the methods available for sizing liposomes. The sizing may be conducted in order to achieve a desired size range and relatively narrow distribution of particle sizes.

Several techniques are available for sizing the particles to a desired size. One sizing method, used for liposomes and equally applicable to the present particles is described in U.S. Pat. No. 4,737,323. Sonicating a particle suspension either by bath or probe sonication produces a progressive size reduction down to particles of less than about 50 nm in size. Homogenization is another method which relies on shearing energy to fragment larger particles into smaller ones. In a typical homogenization procedure, particles are recirculated through a standard emulsion homogenizer until selected particle sizes, typically between about 60 and 80 nm, are observed. In both methods, the particle size distribution can be monitored by conventional laser-beam particle size discrimination, or QELS.

Extrusion of the particles through a small-pore polycarbonate membrane or an asymmetric ceramic membrane is also an effective method for reducing particle sizes to a relatively well-defined size distribution. Typically, the suspension is cycled through the membrane one or more times until the desired particle size distribution is achieved. The particles may be extruded through successively smaller-pore membranes, to achieve a gradual reduction in size.

In another group of embodiments, the present invention provides a method for the preparation of serum-stable nucleic acid-lipid particles, comprising:

(a) preparing a mixture comprising cationic lipids and non-cationic lipids in an organic solvent;

(b) contacting an aqueous solution of nucleic acid with said mixture in step (a) to provide a clear single phase; and

(c) removing said organic solvent to provide a suspension of nucleic acid-lipid particles, wherein said nucleic acid is encapsulated in a lipid bilayer, and said particles are stable in serum and have a size of from about 50 to about 150 nm.

The nucleic acids (or plasmids), cationic lipids and non-cationic lipids which are useful in this group of embodiments are as described for the detergent dialysis methods above.

The selection of an organic solvent will typically involve consideration of solvent polarity and the ease with which the solvent can be removed at the later stages of particle formation. The organic solvent, which is also used as a solubilizing agent, is in an amount sufficient to provide a clear single phase mixture of nucleic acid and lipids. Suitable solvents include, but are not limited to, chloroform, dichloromethane, diethylether, cyclohexane, cyclopentane, benzene, toluene, methanol, or other aliphatic alcohols such as propanol, iso-propanol, butanol, tert-butanol, iso-butanol, pentanol and hexanol. Combinations of two or more solvents may also be used in the present invention.

Contacting the nucleic acid with the organic solution of cationic and non-cationic lipids is accomplished by mixing together a first solution of nucleic acid, which is typically an aqueous solution, and a second organic solution of the lipids. One of skill in the art will understand that this mixing can take place by any number of methods, for example by mechanical means such as by using vortex mixers.

After the nucleic acid has been contacted with the organic solution of lipids, the organic solvent is removed, thus forming an aqueous suspension of serum-stable nucleic acid-lipid particles. The methods used to remove the organic solvent will typically involve evaporation at reduced pressures or blowing a stream of inert gas (e.g., nitrogen or argon) across the mixture.

The serum-stable nucleic acid-lipid particles thus formed will typically be sized from about 50 nm to about 150 nm, more typically about 60 nm to about 130 nm, more typically about 70 nm to about 100 nm, most typically about 70 to about 90 nm. To achieve further size reduction or homogeneity of size in the particles, sizing can be conducted as described above.

In other embodiments, the methods will further comprise adding nonlipid polycations which are useful to effect the delivery to cells using the present compositions. Examples of suitable nonlipid polycations include, but are limited to, hexadimethrine bromide (sold under the brandname POLYBRENE®, from Aldrich Chemical Co., Milwaukee, Wis., USA) or other salts of heaxadimethrine. Other suitable polycations include, for example, salts of poly-L-ornithine, poly-L-arginine, poly-L-lysine, poly-D-lysine, polyallylamine and polyethyleneimine.

In certain embodiments, the formation of the nucleic acid-lipid particles can be carried out either in a mono-phase system (e.g., a Bligh and Dyer monophase or similar mixture of aqueous and organic solvents) or in a two-phase system with suitable mixing.

When formation of the complexes is carried out in a mono-phase system, the cationic lipids and nucleic acids are each dissolved in a volume of the mono-phase mixture. Combination of the two solutions provides a single mixture in which the complexes form. Alternatively, the complexes can form in two-phase mixtures in which the cationic lipids bind to the nucleic acid (which is present in the aqueous phase), and "pull" it into the organic phase.

In another embodiment, the present invention provides a method for the preparation of nucleic acid-lipid particles, comprising:

(a) contacting nucleic acids with a solution comprising non-cationic lipids and a detergent to form a nucleic acid-lipid mixture;

(b) contacting cationic lipids with the nucleic acid-lipid mixture to neutralize a portion of the negative charge of the nucleic acids and form a charge-neutralized mixture of nucleic acids and lipids; and

(c) removing the detergent from the charge-neutralized mixture to provide the nucleic acid-lipid particles in which the nucleic acids are protected from degradation.

In one group of embodiments, the solution of non-cationic lipids and detergent is an aqueous solution. Contacting the nucleic acids with the solution of non-cationic lipids and detergent is typically accomplished by mixing together a first solution of nucleic acids and a second solution of the lipids and detergent. One of skill in the art will understand that this mixing can take place by any number of methods, for

example, by mechanical means such as by using vortex mixers. Preferably, the nucleic acid solution is also a detergent solution. The amount of non-cationic lipid which is used in the present method is typically determined based on the amount of cationic lipid used, and is typically of from about 0.2 to 5 times the amount of cationic lipid, preferably from about 0.5 to about 2 times the amount of cationic lipid used.

In some embodiments, the nucleic acids are precondensed as described in, e.g., U.S. patent application Ser. No. 09/744,103.

The nucleic acid-lipid mixture thus formed is contacted with cationic lipids to neutralize a portion of the negative charge which is associated with the nucleic acids (or other polyanionic materials) present. The amount of cationic lipids used will typically be sufficient to neutralize at least 50% of the negative charge of the nucleic acid. Preferably, the negative charge will be at least 70% neutralized, more preferably at least 90% neutralized. Cationic lipids which are useful in the present invention, include, for example, DLinDMA and, DLenDMA. These lipids and related analogs have been described in U.S. patent application Ser. No. 11/148,430, filed Jun. 7, 2005.

Contacting the cationic lipids with the nucleic acid-lipid mixture can be accomplished by any of a number of techniques, preferably by mixing together a solution of the cationic lipid and a solution containing the nucleic acid-lipid mixture. Upon mixing the two solutions (or contacting in any other manner), a portion of the negative charge associated with the nucleic acid is neutralized. Nevertheless, the nucleic acid remains in an uncondensed state and acquires hydrophilic characteristics.

After the cationic lipids have been contacted with the nucleic acid-lipid mixture, the detergent (or combination of detergent and organic solvent) is removed, thus forming the nucleic acid-lipid particles. The methods used to remove the detergent will typically involve dialysis. When organic solvents are present, removal is typically accomplished by evaporation at reduced pressures or by blowing a stream of inert gas (e.g., nitrogen or argon) across the mixture.

The particles thus formed will typically be sized from about 50 nm to several microns, more typically about 50 nm to about 150 nm, more typically about 60 nm to about 130 nm, more typically about 70 nm to about 110 nm, most typically about 70 to about 90 nm. To achieve further size reduction or homogeneity of size in the particles, the nucleic acid-lipid particles can be sonicated, filtered or subjected to other sizing techniques which are used in liposomal formulations and are known to those of skill in the art.

In other embodiments, the methods will further comprise adding nonlipid polycations which are useful to effect the lipofection of cells using the present compositions. Examples of suitable nonlipid polycations include, hexadimethrine bromide (sold under the brandname POLYBRENE®, from Aldrich Chemical Co., Milwaukee, Wis., USA) or other salts of hexadimethrine. Other suitable polycations include, for example, salts of poly-L-ornithine, poly-L-arginine, poly-L-lysine, poly-D-lysine, polyallylamine and polyethyleneimine. Addition of these salts is preferably after the particles have been formed.

In another aspect, the present invention provides methods for the preparation of nucleic acid-lipid particles, comprising:

(a) contacting an amount of cationic lipids with nucleic acids in a solution; the solution comprising from about 15-35% water and about 65-85% organic solvent and the amount of cationic lipids being sufficient to produce a +/−charge ratio of from about 0.85 to about 2.0, to provide a hydrophobic nucleic acid-lipid complex;

(b) contacting the hydrophobic, nucleic acid-lipid complex in solution with non-cationic lipids, to provide a nucleic acid-lipid mixture; and

(c) removing the organic solvents from the nucleic acid-lipid mixture to provide nucleic acid-lipid particles in which the nucleic acids are protected from degradation.

The nucleic acids, non-cationic lipids, cationic lipids and organic solvents which are useful in this aspect of the invention are the same as those described for the methods above which used detergents. In one group of embodiments, the solution of step (a) is a mono-phase. In another group of embodiments, the solution of step (a) is two-phase.

In preferred embodiments, the non-cationic lipids are ESM, DOPE, DOPC, polyethylene glycol-based polymers (e.g., PEG 2000, PEG 5000, PEG-modified diacylglycerols, or PEG-modified dialkyloxypropyls), distearoylphosphatidylcholine (DSPC), DPPE, DMPE, 16:0 Monomethyl Phosphatidylethanolamine, 16:0 Dimethyl Phosphatidylethanolamine, 18:1 Trans Phosphatidylethanolamine, 18:0 18:1 Phosphatidylethanolamine (SOPE), 1,2-dielaidoyl-sn-glycero-3-phophoethanolamine (transDOPE), 16:0 18:1 Phosphatidylethanolamine, DSPE, cholesterol, or combinations thereof. In still other preferred embodiments, the organic solvents are methanol, chloroform, methylene chloride, ethanol, diethyl ether or combinations thereof.

In one embodiment, the nucleic acid is a plasmid from which an interfering RNA is transcribed; the cationic lipid is DLinDMA, DLenDMA, DODAC, DDAB, DOTMA, DOSPA, DMRIE, DOGS or combinations thereof; the non-cationic lipid is ESM, DOPE, DAG-PEGs, distearoylphosphatidylcholine (DSPC), DPPE, DMPE, 16:0 Monomethyl Phosphatidylethanolamine, 16:0 Dimethyl Phosphatidylethanolamine, 18:1 Trans Phosphatidylethanolamine, 18:0 18:1 Phosphatidylethanolamine (SOPE), 1,2-dielaidoyl-sn-glycero-3-phophoethanolamine (transDOPE), 16:0 18:1 Phosphatidylethanolamine DSPE, cholesterol, or combinations thereof (e.g. DSPC and PEG-DAA); and the organic solvent is methanol, chloroform, methylene chloride, ethanol, diethyl ether or combinations thereof.

As above, contacting the nucleic acids with the cationic lipids is typically accomplished by mixing together a first solution of nucleic acids and a second solution of the lipids, preferably by mechanical means such as by using vortex mixers. The resulting mixture contains complexes as described above. These complexes are then converted to particles by the addition of non-cationic lipids and the removal of the organic solvent. The addition of the non-cationic lipids is typically accomplished by simply adding a solution of the non-cationic lipids to the mixture containing the complexes. A reverse addition can also be used. Subsequent removal of organic solvents can be accomplished by methods known to those of skill in the art and also described above.

The amount of non-cationic lipids which is used in this aspect of the invention is typically an amount of from about 0.2 to about 15 times the amount (on a mole basis) of cationic lipids which was used to provide the charge-neutralized nucleic acid-lipid complex. Preferably, the amount is from about 0.5 to about 9 times the amount of cationic lipids used.

In yet another aspect, the present invention provides nucleic acid-lipid particles which are prepared by the methods described above. In these embodiments, the nucleic acid-lipid particles are either net charge neutral or carry an overall charge which provides the particles with greater gene lipofection activity. Preferably, the nucleic acid component of the particles is a nucleic acid which interferes with the production of an undesired protein. In some embodiments, the nucleic acid comprises an interfering RNA, the non-cationic lipid is

egg sphingomyelin and the cationic lipid is DLinDMA or DLenDMA. In some embodiments, the nucleic acid comprises an interfering RNA, the non-cationic lipid is a mixture of DSPC and cholesterol, and the cationic lipid is DLinDMA or DLenDMA. In other preferred embodiments, the non-cationic lipid may further comprise cholesterol.

A variety of general methods for making SNALP-CPLs (CPL-containing SNALPs) are discussed herein. Two general techniques include "post-insertion" technique, that is, insertion of a CPL into for example, a pre-formed SNALP, and the "standard" technique, wherein the CPL is included in the lipid mixture during for example, the SNALP formation steps. The post-insertion technique results in SNALPs having CPLs mainly in the external face of the SNALP bilayer membrane, whereas standard techniques provide SNALPs having CPLs on both internal and external faces. The method is especially useful for vesicles made from phospholipids (which can contain cholesterol) and also for vesicles containing PEG-lipids (such as PEG-DAAs and PEG-DAGs). Methods of making SNALP-CPL, are taught, for example, in U.S. Pat. Nos. 5,705,385, 6,586,410, 5,981,501 6,534,484; 6,852,334; U.S. Patent Publication No. 20020072121; and WO 00/62813.

VII. Kits

The present invention also provides nucleic acid-lipid particles in kit form. The kit will typically be comprised of a container which is compartmentalized for holding the various elements of the nucleic acid-lipid particles. The kit will contain the compositions of the present inventions, preferably in dehydrated form, with instructions for their rehydration and administration. In still other embodiments, the particles and/or compositions comprising the particles will have a targeting moiety attached to the surface of the particle. Methods of attaching targeting moieties (e.g., antibodies, proteins) to lipids (such as those used in the present particles) are known to those of skill in the art.

VIII. Administration of Nucleic Acid-Lipid Particles

Once formed, the serum-stable nucleic acid-lipid particles of the present invention are useful for the introduction of nucleic acids (i.e., siRNA that silences expression of gene expressed in cancer such as an Eg5, EGFR and/or XIAP gene) into cells. Accordingly, the present invention also provides methods for introducing a nucleic acids (e.g., a plasmid or and siRNA) into a cell. The methods are carried out in vitro or in vivo by first forming the particles as described above and then contacting the particles with the cells for a period of time sufficient for delivery of the nucleic acid to the cell to occur.

The nucleic acid-lipid particles of the present invention can be adsorbed to almost any cell type with which they are mixed or contacted. Once adsorbed, the particles can either be endocytosed by a portion of the cells, exchange lipids with cell membranes, or fuse with the cells. Transfer or incorporation of the nucleic acid portion of the particle can take place via any one of these pathways. In particular, when fusion takes place, the particle membrane is integrated into the cell membrane and the contents of the particle combine with the intracellular fluid.

The nucleic acid-lipid particles of the present invention can be administered either alone or in mixture with a physiologically-acceptable carrier (such as physiological saline or phosphate buffer) selected in accordance with the route of administration and standard pharmaceutical practice. Generally, normal saline will be employed as the pharmaceutically acceptable carrier. Other suitable carriers include, e.g., water, buffered water, 0.4% saline, 0.3% glycine, and the like, including glycoproteins for enhanced stability, such as albumin, lipoprotein, globulin, etc.

The pharmaceutical carrier is generally added following particle formation. Thus, after the particle is formed, the particle can be diluted into pharmaceutically acceptable carriers such as normal saline.

The concentration of particles in the pharmaceutical formulations can vary widely, i.e., from less than about 0.05%, usually at or at least about 2-5% to as much as 10 to 30% by weight and will be selected primarily by fluid volumes, viscosities, etc., in accordance with the particular mode of administration selected. For example, the concentration may be increased to lower the fluid load associated with treatment. This may be particularly desirable in patients having atherosclerosis-associated congestive heart failure or severe hypertension. Alternatively, particles composed of irritating lipids may be diluted to low concentrations to lessen inflammation at the site of administration.

The pharmaceutical compositions of the present invention may be sterilized by conventional, well known sterilization techniques. Aqueous solutions can be packaged for use or filtered under aseptic conditions and lyophilized, the lyophilized preparation being combined with a sterile aqueous solution prior to administration. The compositions can contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions, such as pH adjusting and buffering agents, tonicity adjusting agents and the like, for example, sodium acetate, sodium lactate, sodium chloride, potassium chloride, and calcium chloride. Additionally, the particle suspension may include lipid-protective agents which protect lipids against free-radical and lipid-peroxidative damages on storage. Lipophilic free-radical quenchers, such as alphatocopherol and water-soluble iron-specific chelators, such as ferrioxamine, are suitable.

The nucleic acid-lipid particles can be incorporated into a broad range of topical dosage forms including, but not limited to, gels, oils, emulsions, topical creams, pastes, ointments, lotions and the like.

A. In Vivo Administration

Systemic delivery for in vivo therapy, i.e., delivery of a therapeutic nucleic acid to a distal target cell via body systems such as the circulation, has been achieved using nucleic acid-lipid particles such as those disclosed in WO 96/40964 and U.S. Pat. Nos. 5,705,385, 5,976,567, 5,981,501 and 6,410,328. This latter format provides a fully encapsulated nucleic acid-lipid particle that protects the nucleic acid from nuclease degradation in serum, is nonimmunogenic, is small in size and is suitable for repeat dosing.

For in vivo administration, administration can be in any manner known in the art, e.g., by injection, oral administration, inhalation (e.g., intransal or intratracheal), transdermal application, or rectal administration. Administration can be accomplished via single or divided doses. The pharmaceutical compositions can be administered parenterally, i.e., intraarticularly, intravenously, intraperitoneally, subcutaneously, intramuscularly, or intratumorally. In some embodiments, the pharmaceutical compositions are administered intravenously or intraperitoneally by a bolus injection (see, e.g., Stadler, et al., U.S. Pat. No. 5,286,634) or by pump infusion. Intracellular nucleic acid delivery has also been discussed in Straubringer, et al., *Methods Enzymol*, Academic Press, New York. 101:512 (1983); Mannino, et al., *Biotechniques* 6:682 (1988); Nicolau, et al., *Crit. Rev. Ther. Drug Carrier Syst.* 6:239 (1989), and Behr, *Acc. Chem. Res.* 26:274 (1993). Still other methods of administering lipid based therapeutics are described in, for example, Rahman et al., U.S. Pat.

No. 3,993,754; Sears, U.S. Pat. No. 4,145,410; Papahadjopoulos et al., U.S. Pat. No. 4,235,871; Schneider, U.S. Pat. No. 4,224,179; Lenk et al., U.S. Pat. No. 4,522,803; and Fountain et al., U.S. Pat. No. 4,588,578. The lipid nucleic acid particles can be administered by direct injection at the site of disease or by injection at a site distal from the site of disease (see, e.g., Culver, HUMAN GENE THERAPY, MaryAnn Liebert, Inc., Publishers, New York. pp. 70-71 (1994)).

The compositions of the present invention, either alone or in combination with other suitable components, can be made into aerosol formulations (i.e., they can be "nebulized") to be administered via inhalation (e.g., intranasally or intratracheally) (see, Brigham, et al., *Am. J. Sci.* 298(4):278 (1989)). Aerosol formulations can be placed into pressurized acceptable propellants, such as dichlorodifluoromethane, propane, nitrogen, and the like.

Formulations suitable for parenteral administration, such as, for example, by intraarticular (in the joints), intravenous, intramuscular, intradermal, intraperitoneal, and subcutaneous routes, include aqueous and non-aqueous, isotonic sterile injection solutions, which can contain antioxidants, buffers, bacteriostats, and solutes that render the formulation isotonic with the blood of the intended recipient, and aqueous and non-aqueous sterile suspensions that can include suspending agents, solubilizers, thickening agents, stabilizers, and preservatives. In the practice of this invention, compositions can be administered, for example, by intravenous infusion, orally, topically, intraperitoneally, intravesically or intrathecally.

Formulations suitable for oral administration can consist of (a) liquid solutions, such as an effective amount of the packaged nucleic acid suspended in diluents, such as water, saline or PEG 400; (b) capsules, sachets or tablets, each containing a predetermined amount of the active ingredient, as liquids, solids, granules or gelatin; (c) suspensions in an appropriate liquid; and (d) suitable emulsions. Tablet forms can include one or more of lactose, sucrose, mannitol, sorbitol, calcium phosphates, corn starch, potato starch, microcrystalline cellulose, gelatin, colloidal silicon dioxide, talc, magnesium stearate, stearic acid, and other excipients, colorants, fillers, binders, diluents, buffering agents, moistening agents, preservatives, flavoring agents, dyes, disintegrating agents, and pharmaceutically compatible carriers. Lozenge forms can comprise the active ingredient in a flavor, e.g., sucrose, as well as pastilles comprising the active ingredient in an inert base, such as gelatin and glycerin or sucrose and acacia emulsions, gels, and the like containing, in addition to the active ingredient, carriers known in the art.

Generally, when administered intravenously, the nucleic acid-lipid formulations are formulated with a suitable pharmaceutical carrier. Many pharmaceutically acceptable carriers may be employed in the compositions and methods of the present invention. Suitable formulations for use in the present invention are found, for example, in REMINGTON'S PHARMACEUTICAL SCIENCES, Mack Publishing Company, Philadelphia, Pa., 17th ed. (1985). A variety of aqueous carriers may be used, for example, water, buffered water, 0.4% saline, 0.3% glycine, and the like, and may include glycoproteins for enhanced stability, such as albumin, lipoprotein, globulin, etc. Generally, normal buffered saline (135-150 mM NaCl) will be employed as the pharmaceutically acceptable carrier, but other suitable carriers will suffice. These compositions can be sterilized by conventional liposomal sterilization techniques, such as filtration. The compositions may contain pharmaceutically acceptable auxiliary substances as required to approximate physiological conditions, such as pH adjusting and buffering agents, tonicity adjusting agents, wetting agents and the like, for example, sodium acetate, sodium lactate, sodium chloride, potassium chloride, calcium chloride, sorbitan monolaurate, triethanolamine oleate, etc. These compositions can be sterilized using the techniques referred to above or, alternatively, they can be produced under sterile conditions. The resulting aqueous solutions may be packaged for use or filtered under aseptic conditions and lyophilized, the lyophilized preparation being combined with a sterile aqueous solution prior to administration.

The methods of the present invention may be practiced in a variety of hosts. Preferred hosts include mammalian species, such as primates (e.g., humans and chimpanzees as well as other nonhuman primates), canines, felines, equines, bovines, ovines, caprines, rodents (e.g., rats and mice), lagomorphs, and swine.

The amount of particles administered will depend upon the ratio of nucleic acid to lipid; the particular nucleic acid used, the disease state being diagnosed; the age, weight, and condition of the patient and the judgment of the clinician; but will generally be between about 0.01 and about 50 mg per kilogram of body weight; preferably between about 0.1 and about 5 mg/kg of body weight or about 10^8-10^{10} particles per injection.

B. Combination Therapy

In some embodiments, the nucleic acid-lipid particles described herein are administered in combination with a second therapeutic agent for treating or preventing cancer. For example, the nucleic acid-lipid particles may be administered in conjunction with any of the standard treatments for cancer including, but not limited to, chemotherapeutic agents including, e.g., alitretinoin, altretamine, anastrozole, azathioprine, bicalutamide, busulfan, capecitabine, carboplatin, cisplatin, cyclophosphamide, cytarabine, doxorubicin, epirubicin, etoposide, exemestane, finasteride, fluorouracil, fulvestrant, gemtuzumab, ozogamicin, hydroxyurea, ibritumomab, idarubicin, ifosfamide, imatinib, letrozole, megestrol acetate, methotrexate, mifepristone, paclitaxel, rituximab, tamoxifen, temozolomide, tretinoin, triptorelin, vincristine, or vinorelbine, and radiation treatment.

The nucleic acid-lipid particles and the second therapeutic agent may be administered simultaneously or sequentially. For example, the nucleic acid-lipid particles may be administered first, followed by the second therapeutic agent. Alternatively, the second therapeutic agent may be administered first, followed by the nucleic acid-lipid particles. In some cases, the nucleic acid-lipid particles and the second therapeutic agent are administered in the same formulation. In other cases the nucleic acid-lipid particles and nucleic acids and the second therapeutic agent are administered in different formulations.

C. Cells for Delivery of Interfering RNA

The compositions and methods of the present invention are used to treat a wide variety of cell types, in vivo and in vitro. Suitable cells include, e.g., hematopoietic precursor (stem) cells, fibroblasts, keratinocytes, hepatocytes, endothelial cells, skeletal and smooth muscle cells, osteoblasts, neurons, quiescent lymphocytes, terminally differentiated cells, slow or noncycling primary cells, parenchymal cells, lymphoid cells, epithelial cells, bone cells, and the like.

In vivo delivery of nucleic acid-lipid particles encapsulating an interfering RNA is particularly suited for targeting tumor cells of any cell type. In vivo studies show that SNALP's accumulate at tumor sites and predominantly transfect tumor cells. See, Fenske, et al., *Methods Enzymol*, Academic Press, New York 346:36 (2002). The methods and compositions can be employed with cells of a wide variety of vertebrates, including mammals, and especially those of vet-

erinary importance, e.g, canine, feline, equine, bovine, ovine, caprine, rodent, lagomorph, swine, etc., in addition to human cell populations.

To the extent that tissue culture of cells may be required, it is well known in the art. Freshney (1994) (Culture of Animal Cells, a Manual of Basic Technique, third edition Wiley-Liss, New York), Kuchler et al. (1977) Biochemical Methods in Cell Culture and Virology, Kuchler, R. J., Dowden, Hutchinson and Ross, Inc., and the references cited therein provides a general guide to the culture of cells. Cultured cell systems often will be in the form of monolayers of cells, although cell suspensions are also used.

D. Detection of SNALPs

In some embodiments, the nucleic acid-lipid particles are detectable in the subject 8, 12, 24, 48, 60, 72, or 96 hours, 6, 8, 10, 12, 14, 16, 18, 19, 22, 24, 25, or 28 days after administration of the particles. The presence of the particles can be detected in the cells, tissues, or other biological samples from the subject. The particles may be detected, e.g., by direct detection of the particles, detection of the interfering RNA sequence, detection of the target sequence of interest (i.e., by detecting expression or reduced expression of the Eg5, EGFR and/or XIAP sequence of interest), detection of a target protein of interest (e.g., by detecting expression or reduced expression of Eg5, EGFR and/or XIAP protein), detection of a compound modulated directly or indirectly by the Eg5, EGFR and/or XIAP (e.g., tubulin, phosphor-histones, P13 kinase-AKT, STATS, caspases) or by detection of apoptosis and cell viability in the subject or a combination thereof.

1. Detection of Particles

Nucleic acid-lipid particles can be detected using any methods known in the art. For example, a label can be coupled directly or indirectly to a component of the SNALP or other lipid-based carrier system using methods well known in the art. A wide variety of labels can be used, with the choice of label depending on sensitivity required, ease of conjugation with the SNALP component, stability requirements, and available instrumentation and disposal provisions. Suitable labels include, but are not limited to, spectral labels, such as fluorescent dyes (e.g., fluorescein and derivatives, such as fluorescein isothiocyanate (FITC) and Oregon Green™; rhodamine and derivatives, such Texas red, tetrarhodimine isothiocynate (TRITC), etc., digoxigenin, biotin, phycoerythrin, AMCA, CyDyes™, and the like; radiolabels, such as ^{3}H, ^{125}I, ^{35}S, ^{14}C, ^{32}P, ^{33}P, etc.; enzymes, such as horse radish peroxidase, alkaline phosphatase, etc.; spectral colorimetric labels, such as colloidal gold or colored glass or plastic beads, such as polystyrene, polypropylene, latex, etc. The label can be detected using any means known in the art.

2. Detection of Nucleic Acids

Nucleic acids (i.e., siRNA that silence expression of an Eg5, EGFR and/or XIAP gene) are detected and quantified herein by any of a number of means well known to those of skill in the art. The detection of nucleic acids proceeds by well known methods such as Southern analysis, northern analysis, gel electrophoresis, PCR, radiolabeling, scintillation counting, and affinity chromatography. Additional analytic biochemical methods such as spectrophotometry, radiography, electrophoresis, capillary electrophoresis, high performance liquid chromatography (HPLC), thin layer chromatography (TLC), hyperdiffusion chromatography, may also be employed

The selection of a nucleic acid hybridization format is not critical. A variety of nucleic acid hybridization formats are known to those skilled in the art. For example, common formats include sandwich assays and competition or displacement assays. Hybridization techniques are generally described in "Nucleic Acid Hybridization, A Practical Approach," Ed. Hames, B. D. and Higgins, S. J., IRL Press, 1985.

The sensitivity of the hybridization assays may be enhanced through use of a nucleic acid amplification system which multiplies the target nucleic acid being detected. In vitro amplification techniques suitable for amplifying sequences for use as molecular probes or for generating nucleic acid fragments for subsequent subcloning are known. Examples of techniques sufficient to direct persons of skill through such in vitro amplification methods, including the polymerase chain reaction (PCR) the ligase chain reaction (LCR), Qβ-replicase amplification and other RNA polymerase mediated techniques (e.g., NASBA™) are found in Sambrook, et al., In *Molecular Cloning. A Laboratory Manual*, Cold Spring Harbor Laboratory Press, 2000, and Ausubel et al., Short Protocols in Molecular Biology, eds., Current Protocols, a joint venture between Greene Publishing Associates, Inc. and John Wiley & Sons, Inc., (2002), as well as Mullis et al. (1987), U.S. Pat. No. 4,683,202; PCR Protocols A Guide to Methods and Applications (Innis et al. eds) Academic Press Inc. San Diego, Calif. (1990) (Innis); Arnheim & Levinson (Oct. 1, 1990), *C&EN* 36; The *Journal Of NIH Research,* 3:81 (1991); (Kwoh et al., *Proc. Natl. Acad. Sci. USA,* 86:1173 (1989); Guatelli et al., *Proc. Natl. Acad. Sci. USA,* 87:1874 (1990); Lomell et al., *J. Clin. Chem.,* 35:1826 (1989); Landegren et al., *Science,* 241:1077 (1988); Van Brunt, *Biotechnology,* 8:291 (1990); Wu and Wallace, *Gene,* 4:560 (1989); Barringer et al., *Gene,* 89:117 (1990), and Sooknanan and Malek, *Biotechnology,* 13:563 (1995). Improved methods of cloning in vitro amplified nucleic acids are described in Wallace et al., U.S. Pat. No. 5,426,039. Other methods described in the art are the nucleic acid sequence based amplification (NASBA™, Cangene, Mississauga, Ontario) and Q Beta Replicase systems. These systems can be used to directly identify mutants where the PCR or LCR primers are designed to be extended or ligated only when a select sequence is present. Alternatively, the select sequences can be generally amplified using, for example, nonspecific PCR primers and the amplified target region later probed for a specific sequence indicative of a mutation.

Oligonucleotides for use as probes, e.g., in in vitro amplification methods, for use as gene probes, or as inhibitor components are typically synthesized chemically according to the solid phase phosphoramidite triester method described by Beaucage and Caruthers, *Tetrahedron Letts.,* 22(20):1859 1862 (1981), e.g., using an automated synthesizer, as described in Needham VanDevanter et al., *Nucleic Acids Res.,* 12:6159 (1984). Purification of oligonucleotides, where necessary, is typically performed by either native acrylamide gel electrophoresis or by anion exchange HPLC as described in Pearson and Regnier, *J. Chrom.,* 255:137 149 (1983). The sequence of the synthetic oligonucleotides can be verified using the chemical degradation method of Maxam and Gilbert (1980) in Grossman and Moldave (eds.) Academic Press, New York, *Methods in Enzymology,* 65:499.

An alternative means for determining the level of transcription is in situ hybridization. In situ hybridization assays are well known and are generally described in Angerer et al., *Methods Enzymol.,* 152:649 (1987). In an in situ hybridization assay cells are fixed to a solid support, typically a glass slide. If DNA is to be probed, the cells are denatured with heat or alkali. The cells are then contacted with a hybridization solution at a moderate temperature to permit annealing of specific probes that are labeled. The probes are preferably labeled with radioisotopes or fluorescent reporters.

E. Detection of an Immune Response

An immune response to induced by the siRNA (i.e., siRNA that silence expression of an Eg5, EGFR and/or XIAP gene) described herein can be long-lived and can be detected long after administration of the siRNA or nucleic acid-lipid particles containing the siRNA. An immune response to the siRNA can be detected by using immunoassays that detect the presence or absence of cytokines and growth factors e.g., produced by responder cells.

Suitable immunoassays include the double monoclonal antibody sandwich immunoassay technique of David et al. (U.S. Pat. No. 4,376,110); monoclonal-polyclonal antibody sandwich assays (Wide et al., in Kirkham and Hunter, eds., *Radioimmunoassay Methods*, E. and S. Livingstone, Edinburgh (1970)); the "western blot" method of Gordon et al. (U.S. Pat. No. 4,452,901); immunoprecipitation of labeled ligand (Brown et al. (1980) *J. Biol. Chem.* 255:4980-4983); enzyme-linked immunosorbent assays (ELISA) as described, for example, by Raines et al. (1982) *J. Biol. Chem.* 257:5154-5160; immunocytochemical techniques, including the use of fluorochromes (Brooks et al. (1980) *Clin. Exp. Immunol.* 39:477); and neutralization of activity (Bowen-Pope et al. (1984) *Proc. Natl. Acad. Sci. USA* 81:2396-2400). In addition to the immunoassays described above, a number of other immunoassays are available, including those described in U.S. Pat. Nos. 3,817,827; 3,850,752; 3,901,654; 3,935,074; 3,984,533; 3,996,345; 4,034,074; and 4,098,876. Monoclonal antibodies that specifically bind cytokines and growth factors (e.g., II-6, IL-12, TNF-α, IFN-α, and IFN-γ can be generated using methods known in the art (see, e.g., Kohler and Milstein, *Nature* 256: 495-497 (1975) and Harlow and Lane, ANTIBODIES, A LABORATORY MANUAL, Cold Spring Harbor Publication, New York (1999)). Generation of monoclonal antibodies has been previously described and can be accomplished by any means known in the art. (Buhring et al. in Hybridoma 1991, Vol. 10, No. 1, pp. 77-78). For example, an animal such as a guinea pig or rat, preferably a mouse is immunized with an immunogenic polypeptide, the antibody-producing cells, preferably splenic lymphocytes, are collected and fused to a stable, immortalized cell line, preferably a myeloma cell line, to produce hybridoma cells which are then isolated and cloned. (U.S. Pat. No. 6,156,882). In some methods, the monoclonal antibody is labeled to facilitate detection.

The invention will be described in greater detail by way of specific examples. The following examples are offered for illustrative purposes, and are not intended to limit the invention in any manner. Those of skill in the art will readily recognize a variety of noncritical parameters which can be changed or modified to yield essentially the same results.

EXAMPLES

The following examples are provided to illustrate, but not to limit the claimed invention.

Example 1

Materials and Methods

siRNA:

All siRNA used in these studies were chemically synthesized by Protiva Biotherapeutics (Burnaby, BC), University of Calgary (Calgary, AB) or Dharmacon Inc. (Lafayette, Colo.). siRNA were desalted and annealed using standard procedures.

Lipid Encapsulation of siRNA:

Unless otherwise indicated, siRNAs were encapsulated into liposomes composed of the following lipids; synthetic cholesterol (Sigma, St. Louis, Mo.), the phospholipid DSPC (1,2-distearoyl-sn-glycero-3-phosphocholine; Avanti Polar Lipids, Alabaster, Ala.), the PEG-lipid PEG-cDMA (3-N-[(-Methoxy poly(ethylene glycol)2000)carbamoyl]-1,2-dimyrestyloxy-propylamine), and the cationic lipid DLinDMA (1,2-Dilinoleyloxy-3-(N,N-dimethyl)aminopropane) in the molar ratios 48:10:2:40 respectively. In other words, unless otherwise indicated, siRNA's were encapsulated in to liposomes of the following SNALP formulation: 2% PEG-cDMA, 40% DLinDMA, 10% DSPC, 48% cholesterol. For vehicle controls, empty liposomes with identical lipid composition were formed in the absence of siRNA.

Serum Nuclease Protection Assay:

Unmodified naked or lipid encapsulated siRNA (0.25 mg/ml) were incubated in 50% mouse serum at 37° C. At the times indicated, aliquots were taken directly into gel loading buffer containing 0.1% SDS and frozen in liquid nitrogen. After the final timepoint, siRNA samples were run on a non-denaturing 20% polyacrylamide TBE gel and visualized by ethidium bromide staining. To confirm that nuclease protection of siRNA was conferred by lipid encapsulation, 0.1% Triton-X100 was added to disrupt lipid bilayer integrity immediately prior to incubation with serum.

RiboGreen™ Assay:

Equal volumes of diluted RiboGreen™ and SNALP are combined so that the final concentration of siRNA is ~167 ng/mL. 30 μl of a 10% Triton X-100 solution is added to the RiboGreen™/SNALP mixture and the resulting solution is incubated at room temperature for at least 2 minutes. Fluorescence measurements are taken at an appropriate wavelength before and after the addition of triton X-100 to determine the amount of encapsulated siRNA (see, e.g., Muriaux et al., *PNAS USA* 98(9): 5246-5251 (2001)).

In Vivo Cytokine Induction:

Animal studies were completed in accordance with the Canadian Council on Animal Care guidelines following approval by the local Animal Care and Use Committee at Protiva Biotherapeutics. 6-8 week old CD1 ICR mice (Harlan; Indianapolis, Ind.) were subjected to a three week quarantine and acclimation period prior to use. Encapsulated siRNA formulations were administered by standard intravenous injection in the lateral tail vein in 0.2 ml PBS. Blood was collected by cardiac puncture 6 h after administration and processed as plasma for cytokine analysis. In RNAi efficacy experiments, plasma was collected from 50 μl test bleeds 6 h after initial siRNA administration.

Cytokine ELISA:

All cytokines were quantified using sandwich ELISA kits according to manufacturers instructions. These were mouse and human IFN-α (PBL Biomedical; Piscataway, N.J.), human IL-6 and TNF-α (eBioscience; San Diego, Calif.), and mouse IL-6, TNF-α, and IFN-γ (BD Biosciences; San Diego, Calif.); and Mouse IFN-α and IFN-β (BD Biosciences, San Diego, Calif.).

Cell Viability Assay:

Cell viability of in vitro cell cultures was assessed using the commercial reagent CellTiter Blue (Promega Corp. Madison, Wis.), a resazurin dye that is reduced by metabolically active cells to the fluorogenic product resorufin. Various cancer cell lines were cultured in vitro using standard tissue culture techniques. 48-72 hours after treatment with siRNA formulations or small molecule drugs, CellTiter Blue reagent was added to the culture to quantify the metabolic activity of the cells—a measure of cell viability.

Target mRNA Quantitation:

The QuantiGene branched DNA assay (Genospectra) was used to quantify the reduction of target mRNA in cell cultures treated with SNALP. Cell lysates were prepared according to the manufacturer's instructions and used directly for Eg5 (kif11) and GAPDH mRNA quantification. The ratio of Eg5 to GAPDH mRNA was calculated for each cell culture and data expressed relative to the vehicle treated control cells. Specific probe sets used for detection of mRNA were designed by Genospectra to target the following regions: for the Eg5 mRNA, positions 4188-4882 of accession NM_004523; for GAPDH mRNA, positions 1-1303 of accession NM-002046.

Antibody Assay:

An ELISA was developed to detect IgM and IgG antibodies against the PEG-lipid and other lipid components of SNALP using a method described in Judge et al in Molecular Therapy (2006). 13(2) pp. 328-337.10 μg of PEG-cDSA was added in 20 μL 100% ethanol to 96 well plates containing PVDF membranes (Millipore Corp. Bedford, Mass.). PEG-cDSA coated membranes were allowed to completely air dry for 2 hours before blocking for 1 h with 10% FBS in PBS. 100 uL of serially diluted serum samples in blocking buffer were then applied in duplicate wells for 1 h and washed 4 times with 1% FBS in PBS. Plate bound antibodies were detected with HRP-conjugated goat anti-IgM Fcμ, or IgG Fcγ. Bound enzyme was developed with TMB substrate, stopped with 2N sulphuric acid, then read in a spectrophotometer at 450 nm (minus 570 nm).

Apoptosis/Caspase 3/7 Assay

The level of Caspase 3 and 7 enzyme activity in siRNA treated cells was assessed using the commercial reagent Apo-ONE (Promega Corp. Madison, Wis.). This assay is based on the specific enzymatic cleavage of the Caspase 3/7 substrate (Z-DEVD)2-Rhodamine 110 to a fluorogenic product and is used to quantify the level of apoptosis in cultured cells. The relative level of Caspase 3/7 activity was assessed in a number of cancer cell lines at 24-48 hours after treatment with siRNA formulations.

Example 2

Selection of Candidate Eg5, EGFR or XIAP siRNA with Specificity to Mouse and Human Targets

Candidate Eg5, EGFR or XIAP sequences were identified by scanning Eg5 (Genbank Accession Nos. NM_004523 and NM_010615), EGFR (Genbank Accession Nos. NM_005228 and NM_207655), and XIAP (Genbank Accession Nos. NM_001167 and NM_009688) sequences to identify AA dinucleotide motifs and the 19 nucleotides 3' of the motif. The following candidate sequences were eliminated: (1) sequences comprising a stretch of 4 or more of the same base in a row; (2) sequences comprising homopolymers of Gs; (3) sequences comprising triple base motifs (GGG, CCC, AAA, or TTT); and (4) sequences comprising stretches of 7 or more G/Cs in a row.

Reynold's Rational Design criteria was then applied to the remaining candidate sequences to identify sequences with 5 or more of the following criteria:

1. 30%-52% GC content;
2. At least 3 A/Us at positions 15-19 (sense);
3. Absence of internal repeats;
4. A at position 19 (sense);
5. A at position 3 (sense);
6. U at position 10 (sense);
7. No G/C at position 19 (sense); and
8. No G at position 13 (sense).

Only results with a score of 6 or more in the Stockholm rules (see, Chalk, Wahlestedt, and Sonnhammer method described in Chalk et al., *Biochem. Biophys. Res. Commun.*, 319:264-274 (2004)) were retained.

Next, sequences with a high score from, e.g., Classification tree method or Chalk, Wahlestedt, and Sonnhammer method, were retained.

Next, sequences with a score of 3 or more based on the rules of Amarzguioui and Prydz, *Biochem. Biophys. Res. Commun.*, 316:1050-1058 (2004), were retained.

Next, sequences with thermodynamics >0 were eliminated.

Finally, BLASTn was used to compare the sequences with the mouse and human databases and sequences with homology to 15-16 contiguous bp from the center of the target sequence (bp 3-18) against any relevant gene were eliminated. The candidate sequences are shown in Tables 1-9.

The candidate sequences are shown in Tables 1-9.

Example 3

siRNA Targeting the Kinesin Eg5 can Inhibit the Growth of Cancer Cells

A panel of siRNA sequences, including Eg5 2263, were evalulated for their antiproliferative effects against cancer cells. Eg5 2263 was previously described in the literature (see, Weil et al. 2002, *BioTechniques* 33:1244-1248) but the authors do not describe its use as a therapeutic or anti-cancer agent. The RNAi activity of the Eg5 siRNA panel were screened in vitro with HeLa cells (human; FIG. **1**) and Neuro2A cells (mouse; FIG. **2**) using a cell viability assay. The cells were treated with 1, 5, or 25 nM siRNA complexed with lipofectamine. Viability of the cell cultures were measured 48 h after treatment and expressed as mean fluorescence units as shown in FIGS. **1** and **2**.

Example 4

siRNA Formulated as SNALP are Potent Inhibitors of Cell Growth In Vitro

Various Eg5 siRNAs were formulated as SNALP (SNALP formulation: 2% PEG-cDMA, 40% DLinDMA, 10% DSPC, 48% cholesterol) and evaluated for their inhibitory effects on cell growth in vitro. The cells (i.e., Neuro2A cells) were treated with various SNALP formulated Eg5 siRNAs, at different concentrations i.e. 3.1 nM, 6.3 nM, 12.5 nM, 25 nM and 50 nM, and their effect on cell viability was evaluated (FIG. **3**). Viability of cell cultures is expressed as mean fluorescence units.

Example 5

Dose Dependent Silencing of Eg5 mRNA in Human HepG2 Cell by Eg5 SNALP

Human hepatocellular HepG2 cells were treated with either Eg5 2263 SNALP (SNALP formulation: 2% PEG-cDMA, 40% DLinDMA, 10% DSPC, 48% cholesterol) or control (i.e., a non-targeting siRNA) SNALP. Eg5 mRNA levels were measured after 48 h by a branched DNA assay. The results are shown in FIG. **4**: Top Panel—Eg5:GAPD mRNA ratios; Bottom panel—% knockdown of Eg5 mRNA versus non-treated cells. The results confirm that the potent effects of Eg5 SNALP on cell viability is due to the silencing of Eg5 RNA.

Example 6

Cell Phenotype Changes Following Treatment with Eg5 siRNA

Control siRNA treated HeLa cells and Eg5 siRNA treated HeLa cells were analyzed by immunohistological staining (DAPI (DNA), blue; tubulin, green). The staining results showed that the control cells demonstrated typical mitotic phenotypes, while the Eg5 siRNA treated HeLa cells induced aberrant cell mitosis characterized by monoastral spindle formation due to Eg5 inhibition (FIG. **5**).

Example 7

Anti-Proliferative Activity of Chemically Modified Eg5 2273 siRNA's

A panel (8 total) of 2'-OMe modified siRNAs of Eg5 2263 siRNA sequence was prepared and their RNAi activity was evaluated in HeLa human cells or Neuro2A mouse cells. The modifications involved introducing 2'-OMe guanosine or 2'-OMe uridine at selected positions in the sense or antisense strand the sequence modification are shown in (FIG. **6**). The modified Eg5 2263 siRNAs incorporated less than 20% of chemically modified nucleosides. Anti-proliferative activity was evaluated in a cell viability bioassay (FIGS. **7**, HeLa human cells; and FIG. **8** Neuro2A mouse cells). Cell viability of cell cultures was measured 48 hours after treatment and expressed as mean fluorescence units.

Example 8

In Vivo Cytokine Induction by Chemically Modified Eg5 2263 SNALP

Unmodified Eg5 2263 siRNA and certain 2'-OMe modified variants thereof (i.e., U/O, G/O, U/U and G/G) were formulated into SNALP (SNALP formulation: 2% PEG-cDMA, 40% DLinDMA, 10% DSPC, 48% cholesterol). These SNALP formulations were tested in vivo in to look for the induction of an immune response, e.g., cytokine induction. Balb/c mice (n=3/treatment group) were injected with 40 ug of the SNALP formulation and samples were collected 6 h post treatment with SNALP and tested for Interferon-alpha by ELISA assay. The results show that 2'-OMe modifications to Eg5 2263 siRNA abrogate Interferon induction associated with systemic administration of the native (unmodified) duplex (FIG. **9**).

Example 9

Antibody Response Against the Delivery Vehicle for siRNA with Selectively 2'-OMe Modified Eg5 2263

Unmodified Eg5 2263 siRNA and a 2'-OMe modified variant thereof (i.e., Eg5 2263 U/U siRNA) were formulated into SNALP (SNALP formulation: 2% PEG-cDMA, 40% DLinDMA, 10% DSPC, 48% cholesterol) and tested in vivo in mice (protocol: 3×2 mg/kg daily; serum assayed on day 10) to look for the induction of an immune response against the delivery vehicle (PEG). The results show that selective 2'-OMe modification to Eg5 2263 siRNA (e.g. U/U modified) abrogates the antibody response against the delivery vehicle that is associated with systemic administration of the native (unmodified) duplex. (FIG. **10**). In FIG. **10**, the top panel show PEG antibody levels in individual mice treated with unmodified Eg5 SNALP or with U/U modified Eg5 SNALP.

Example 10

The Anti-Cancer Activity of Eg5 U/U SNALP in a Range of Cancer Cell Lines

The anti-cancer activity of Eg5 U/U SNALP was demonstrated against a range of cancer cell lines. Activity against the cell lines was monitored by a cell viability assay, and by an apoptosis assay as measured by Caspase 3/7 activation. Eg5 U/U SNALP specificity is confirmed by comparison with control SNALP containing non-targeting siRNA. FIG. **11** illustrates a decrease in cell viability in all cell lines tested after treatment with Eg5 U/U SNALP as compared to control. Upper left panel: LS174T human colorectal adenocarcinoma; Upper right panel: HT29 human colorectal adenocarcinoma; lower left panel: HepG2 human hepatocellular carcinoma; Lower right panel; Neuro2A murine Neuroblastoma. The induction of apoptosis by Eg5 SNALP U/U modified siRNA, as measured by Caspase 3/7 activity, was measured in human hepatocellular carcinoma cells and human colorectal cancer cells after 24 hours and after 48 hours. The Caspase 3/7 activity is expressed as fold induction over media only treated cells. FIG. **12** illustrates that apoptosis induction in human hepatocarcinoma cells is increased in Eg5 2263 U/U SNALP as compared to control siRNA. FIG. **13** illustrates that apoptosis induction is increased in Eg5 2263 U/U SNALP in human colorectal cancer cells (HT-29 and LS 174T) as compared to control.

Example 11

Comparison Between Eg5 2263 U/U SNALP Vs. Small Molecule Eg5 Inhibitor Drug

There are currently several small molecule Eg5 inhibitors under clinical evaluation. Recent publications indicate that certain cancer cell lines (e.g., HT-29 colorectal adenocarcinoma cells) are resistant to apoptosis induction by small molecule Eg5 inhibitors. A comparison of apoptosis activity, via a comparison of Caspase 3/7 induction activity, in HT-29 colorectal adenocarcinoma cells (a small molecule Eg5 inhibitor resistant cell type) after treatment with a small molecule Eg5 inhibitor (i.e, Monastrol at 50 or 100 uM concentration), or with Eg5 2263 U/U SNALP (at 25 or 50 nM concentration) demonstrates that cells lines that are resistant to small molecule Eg5 inhibitors are highly sensitive to Eg5 SNALP (FIG. **14**). A comparison of Eg5 2263 U/U SNALP with the small molecule Eg5 inhibitor, monastrol, in the inhibition of various cancer cell lines, as measure by cell viability assays, demonstrates that Eg5 2263 U/U SNALP is superior at inhibiting cell growth in these cancer cell lines than monastrol (FIG. **15**). The results of these experiments shows that SNALP can confer advantages over conventional small molecule drugs as anti-cancer agents.

Example 12

Serum Nuclease Protection Assay

Naked Eg5 siRNA and SNALP encapsulated Eg5 siRNA were subjected to serum nuclease degredation. The result in the serum nuclease protection assay (presented in FIG. **16**)

shows that SNALP encapsulation provide the protection from serum nuclease required for in vivo use of siRNA.

Example 13

In Vivo Activity of Eg5 SNALP in Tumor Bearing Mice

Anti-tumor effects of Eg5 2263 U/U SNALP (2% PEG-cDSA, 40% DLinDMA, 10% DSPC, 48% cholesterol), as compared to SNALP containing control siRNA (Luc), was evalulated in a subcutaneous model in mice. A/J mice bearing s.c. Neuro2A tumors were treated with SNALP at 5×2 mg/kg daily (d6-10) by i.v. administration. Tumors were measured by calipers and recorded as tumor volume. The results of this study demonstrates that Eg5 2263 U/U SNALP exerts a specific anti-tumor effect in a s.c. tumor model (FIG. **17**). Additionally, therapeutic dosing is well tolerated in tumor-bearing mice (FIG. **18**).

Example 14

In Vivo Activity of Eg5 SNALP in Tumor Bearing Mice

Anti-tumor effects of Eg5 2263 U/U SNALP (2% PEG-cDMA, 40% DLinDMA, 10% DSPC, 48% cholesterol), as compared to SNALP containing control siRNA (Luc), was evalulated in an intrahepatic tumor model in mice. In this study, A/J mice were seeded with 100,000 Neuro2A cells by intrahepatic injection. On day 12, the mice were treated with Eg5 2263 U/U SNALP (n=6) or control siRNA (Luc SNALP; n=5). The mice were dosed at 3 mg/kg at t=0 h and at t=6 h, for a cumulative dosage of 6 mg/kg. The livers were collected 30 h after the first dose (d13), and formalin-fixed for conventional histology. The tissues were processed and stained with H&E. Tumor histology showed that Eg5 2263 U/U SNALP treated mice induced extensive phenotypic changes (e.g., aberrant mitosis and apoptosis) in the intrahepatic tumor cells, which is characteristic of Eg5 inhibition, as compared to control treated subjects. FIG. **19** shows the tumor histopathology of the intrahepatic Neuro2A tumor that was treated with Eg5 2263 U/U SNALP. Histology shows numerous tumor cells with atypical mitotic figures and apoptotic bodies characteristic of Eg5 inhibition. FIG. **20** shows the tumor histopathology of the intrahepatic Neuro2A tumor that was treated with control SNALP. Histology results shows numerous tumor cells with normal mitotic figures.

Example 15

In Vitro Activity of EGFr siRNA

A431 carcinoma cells were treated with increasing concentrations of lipofectamine complexed EGFr or non-targeting control siRNA. EGFr mRNA levels were quantitated by branched DNA assay after 48 h culture. EGFr mRNA values are expressed as % of media treated cells. As shown in FIG. **30**, EGFr sequences 817 and 1252 and 1986 displayed the greatest levels of mRNA silencing.

Cell viability was also quantitated by CellTiter Blue fluorescence assay after 48 h culture. inability scores are expressed as % of media treated cells. As shown in FIG. **31**, EGFr sequences 817 and 1252 and 1986 that displayed the greatest levels of mRNA silencing also show the most significant effects on cell viability.

Example 16

In Vitro Activity of EGFr siRNA

HT-29 tumor cells were treated with increasing concentrations of EGFr sequences 817 and 1252 and 1986 siRNA sequences or a non-targeting control siRNA formulated in SNALP. EGFr mRNA levels were measured 48 h after SNALP treatment by bDNA assay. As shown in FIG. **32**, EGFr sequences 817 and 1252 and 1986 siRNA formulated in SNALP silence EGFR siRNA.

Example 17

In Vitro Activity of XIAP SNALP

SNALP containing XIAP-113, XIAP-300 or non-targeting control siRNA were applied to HT-29 cells in vitro at various concentrations. 48 h later, XIAP mRNA levels were measured by bDNA assay and expressed as % of media treated cells. As shown in FIG. **33**, XIAP-113 SNALP causes significant, dose-dependent decreases in XIAP mRNA levels

Example 18

In Vitro Activity of XIAP SNALP

SNALP containing XIAP-113, XIAP-300 or non-targeting control siRNA were applied to LS174T colon adenocarcinoma cells in vitro at 35 nM siRNA. Cells were then treated with monastrol, a small molecule inhibitor of Eg5. Viability of cell cultures was assessed after 48 h. As shown in FIG. **34**, XIAP-113 and -300 SNALP sensitize human colon cancer cells to the cytotoxic effects of the Eg5 inhibitor. Degree of sensitization correlates with the relative potency of mRNA silencing by these SNALP

Example 19

In Vitro Activity of Eg5 SNALP in in Combination with XIAP SNALP

HT29 colon cancer cells were co-cultured with 10 nM or 30 nM XIAP-113 SNALP plus increasing concentrations of Eg5 2263 SNALP. Cell viability and caspase 3/7 activity were assayed after 48 h culture. As shown in FIG. **35**, co-administration of XIAP SNALP sensitizes HT29 cells to killing by Eg5 SNALP, as demonstrated by significant increases in the level of apoptosis and corresponding decrease in cell viability in the cultures.

It is to be understood that the above description is intended to be illustrative and not restrictive. Many embodiments will be apparent to those of skill in the art upon reading the above description. The scope of the invention should, therefore, be determined not with reference to the above description, but should instead be determined with reference to the appended claims, along with the full scope of equivalents to which such claims are entitled. The disclosures of all articles and references, including patent applications, patents, PCT publications, and Accession Nos. are incorporated herein by reference for all purposes.

SEQUENCE LISTING

The patent contains a lengthy "Sequence Listing" section. A copy of the "Sequence Listing" is available in electronic form from the USPTO web site (http://seqdata.uspto.gov/?pageRequest=docDetail&DocID=US08598333B2). An electronic copy of the "Sequence Listing" will also be available from the USPTO upon request and payment of the fee set forth in 37 CFR 1.19(b)(3).

What is claimed is:

1. An siRNA molecule that silences Eg5 expression comprising a sense strand and a complementary antisense strand, wherein the antisense strand consists of the nucleic acid sequence of SEQ ID NO:44.

2. The siRNA molecule of claim **1**, wherein the siRNA molecule is chemically synthesized.

3. The siRNA molecule of claim **1**, wherein the sense strand comprises the nucleic acid sequence of SEQ ID NO:20.

4. The siRNA molecule of claim **1**, wherein the sense strand consists of the nucleic acid sequence of SEQ ID NO:43.

5. The siRNA molecule of claim **1**, wherein the siRNA molecule comprises at least one modified nucleotide.

6. The siRNA molecule of claim **5**, wherein the modified nucleotide is a 2'-O-methyl (2'OMe) nucleotide.

7. A composition comprising the siRNA molecule of claim **1** and a pharmaceutically acceptable carrier.

8. A nucleic acid-lipid particle comprising:

(a) the siRNA molecule of claim **1**;

(b) a cationic lipid; and

(c) a non-cationic lipid.

* * * * *

UNITED STATES PATENT AND TRADEMARK OFFICE

CERTIFICATE OF CORRECTION

PATENT NO.	: 8,598,333 B2
APPLICATION NO.	: 11/807872
DATED	: December 3, 2013
INVENTOR(S)	: MacLachlan et al.

It is certified that error appears in the above-identified patent and that said Letters Patent is hereby corrected as shown below:

On the Title Page:

The first or sole Notice should read --

Subject to any disclaimer, the term of this patent is extended or adjusted under 35 U.S.C. 154(b) by 1404 days.

Signed and Sealed this
Seventh Day of July, 2015

Michelle K. Lee

Michelle K. Lee
Director of the United States Patent and Trademark Office